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OM protein - protein search, using sw model

Run on: July 15, 2006, 00:24:42 ; Search time 50 Seconds
(without alignments)
29.760 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58

Perfect score: 96
Sequence: 1 FEHCNFDVTRLRENE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 362972

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	33	34.4	35	2	US-09-270-767-60767
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405	27	28.1	30	2	US-09-671-773C-167	Sequence 167, App	478	27	28.1	31	2	US-09-671-773C-97	Sequence 97, Appl
406	27	28.1	30	2	US-09-671-773C-168	Sequence 168, App	479	27	28.1	31	2	US-09-671-773C-175	Sequence 175, App
407	27	28.1	30	2	US-09-671-773C-169	Sequence 169, App	480	27	28.1	31	2	US-10-131-546-9	Sequence 9, Appl
408	27	28.1	30	2	US-09-671-773C-170	Sequence 170, App	481	27	28.1	31	2	US-10-131-546-10	Sequence 10, Appl
409	27	28.1	30	2	US-09-671-773C-171	Sequence 171, App	482	27	28.1	31	2	US-10-131-546-16	Sequence 16, Appl
410	27	28.1	30	2	US-09-671-773C-172	Sequence 172, App	483	27	28.1	32	1	US-07-925-732-1	Sequence 1, Appl
411	27	28.1	30	2	US-09-671-773C-173	Sequence 173, App	484	27	28.1	33	2	US-09-333-842-2	Sequence 2, Appl
412	27	28.1	30	2	US-09-671-773C-322	Sequence 322, App	485	27	28.1	33	2	US-10-100-256B-2	Sequence 2, Appl
413	27	28.1	30	2	US-09-671-773C-323	Sequence 323, App	486	27	28.1	34	1	US-08-014-153D-23	Sequence 23, Appl
414	27	28.1	30	2	US-09-671-773C-324	Sequence 324, App	487	27	28.1	34	1	US-08-014-153D-30	Sequence 30, Appl
415	27	28.1	30	2	US-09-671-773C-325	Sequence 325, App	488	27	28.1	34	1	US-08-014-153D-31	Sequence 31, Appl
416	27	28.1	30	2	US-09-671-773C-326	Sequence 326, App	489	27	28.1	34	1	US-08-178-477B-26	Sequence 26, Appl
417	27	28.1	30	2	US-09-671-773C-327	Sequence 327, App	490	27	28.1	34	2	US-09-270-767-59606	Sequence 59606, A
418	27	28.1	30	2	US-09-671-773C-328	Sequence 328, App	491	27	28.1	35	2	US-09-640-957B-44	Sequence 44, Appl
419	27	28.1	30	2	US-09-671-773C-329	Sequence 329, App	492	27	28.1	35	2	US-09-270-767-61805	Sequence 61805, A
420	27	28.1	30	2	US-09-671-773C-330	Sequence 330, App	493	27	28.1	36	1	US-08-441-534A-7	Sequence 7, Appl
421	27	28.1	30	2	US-09-671-773C-331	Sequence 331, App	494	27	28.1	36	1	US-08-629-752-7	Sequence 7, Appl
422	27	28.1	30	2	US-09-671-773C-332	Sequence 332, App	495	27	28.1	36	1	US-08-802-991-7	Sequence 7, Appl
423	27	28.1	30	2	US-09-671-773C-333	Sequence 333, App	496	27	28.1	36	1	US-08-867-087B-58	Sequence 58, Appl
424	27	28.1	30	2	US-09-671-773C-334	Sequence 334, App	497	27	28.1	38	1	US-08-488-161-4	Sequence 4, Appl
425	27	28.1	30	2	US-09-671-773C-335	Sequence 335, App	498	27	28.1	38	2	US-09-273-685-4	Sequence 4, Appl
426	27	28.1	30	2	US-09-671-773C-336	Sequence 336, App	499	27	28.1	38	2	US-09-270-767-57878	Sequence 57878, A
427	27	28.1	30	2	US-09-671-773C-337	Sequence 337, App	500	27	28.1	38	2	US-09-270-767-62125	Sequence 62125, A
428	27	28.1	30	2	US-09-671-773C-338	Sequence 338, App	501	27	28.1	38	5	PCT-US95-11934-4	Sequence 4, Appl
429	27	28.1	30	2	US-09-671-773C-339	Sequence 339, App	502	27	28.1	39	2	US-09-149-476-352	Sequence 352, App
430	27	28.1	30	2	US-09-671-773C-340	Sequence 340, App	503	27	28.1	40	2	US-09-270-767-33566	Sequence 33566, A
431	27	28.1	30	2	US-09-671-773C-341	Sequence 341, App	504	27	28.1	40	2	US-09-270-767-48783	Sequence 48783, A
432	27	28.1	31	1	US-07-925-732-2	Sequence 2, Appl	505	27	28.1	40	2	US-09-671-773C-174	Sequence 174, App
433	27	28.1	31	1	US-08-201-092-3	Sequence 3, Appl	506	26.5	27.6	15	1	US-08-218-025A-105	Sequence 105, App
434	27	28.1	31	1	US-08-243-082-5	Sequence 5, Appl	507	26.5	27.6	21	1	US-08-447-411-37	Sequence 37, Appl
435	27	28.1	31	1	US-08-243-082-6	Sequence 6, Appl	508	26.5	27.6	21	1	US-09-708-606-19	Sequence 19, Appl
436	27	28.1	31	1	US-08-414-424-2	Sequence 2, Appl	509	26.5	27.6	24	1	US-08-248-021A-16	Sequence 16, Appl
437	27	28.1	31	1	US-08-414-424-3	Sequence 3, Appl	510	26.5	27.6	24	1	US-08-248-021A-17	Sequence 17, Appl
438	27	28.1	31	2	US-08-930-845-3	Sequence 3, Appl	511	26.5	27.6	27	1	US-08-248-021A-15	Sequence 15, Appl
439	27	28.1	31	2	US-08-893-749-22	Sequence 22, Appl	512	26.5	27.6	29	2	US-08-817-811-51	Sequence 51, Appl
440	27	28.1	31	2	US-09-289-612-4	Sequence 4, Appl	513	26.5	27.6	31	1	US-08-248-021A-13	Sequence 13, Appl
441	27	28.1	31	2	US-09-289-612-5	Sequence 5, Appl	514	26.5	27.6	31	2	US-09-308-345A-34	Sequence 34, Appl
442	27	28.1	31	2	US-10-131-346-9	Sequence 9, Appl	515	26.5	27.6	33	2	US-09-084-303B-286	Sequence 286, App
443	27	28.1	31	2	US-10-131-346-10	Sequence 10, Appl	516	26.5	27.6	36	1	US-08-039-137-38	Sequence 38, App
444	27	28.1	31	2	US-10-131-346-16	Sequence 16, Appl	517	26.5	27.6	36	1	US-08-039-137-43	Sequence 43, Appl
445	27	28.1	31	2	US-10-131-543-9	Sequence 9, Appl	518	26.5	27.6	40	2	US-09-962-756-1707	Sequence 1707, App
446	27	28.1	31	2	US-10-131-543-10	Sequence 10, Appl	519	26	27.1	11	2	US-09-224-785-22	Sequence 22, Appl
447	27	28.1	31	2	US-10-131-543-16	Sequence 16, Appl	520	26	27.1	11	2	US-09-224-785-25	Sequence 25, Appl
448	27	28.1	31	2	US-09-671-773C-12	Sequence 12, Appl	521	26	27.1	11	2	US-09-756-594-22	Sequence 22, Appl
449	27	28.1	31	2	US-09-671-773C-15	Sequence 15, Appl	522	26	27.1	11	2	US-09-756-594-25	Sequence 25, Appl
450	27	28.1	31	2	US-09-671-773C-17	Sequence 17, Appl	523	26	27.1	12	1	US-07-778-233B-33	Sequence 33, Appl
451	27	28.1	31	2	US-09-671-773C-19	Sequence 19, Appl	524	26	27.1	12	1	US-07-963-321-33	Sequence 33, Appl
452	27	28.1	31	2	US-09-671-773C-20	Sequence 20, Appl	525	26	27.1	12	1	US-08-290-641-33	Sequence 33, Appl
453	27	28.1	31	2	US-09-671-773C-21	Sequence 21, Appl	526	26	27.1	12	1	US-08-548-540-33	Sequence 33, Appl
454	27	28.1	31	2	US-09-671-773C-22	Sequence 22, Appl	527	26	27.1	12	3	US-08-816-454B-208	Sequence 208, App
455	27	28.1	31	2	US-09-671-773C-23	Sequence 23, Appl	528	26	27.1	12	5	PCT-US96-09809-33	Sequence 33, Appl
456	27	28.1	31	2	US-09-671-773C-24	Sequence 24, Appl	529	26	27.1	14	1	US-08-413-708B-5	Sequence 5, Appl
457	27	28.1	31	2	US-09-671-773C-25	Sequence 25, Appl	530	26	27.1	14	2	US-09-192-048-24	Sequence 24, Appl
458	27	28.1	31	2	US-09-671-773C-26	Sequence 26, Appl	531	26	27.1	15	2	US-09-828-574A-7	Sequence 7, Appl
459	27	28.1	31	2	US-09-671-773C-32	Sequence 32, Appl	532	26	27.1	16	2	US-09-164-186-5	Sequence 5, Appl
460	27	28.1	31	2	US-09-671-773C-44	Sequence 44, Appl	533	26	27.1	16	2	US-09-700-993-9	Sequence 9, Appl
461	27	28.1	31	2	US-09-671-773C-47	Sequence 47, Appl	534	26	27.1	17	2	US-08-706-344C-15	Sequence 15, Appl
462	27	28.1	31	2	US-09-671-773C-48	Sequence 48, Appl	535	26	27.1	18	2	US-09-646-691B-82	Sequence 82, Appl
463	27	28.1	31	2	US-09-671-773C-51	Sequence 51, Appl	536	26	27.1	18	2	US-09-834-240-27	Sequence 27, Appl
464	27	28.1	31	2	US-09-671-773C-63	Sequence 63, Appl	537	26	27.1	18	3	US-09-549-855-27	Sequence 27, Appl

538	26	27.1	19	2	US-09-627-1658-51	Sequence 51, Appl	611	26	27.1	35	2	US-09-082-279B-22	Sequence 22, Appl
539	26	27.1	20	2	US-09-623-548A-1417	Sequence 1417, Ap	612	26	27.1	35	2	US-09-082-279B-138	Sequence 138, App
540	26	27.1	20	2	US-09-657-276-1417	Sequence 1417, Ap	613	26	27.1	35	2	US-09-082-279B-139	Sequence 139, App
541	26	27.1	23	2	US-09-700-993-32	Sequence 32, Appl	614	26	27.1	35	2	US-09-082-279B-140	Sequence 140, App
542	26	27.1	24	1	US-08-248-021A-9	Sequence 9, Appli	615	26	27.1	35	2	US-09-082-279B-141	Sequence 141, App
543	26	27.1	24	1	US-08-248-021A-10	Sequence 10, Appl	616	26	27.1	35	2	US-09-082-279B-142	Sequence 142, App
544	26	27.1	24	1	US-08-248-021A-11	Sequence 11, Appl	617	26	27.1	35	2	US-09-082-279B-143	Sequence 143, App
545	26	27.1	24	1	US-08-248-021A-21	Sequence 21, Appl	618	26	27.1	35	2	US-09-082-279B-144	Sequence 144, App
546	26	27.1	24	1	US-08-248-021A-22	Sequence 22, Appl	619	26	27.1	35	2	US-09-082-279B-145	Sequence 145, App
547	26	27.1	24	2	US-10-005-920-1	Sequence 1, Appli	620	26	27.1	35	2	US-09-082-279B-146	Sequence 146, App
548	26	27.1	25	1	US-08-473-475A-21	Sequence 21, Appl	621	26	27.1	35	2	US-09-082-279B-147	Sequence 147, App
549	26	27.1	26	1	US-08-620-151-114	Sequence 114, App	622	26	27.1	35	2	US-09-082-279B-148	Sequence 148, App
550	26	27.1	26	2	US-09-224-785-40	Sequence 40, Appl	623	26	27.1	35	2	US-09-082-279B-149	Sequence 149, App
551	26	27.1	26	2	US-09-756-594-40	Sequence 40, Appl	624	26	27.1	35	2	US-09-082-279B-150	Sequence 150, App
552	26	27.1	28	1	US-07-690-300B-39	Sequence 39, Appl	625	26	27.1	35	2	US-09-082-279B-151	Sequence 151, App
553	26	27.1	28	1	US-07-690-300B-53	Sequence 53, Appl	626	26	27.1	35	2	US-08-474-349A-228	Sequence 228, App
554	26	27.1	28	1	US-07-690-300B-54	Sequence 54, Appl	627	26	27.1	35	2	US-09-085-761A-68	Sequence 68, Appl
555	26	27.1	28	1	US-07-690-300B-55	Sequence 55, Appl	628	26	27.1	35	2	US-09-315-304B-22	Sequence 22, Appl
556	26	27.1	28	1	US-07-690-300B-64	Sequence 64, Appl	629	26	27.1	35	2	US-09-315-304B-138	Sequence 138, App
557	26	27.1	28	1	US-07-690-300B-71	Sequence 71, Appl	630	26	27.1	35	2	US-09-315-304B-139	Sequence 139, App
558	26	27.1	28	1	US-08-308-729-41	Sequence 41, Appl	631	26	27.1	35	2	US-09-315-304B-140	Sequence 140, App
559	26	27.1	28	1	US-08-308-729-54	Sequence 54, Appl	632	26	27.1	35	2	US-09-315-304B-141	Sequence 141, App
560	26	27.1	28	2	US-09-082-279B-18	Sequence 18, Appl	633	26	27.1	35	2	US-09-315-304B-142	Sequence 142, App
561	26	27.1	28	2	US-09-082-279B-19	Sequence 19, Appl	634	26	27.1	35	2	US-09-315-304B-143	Sequence 143, App
562	26	27.1	28	2	US-09-082-279B-21	Sequence 21, Appl	635	26	27.1	35	2	US-09-315-304B-144	Sequence 144, App
563	26	27.1	28	2	US-08-474-349A-224	Sequence 224, App	636	26	27.1	35	2	US-09-315-304B-145	Sequence 145, App
564	26	27.1	28	2	US-08-474-349A-225	Sequence 225, App	637	26	27.1	35	2	US-09-315-304B-146	Sequence 146, App
565	26	27.1	28	2	US-08-474-349A-227	Sequence 227, App	638	26	27.1	35	2	US-09-315-304B-147	Sequence 147, App
566	26	27.1	28	2	US-09-315-304B-18	Sequence 18, Appl	639	26	27.1	35	2	US-09-315-304B-148	Sequence 148, App
567	26	27.1	28	2	US-09-315-304B-19	Sequence 19, Appl	640	26	27.1	35	2	US-09-315-304B-149	Sequence 149, App
568	26	27.1	28	2	US-09-315-304B-21	Sequence 21, Appl	641	26	27.1	35	2	US-09-315-304B-150	Sequence 150, App
569	26	27.1	28	2	US-09-834-784-18	Sequence 18, Appl	642	26	27.1	35	2	US-09-315-304B-151	Sequence 151, App
570	26	27.1	28	2	US-09-834-784-19	Sequence 19, Appl	643	26	27.1	35	2	US-09-834-784-22	Sequence 22, Appl
571	26	27.1	28	2	US-09-834-784-21	Sequence 21, Appl	644	26	27.1	35	2	US-09-834-784-138	Sequence 138, App
572	26	27.1	28	2	US-09-515-965A-18	Sequence 18, Appl	645	26	27.1	35	2	US-09-834-784-139	Sequence 139, App
573	26	27.1	28	2	US-09-515-965A-19	Sequence 19, Appl	646	26	27.1	35	2	US-09-834-784-140	Sequence 140, App
574	26	27.1	28	2	US-09-515-965A-21	Sequence 21, Appl	647	26	27.1	35	2	US-09-834-784-141	Sequence 141, App
575	26	27.1	28	2	US-09-528-200-94	Sequence 94, Appl	648	26	27.1	35	2	US-09-834-784-142	Sequence 142, App
576	26	27.1	28	2	US-09-528-200-95	Sequence 95, Appl	649	26	27.1	35	2	US-09-834-784-143	Sequence 143, App
577	26	27.1	28	2	US-09-528-200-96	Sequence 96, Appl	650	26	27.1	35	2	US-09-834-784-144	Sequence 144, App
578	26	27.1	28	2	US-09-528-200-97	Sequence 97, Appl	651	26	27.1	35	2	US-09-834-784-145	Sequence 145, App
579	26	27.1	28	2	US-09-350-641C-18	Sequence 18, Appl	652	26	27.1	35	2	US-09-834-784-146	Sequence 146, App
580	26	27.1	28	2	US-09-350-641C-19	Sequence 19, Appl	653	26	27.1	35	2	US-09-834-784-147	Sequence 147, App
581	26	27.1	28	2	US-09-350-641C-21	Sequence 21, Appl	654	26	27.1	35	2	US-09-834-784-148	Sequence 148, App
582	26	27.1	28	2	US-09-350-841A-18	Sequence 18, Appl	655	26	27.1	35	2	US-09-834-784-149	Sequence 149, App
583	26	27.1	28	2	US-09-350-841A-19	Sequence 19, Appl	656	26	27.1	35	2	US-09-834-784-150	Sequence 150, App
584	26	27.1	28	2	US-09-350-841A-21	Sequence 21, Appl	657	26	27.1	35	2	US-09-834-784-151	Sequence 151, App
585	26	27.1	28	2	US-09-623-548A-442	Sequence 442, App	658	26	27.1	35	2	US-09-515-965A-22	Sequence 22, Appl
586	26	27.1	28	2	US-09-657-276-442	Sequence 442, App	659	26	27.1	35	2	US-09-515-965A-138	Sequence 138, App
587	26	27.1	28	3	US-09-719-748-12	Sequence 12, Appl	660	26	27.1	35	2	US-09-515-965A-139	Sequence 139, App
588	26	27.1	29	1	US-08-776-815B-8	Sequence 8, Appli	661	26	27.1	35	2	US-09-515-965A-140	Sequence 140, App
589	26	27.1	29	2	US-09-270-767-57553	Sequence 57553, A	662	26	27.1	35	2	US-09-515-965A-141	Sequence 141, App
590	26	27.1	30	1	US-08-776-815B-9	Sequence 9, Appli	663	26	27.1	35	2	US-09-515-965A-142	Sequence 142, App
591	26	27.1	30	1	US-08-776-815B-10	Sequence 10, Appl	664	26	27.1	35	2	US-09-515-965A-143	Sequence 143, App
592	26	27.1	30	2	US-09-037-179B-11	Sequence 11, Appl	665	26	27.1	35	2	US-09-515-965A-144	Sequence 144, App
593	26	27.1	30	2	US-10-005-920-5	Sequence 5, Appli	666	26	27.1	35	2	US-09-515-965A-145	Sequence 145, App
594	26	27.1	30	2	US-09-929-315-11	Sequence 11, Appl	667	26	27.1	35	2	US-09-515-965A-146	Sequence 146, App
595	26	27.1	31	1	US-07-690-300B-18	Sequence 18, Appl	668	26	27.1	35	2	US-09-515-965A-147	Sequence 147, App
596	26	27.1	31	1	US-07-690-300B-84	Sequence 84, Appl	669	26	27.1	35	2	US-09-515-965A-148	Sequence 148, App
597	26	27.1	31	1	US-08-248-021A-19	Sequence 19, Appl	670	26	27.1	35	2	US-09-515-965A-149	Sequence 149, App
598	26	27.1	31	1	US-08-248-021A-20	Sequence 20, Appl	671	26	27.1	35	2	US-09-515-965A-150	Sequence 150, App
599	26	27.1	31	1	US-08-776-815B-11	Sequence 11, Appl	672	26	27.1	35	2	US-09-515-965A-151	Sequence 151, App
600	26	27.1	31	1	US-08-776-815B-12	Sequence 12, Appl	673	26	27.1	35	2	US-09-350-641C-22	Sequence 22, Appl
601	26	27.1	31	1	US-08-776-815B-13	Sequence 13, Appl	674	26	27.1	35	2	US-09-350-641C-138	Sequence 138, App
602	26	27.1	31	2	US-09-205-258-1105	Sequence 1105, Ap	675	26	27.1	35	2	US-09-350-641C-139	Sequence 139, App
603	26	27.1	31	2	US-09-623-548A-443	Sequence 443, App	676	26	27.1	35	2	US-09-350-641C-140	Sequence 140, App
604	26	27.1	31	2	US-09-657-276-443	Sequence 443, App	677	26	27.1	35	2	US-09-350-641C-141	Sequence 141, App
605	26	27.1	31	2	US-10-004-860-1105	Sequence 1105, Ap	678	26	27.1	35	2	US-09-350-641C-142	Sequence 142, App
606	26	27.1	32	2	US-09-270-767-61305	Sequence 61305, A	679	26	27.1	35	2	US-09-350-641C-143	Sequence 143, App
607	26	27.1	32	2	US-09-164-186-9	Sequence 9, Appli	680	26	27.1	35	2	US-09-350-641C-144	Sequence 144, App
608	26	27.1	34	1	US-08-867-087B-62	Sequence 62, Appl	681	26	27.1	35	2	US-09-350-641C-145	Sequence 145, App
609	26	27.1	35	2	US-09-053-197A-63	Sequence 63, Appl	682	26	27.1	35	2	US-09-350-641C-146	Sequence 146, App
610	26	27.1	35	2	US-08-485-264A-210	Sequence 210, App	683	26	27.1	35	2	US-09-350-641C-147	Sequence 147, App

684	26	27.1	35	2	US-09-350-641C-148	Sequence 148, App	757	25	26.0	13	2	US-09-196-390-8	Sequence 8, Appli
685	26	27.1	35	2	US-09-350-641C-149	Sequence 149, App	758	25	26.0	13	2	US-09-606-304-17	Sequence 17, Appl
686	26	27.1	35	2	US-09-350-641C-150	Sequence 150, App	759	25	26.0	13	2	US-09-952-677-8	Sequence 8, Appli
687	26	27.1	35	2	US-09-350-641C-151	Sequence 151, App	760	25	26.0	15	1	US-08-221-583-17	Sequence 17, Appl
688	26	27.1	35	2	US-09-350-641A-22	Sequence 22, Appl	761	25	26.0	15	1	US-08-221-583-18	Sequence 18, Appl
689	26	27.1	35	2	US-09-350-841A-138	Sequence 138, App	762	25	26.0	15	1	US-08-221-583-19	Sequence 19, Appl
690	26	27.1	35	2	US-09-350-841A-139	Sequence 139, App	763	25	26.0	15	1	US-08-310-341B-1	Sequence 1, Appli
691	26	27.1	35	2	US-09-350-841A-140	Sequence 140, App	764	25	26.0	15	1	US-10-211-689-66	Sequence 66, Appl
692	26	27.1	35	2	US-09-350-841A-141	Sequence 141, App	765	25	26.0	15	5	PCT-US95-04018-17	Sequence 17, Appl
693	26	27.1	35	2	US-09-350-841A-142	Sequence 142, App	766	25	26.0	15	5	PCT-US95-04018-18	Sequence 18, Appl
694	26	27.1	35	2	US-09-350-841A-143	Sequence 143, App	767	25	26.0	15	5	PCT-US95-04018-19	Sequence 19, Appl
695	26	27.1	35	2	US-09-350-841A-144	Sequence 144, App	768	25	26.0	15	5	PCT-US95-05657-1	Sequence 1, Appli
696	26	27.1	35	2	US-09-350-841A-145	Sequence 145, App	769	25	26.0	16	2	US-09-352-548-43	Sequence 43, Appl
697	26	27.1	35	2	US-09-350-841A-146	Sequence 146, App	770	25	26.0	16	2	US-09-671-089-53	Sequence 53, Appl
698	26	27.1	35	2	US-09-350-841A-147	Sequence 147, App	771	25	26.0	17	2	US-09-082-279B-848	Sequence 848, App
699	26	27.1	35	2	US-09-350-841A-148	Sequence 148, App	772	25	26.0	17	2	US-09-315-304B-848	Sequence 848, App
700	26	27.1	35	2	US-09-350-841A-149	Sequence 149, App	773	25	26.0	17	2	US-09-834-784-848	Sequence 848, App
701	26	27.1	35	2	US-09-350-841A-150	Sequence 150, App	774	25	26.0	17	2	US-09-515-965A-848	Sequence 848, App
702	26	27.1	35	2	US-09-350-841A-151	Sequence 151, App	775	25	26.0	17	2	US-09-350-641C-848	Sequence 848, App
703	26	27.1	36	1	US-08-039-137-39	Sequence 39, Appl	776	25	26.0	17	2	US-09-350-841A-848	Sequence 848, App
704	26	27.1	36	1	US-08-039-137-40	Sequence 40, Appl	777	25	26.0	18	2	US-09-834-240-6	Sequence 6, Appli
705	26	27.1	36	1	US-08-039-137-41	Sequence 41, Appl	778	25	26.0	18	2	US-09-896-841A-74	Sequence 74, Appl
706	26	27.1	36	1	US-08-039-137-42	Sequence 42, Appl	779	25	26.0	18	3	US-09-549-855-6	Sequence 6, Appli
707	26	27.1	37	2	US-08-919-597-210	Sequence 210, App	780	25	26.0	20	1	US-08-557-892-11	Sequence 11, Appl
708	26	27.1	37	2	US-08-919-597-211	Sequence 211, App	781	25	26.0	20	1	US-08-387-858A-11	Sequence 11, Appl
709	26	27.1	37	2	US-08-919-597-212	Sequence 212, App	782	25	26.0	20	2	US-09-294-384B-11	Sequence 11, Appl
710	26	27.1	37	2	US-08-277-078-48	Sequence 212, App	783	25	26.0	20	2	US-08-818-112-120	Sequence 120, App
711	26	27.1	37	2	US-08-470-896-210	Sequence 210, App	784	25	26.0	20	2	US-08-818-111-115	Sequence 115, App
712	26	27.1	37	2	US-08-470-896-211	Sequence 211, App	785	25	26.0	20	2	US-09-056-556-120	Sequence 120, App
713	26	27.1	37	2	US-08-470-896-212	Sequence 212, App	786	25	26.0	20	2	US-08-717-079-11	Sequence 11, Appl
714	26	27.1	37	2	US-08-484-741-210	Sequence 211, App	787	25	26.0	20	2	US-09-072-596-115	Sequence 115, App
715	26	27.1	37	2	US-08-484-741-211	Sequence 211, App	788	25	26.0	20	2	US-09-072-967-120	Sequence 120, App
716	26	27.1	37	2	US-08-484-741-212	Sequence 212, App	789	25	26.0	20	2	US-09-171-432A-73	Sequence 73, Appl
717	26	27.1	37	3	US-10-000-986A-136	Sequence 136, App	790	25	26.0	20	2	US-09-171-432A-74	Sequence 74, Appl
718	26	27.1	38	2	US-09-646-691B-54	Sequence 54, Appl	791	25	26.0	20	2	US-10-193-002-115	Sequence 115, App
719	26	27.1	40	2	US-09-647-143-16	Sequence 16, Appl	792	25	26.0	20	2	US-10-076-622-612	Sequence 612, App
720	26	27.1	40	2	US-09-270-767-59425	Sequence 59425, A	793	25	26.0	20	2	US-10-084-843-120	Sequence 120, App
721	26	27.1	40	2	US-10-038-612-57	Sequence 57, Appl	794	25	26.0	20	2	US-10-124-805-612	Sequence 612, App
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724	25.5	26.6	12	2	US-08-590-563-22	Sequence 22, Appl	797	25	26.0	22	1	US-08-484-635-181	Sequence 181, App
725	25.5	26.6	12	2	US-09-770-621-22	Sequence 22, Appl	798	25	26.0	22	1	US-08-484-631-181	Sequence 181, App
726	25.5	26.6	12	2	US-09-235-832-22	Sequence 22, Appl	799	25	26.0	22	1	US-08-827-570-181	Sequence 181, App
727	25.5	26.6	15	1	US-08-221-583-15	Sequence 15, Appl	800	25	26.0	22	2	US-10-038-612-79	Sequence 79, Appl
728	25.5	26.6	20	5	PCT-US95-04018-15	Sequence 15, Appl	801	25	26.0	23	1	US-08-245-853-21	Sequence 21, Appl
729	25.5	26.6	37	2	US-09-894-912A-20	Sequence 20, Appl	802	25	26.0	23	1	US-08-573-675-21	Sequence 21, Appl
730	25	26.0	6	1	US-08-375-911A-5	Sequence 5, Appli	803	25	26.0	23	1	US-08-493-235-11	Sequence 11, Appl
731	25	26.0	7	2	US-09-187-859-1592	Sequence 1592, Ap	804	25	26.0	23	2	US-10-211-689-68	Sequence 68, Appl
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733	25	26.0	7	2	US-10-006-869-1592	Sequence 1592, Ap	806	25	26.0	24	2	US-09-721-108-239	Sequence 239, App
734	25	26.0	8	3	US-08-641-528B-19948	Sequence 19948, A	807	25	26.0	24	2	US-09-574-779B-5	Sequence 5, Appli
735	25	26.0	9	2	US-09-502-600-69	Sequence 69, Appl	808	25	26.0	24	2	US-10-360-101-162	Sequence 162, App
736	25	26.0	9	2	US-09-918-243-69	Sequence 69, Appl	809	25	26.0	25	1	US-08-684-862-7	Sequence 7, Appli
737	25	26.0	9	3	US-09-641-528B-11723	Sequence 11723, A	810	25	26.0	25	1	US-08-484-635-145	Sequence 145, App
738	25	26.0	9	3	US-09-641-528B-17690	Sequence 17690, A	811	25	26.0	25	1	US-08-484-631-145	Sequence 145, App
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740	25	26.0	9	3	US-09-641-528B-45234	Sequence 45234, A	813	25	26.0	25	2	US-09-004-730A-108	Sequence 108, App
741	25	26.0	10	1	US-08-764-640-67	Sequence 67, Appl	814	25	26.0	25	2	US-08-981-799A-108	Sequence 108, App
742	25	26.0	10	2	US-08-973-225-67	Sequence 67, Appl	815	25	26.0	25	2	US-10-666-480-110	Sequence 110, App
743	25	26.0	10	2	US-09-244-298A-67	Sequence 67, Appl	816	25	26.0	26	1	US-08-467-587A-19	Sequence 19, Appl
744	25	26.0	10	2	US-09-516-704-67	Sequence 67, Appl	817	25	26.0	26	2	US-09-224-785-41	Sequence 41, Appl
745	25	26.0	10	2	US-09-549-090-67	Sequence 67, Appl	818	25	26.0	26	2	US-09-756-594-41	Sequence 41, Appl
746	25	26.0	10	2	US-08-832-230A-67	Sequence 67, Appl	819	25	26.0	26	2	US-09-860-793-6	Sequence 6, Appli
747	25	26.0	10	3	US-09-641-528B-19934	Sequence 19934, A	820	25	26.0	26	2	US-09-084-303B-243	Sequence 243, App
748	25	26.0	10	3	US-09-641-528B-20286	Sequence 20286, A	821	25	26.0	26	2	US-09-774-639-300	Sequence 300, App
749	25	26.0	11	2	US-09-224-785-29	Sequence 29, Appl	822	25	26.0	27	1	US-08-165-038-13	Sequence 13, Appl
750	25	26.0	11	2	US-09-756-594-29	Sequence 29, Appl	823	25	26.0	27	1	US-08-876-781-13	Sequence 13, Appl
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752	25	26.0	11	3	US-09-641-528B-17911	Sequence 17911, A	825	25	26.0	27	1	US-08-387-858A-3	Sequence 3, Appli
753	25	26.0	11	3	US-09-641-528B-19923	Sequence 19923, A	826	25	26.0	27	2	US-08-408-264A-20	Sequence 20, Appl
754	25	26.0	11	3	US-09-641-528B-38756	Sequence 38756, A	827	25	26.0	27	2	US-09-294-384B-3	Sequence 3, Appli
755	25	26.0	11	3	US-09-641-528B-44627	Sequence 44627, A	828	25	26.0	27	2	US-09-264-709A-15	Sequence 15, Appl
756	25	26.0	13	2	US-08-836-567-17	Sequence 17, Appl	829	25	26.0	27	2	US-09-421-097-20	Sequence 20, Appl

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833	25	26.0	28	2	US-09-428-082B-590	Sequence 590, App	906	24	25.0	8	5	PCT-US91-02166-14	Sequence 14, Appl
834	25	26.0	28	2	US-09-428-082B-591	Sequence 591, App	907	24	25.0	9	2	US-09-518-046-74	Sequence 74, Appl
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836	25	26.0	30	1	US-08-484-107-3	Sequence 3, Appli	909	24	25.0	9	2	US-09-650-371-74	Sequence 74, Appl
837	25	26.0	30	2	US-09-205-258-646	Sequence 646, App	910	24	25.0	9	2	US-09-650-371-133	Sequence 133, App
838	25	26.0	30	2	US-09-270-767-60358	Sequence 60358, A	911	24	25.0	9	3	US-09-641-528B-1789	Sequence 1789, App
839	25	26.0	30	2	US-09-627-165B-53	Sequence 53, Appl	912	24	25.0	9	3	US-09-641-528B-13672	Sequence 13672, A
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846	25	26.0	32	2	US-09-834-784-840	Sequence 840, App	919	24	25.0	10	3	US-09-641-528B-4918	Sequence 4918, App
847	25	26.0	32	2	US-09-638-524A-14	Sequence 14, Appl	920	24	25.0	10	3	US-09-641-528B-21738	Sequence 21738, A
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851	25	26.0	32	2	US-09-638-524A-19	Sequence 19, Appl	924	24	25.0	11	2	US-09-224-785-6	Sequence 6, Appli
852	25	26.0	32	2	US-09-638-524A-20	Sequence 20, Appl	925	24	25.0	11	2	US-09-224-785-24	Sequence 24, Appl
853	25	26.0	32	2	US-09-638-524A-21	Sequence 21, Appl	926	24	25.0	11	2	US-09-224-785-25	Sequence 25, Appl
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856	25	26.0	32	2	US-09-350-641C-840	Sequence 840, App	929	24	25.0	11	2	US-09-025-596-26	Sequence 26, Appl
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858	25	26.0	32	2	US-10-125-062-11	Sequence 11, Appl	931	24	25.0	11	2	US-09-756-594-24	Sequence 24, Appl
859	25	26.0	33	1	US-07-859-923A-13	Sequence 13, Appl	932	24	25.0	11	2	US-09-756-594-26	Sequence 26, Appl
860	25	26.0	33	1	US-08-484-107-13	Sequence 13, Appl	933	24	25.0	11	2	US-09-756-594-27	Sequence 27, Appl
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864	25	26.0	36	1	US-08-867-087B-59	Sequence 59, Appl	937	24	25.0	11	3	US-09-641-528B-769	Sequence 769, App
865	25	26.0	36	2	US-09-082-279B-844	Sequence 844, App	938	24	25.0	11	3	US-09-641-528B-4906	Sequence 4906, App
866	25	26.0	36	2	US-09-315-304B-844	Sequence 844, App	939	24	25.0	11	3	US-09-641-528B-9372	Sequence 9372, App
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874	25	26.0	38	2	US-08-348-518C-11	Sequence 11, Appl	947	24	25.0	12	1	US-08-556-597-58	Sequence 58, Appl
875	25	26.0	38	2	US-08-476-509B-11	Sequence 11, Appl	948	24	25.0	13	2	US-09-489-156-17	Sequence 17, Appl
876	25	26.0	38	2	US-10-125-062-12	Sequence 12, Appl	949	24	25.0	15	1	US-08-221-583-26	Sequence 26, Appl
877	25	26.0	39	1	US-08-050-319B-40	Sequence 40, Appl	950	24	25.0	15	1	US-08-221-583-27	Sequence 27, Appl
878	25	26.0	39	1	US-08-465-982-40	Sequence 40, Appl	951	24	25.0	15	1	US-08-221-583-28	Sequence 28, Appl
879	25	26.0	39	2	US-09-698-286A-30	Sequence 30, Appl	952	24	25.0	15	1	US-08-218-025A-141	Sequence 141, App
880	25	26.0	39	2	US-09-270-767-37736	Sequence 37736, A	953	24	25.0	15	1	US-08-179-481-59	Sequence 59, Appl
881	25	26.0	39	2	US-10-125-062-16	Sequence 16, Appl	954	24	25.0	15	2	US-09-526-195-13	Sequence 13, Appl
882	25	26.0	40	2	US-10-038-612-58	Sequence 58, Appl	955	24	25.0	15	2	US-09-142-524D-108	Sequence 108, App
883	25	26.0	40	2	US-09-954-968-4	Sequence 4, Appli	956	24	25.0	15	2	US-10-038-407-13	Sequence 13, Appl
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888	24.5	25.5	40	1	US-08-662-227-26	Sequence 26, Appl	961	24	25.0	15	5	PCT-US95-04018-27	Sequence 27, Appl
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891	24.5	25.5	40	1	US-08-210-762B-12	Sequence 12, Appl	964	24	25.0	16	2	US-08-975-698A-5	Sequence 5, Appli
892	24.5	25.5	40	1	US-08-210-762B-10	Sequence 10, Appl	965	24	25.0	16	2	US-09-417-090-5	Sequence 5, Appli
893	24.5	25.5	40	1	US-08-210-762B-11	Sequence 11, Appl	966	24	25.0	16	2	US-08-492-411A-13	Sequence 13, Appl
894	24.5	25.5	40	1	US-08-210-762B-15	Sequence 15, Appl	967	24	25.0	16	2	US-09-727-578-5	Sequence 5, Appli
895	24.5	25.5	40	1	US-09-106-075A-10	Sequence 10, Appl	968	24	25.0	16	2	US-09-555-352-13	Sequence 13, Appl
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897	24.5	25.5	40	1	US-09-106-075A-14	Sequence 14, Appl	970	24	25.0	16	2	US-10-105-774-15	Sequence 15, Appl
898	24.5	25.5	40	1	US-08-665-259-17	Sequence 17, Appl	971	24	25.0	16	2	US-09-962-756-1803	Sequence 1803, App
899	24.5	25.5	40	1	US-08-762-500-17	Sequence 17, Appl	972	24	25.0	16	2	US-09-825-517A-70	Sequence 70, Appl
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901	24	25.0	8	1	US-08-672-610A-53	Sequence 53, Appl	974	24	25.0	17	2	US-09-515-965A-1523	Sequence 1523, App
902	24	25.0	8	2	US-09-206-786A-53	Sequence 53, Appl	975	24	25.0	17	2	US-09-350-641C-1523	Sequence 1523, App

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976      24      25.0      17      2      US-09-350-841A-1523      Sequence 1523, Ap
977      24      25.0      17      2      US-09-700-993-21      Sequence 21, Appl
978      24      25.0      17      2      US-10-117-846-35      Sequence 35, Appl
979      24      25.0      17      2      US-10-117-846-38      Sequence 38, Appl
980      24      25.0      17      2      US-10-117-846-39      Sequence 39, Appl
981      24      25.0      17      2      US-10-117-846-39      Patent No. 5183805
982      24      25.0      17      7      5183805-1      Patent No. 5183805
983      24      25.0      17      7      5183805-2      Patent No. 5183805
984      24      25.0      18      2      US-09-328-501-3      Sequence 3, Appl
985      24      25.0      18      2      US-09-777-710A-3      Sequence 3, Appl
986      24      25.0      18      2      US-09-896-841A-75      Sequence 75, Appl
987      24      25.0      18      2      US-08-495-606E-19      Sequence 19, Appl
988      24      25.0      18      5      PCT-US94-01234-19      Sequence 19, Appl
989      24      25.0      18      5      PCT-US94-01234-32      Sequence 32, Appl
990      24      25.0      18      6      US-10-191-289A-3      Sequence 3, Appl
991      24      25.0      20      1      US-08-218-025A-59      Sequence 59, Appl
992      24      25.0      20      1      US-08-306-116A-17      Sequence 17, Appl
993      24      25.0      20      1      US-08-484-135-72      Sequence 72, Appl
994      24      25.0      20      1      US-08-484-135-90      Sequence 90, Appl
995      24      25.0      20      1      US-08-484-635-30      Sequence 30, Appl
996      24      25.0      20      1      US-08-484-635-53      Sequence 53, Appl
997      24      25.0      20      1      US-08-484-631-30      Sequence 30, Appl
998      24      25.0      20      1      US-08-484-631-53      Sequence 53, Appl
999      24      25.0      20      1      US-08-934-915-131      Sequence 131, App
1000     24      25.0      20      1      US-08-827-570-30      Sequence 30, Appl
          24      25.0      20      1      US-08-827-570-53      Sequence 53, Appl

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ALIGNMENTS

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RESULT 1
US-09-835-752-1
; Sequence 1, Application US/09835752
; Patent No. 6835545
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
; FILE REFERENCE: H0498/7137(ERG)
; CURRENT APPLICATION NUMBER: US/09/835,752
; CURRENT FILING DATE: 2001-04-16
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 06/203,254
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-752-1

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Query Match      44.8%; Score 43; DB 2; Length 15;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 PEHCNFD 8
Db      7 PEHANFD 14

RESULT 2
US-10-038-407-2
; Sequence 2, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 VI/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679

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; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-2

```

```

Query Match      35.9%; Score 34.5; DB 2; Length 34;
Best Local Similarity 42.9%; Pred. No. 75;
Matches 6; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

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Qy      2 EHCNFDVTRLRE 15
Db      4 KNCSEFN-ITTSIRD 16
          ::|||::|||:

```

```

RESULT 3
US-08-143-311B-18
; Sequence 18, Application US/08143311B
; Patent No. 5863540
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: HALE, LAURA P.
; APPLICANT: PATTON, KAREN L.
; APPLICANT: TELEN, MARILYN J.
; APPLICANT: LIAO, HUA-XIN
; TITLE OF INVENTION: AN ADHESION MOLECULE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/143,311B
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,339
; FILING DATE: 30-OCT-1992
; CLASSIFICATION: 436
; APPLICATION NUMBER: 07/669,730
; FILING DATE: 15-MAR-1991
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-50
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-143-311B-18

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```

Query Match      35.4%; Score 34; DB 1; Length 19;
Best Local Similarity 58.3%; Pred. No. 48;

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Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 CNFNDVTVTLRLRE 15
||| ||| |
Db 1 CNRNDVTGGRRD 12

RESULT 4

US-10-038-612-56
; Sequence 56, Application US/10038612
; Patent No. 6723830

GENERAL INFORMATION:

; APPLICANT: Ben-Gasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; FILE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 40
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: PDGFR-b
US-10-038-612-56

Query Match 35.4%; Score 34; DB 2; Length 40;
Best Local Similarity 31.2%; Pred. No. 1.1e+02;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 EHCNFDVTVTLRLRE 17
|:|:|:|:|:|:|:
Db 2 EYCRYGDLVDYLHNRK 17

RESULT 5

US-08-218-025A-44
; Sequence 44, Application US/08218025A
; Patent No. 5556744

GENERAL INFORMATION:

; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-218-025A-44

Query Match 34.9%; Score 33.5; DB 1; Length 20;
Best Local Similarity 46.2%; Pred. No. 61;
Matches 6; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 3 HCNFNDVTVTLRLRE 15
:|:|:|:|:|:|:
Db 1 NCSFN-ITTSIRD 12

RESULT 6

US-08-893-749-23
; Sequence 23, Application US/08893749
; Patent No. 6126916

; GENERAL INFORMATION:
; APPLICANT: MCBRIDE, William J.
; APPLICANT: GRIFFITHS, Gary L.
; TITLE OF INVENTION: RADIOMETAL-BINDING PEPTIDE ANALOGUES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,749
; FILING DATE: 11-JUL-1997
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,662
; FILING DATE: 12-JUL-1996

ATTORNEY/AGENT INFORMATION:

; NAME: Saxe, Bern D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 018733/0804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-893-749-23

Query Match 34.4%; Score 33; DB 2; Length 27;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 CNFNDVTVTLRLRE 15
|:|:|:|:|:|:|:
Db 3 CVFTDNYTLRLK 14

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RESULT 7
US-09-270-767-60767
; Sequence 60767, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60767
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60767
Query Match 34.4%; Score 33; DB 2; Length 35;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CNFNDVTTRL 13
|||:|:|
Db 10 CNMNCITILL 19

RESULT 8
US-08-232-513A-11
; Sequence 11, Application US/08232513A
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; FILE REFERENCE: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..17

; OTHER INFORMATION: /label= HEPO
US-08-232-513A-11
Query Match 33.3%; Score 32; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFNDVTT 11
|||:|:|
Db 2 EHCSLNENIT 11

RESULT 9
US-09-231-159-16
; Sequence 16, Application US/09231159
; Patent No. 6268347
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain
; FILE REFERENCE: Using Prosaposin-Derived Peptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,159
; FILING DATE:
; CLASSIFICATION:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,159
; FILING DATE: 05-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1928
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-231-159-16
Query Match 33.3%; Score 32; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFNDVTT 11
|||:|:|
Db 2 EHCSLNENIT 11

RESULT 10
US-08-611-307-16
; Sequence 16, Application US/08611307
; Patent No. 6271196
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain
; FILE REFERENCE: Using Prosaposin-Derived Peptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,307
FILING DATE: 05-MAR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1928
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-611-307-16

Query Match 33.3%; Score 32; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
|||:|:
Db 2 EHCSLNENIT 11

RESULT 11
US-08-928-074-16
Sequence 16, Application US/08928074
Patent No. 6849602
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,074
FILING DATE: 11-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,307
FILING DATE: 05-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04143
FILING DATE: 05-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07256/024001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-928-074-16
Query Match 33.3%; Score 32; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 EHCNFDVTT 11
|||:|:
Db 2 EHCSLNENIT 11

RESULT 12
US-09-625-191B-26
Sequence 26, Application US/09625191B
Patent No. 6962974
GENERAL INFORMATION:
APPLICANT: Kalluri, Raghuram
TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE THEREOF
FILE REFERENCE: 2312/2085C (formerly 1440.1027006)
CURRENT APPLICATION NUMBER: US/09/625,191B
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 09/543,371
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: US 09/335,224
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/126,175
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/089,689
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 20
TYPE: PPT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(20)
OTHER INFORMATION: T3 peptide
US-09-625-191B-26

Query Match 33.3%; Score 32; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FEHCNFDV 9
|:|:|:
Db 9 FLFCNVNDV 17

RESULT 13
US-09-528-200-69
Sequence 69, Application US/09528200
Patent No. 6630570
GENERAL INFORMATION:
APPLICANT: LUCHA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: SEMMLER, WOLFHARD
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: HESSNIUS, CARSTEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
FILE REFERENCE: SCH-1731

;; CURRENT APPLICATION NUMBER: US/09/528,200
;; CURRENT FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: DE 199 17 713.9
;; PRIOR FILING DATE: 1999-09-04
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 69
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-09-528-200-69

Query Match 33.3%; Score 32; DB 2; Length 28;
Best Local Similarity 53.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 HCNFNDVTRLRE 15
| | | | |
Db 3 HAVFTDNYTRUK 15

RESULT 14

PCT-US94-04361-50
;; Sequence 50, Application PC/TUS9404361
;; GENERAL INFORMATION:

;; APPLICANT: Brigham and Women's Hospital
;; APPLICANT: 75 Francis Street
;; APPLICANT: Boston, MA 02115
;; APPLICANT: Bunn, H. Franklin
;; APPLICANT: Wen, Danyi
;; APPLICANT: Showers, Mark O.

;; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
;; TITLE OF INVENTION: Activity
;; NUMBER OF SEQUENCES: 59
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Sterne, Keseler, Goldstein & Fox
;; STREET: 1100 New York Avenue, Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.

;; ZIP: 20005-3934

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US94/04361

;; FILING DATE: Herewith

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/049,802

;; FILING DATE: 21-APR-1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Cimbala, Michele A.

;; REGISTRATION NUMBER: 33,851

;; REFERENCE/DOCKET NUMBER: 0627.336PC01

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202) 371-2600

;; TELEFAX: (202) 371-2540

;; INFORMATION FOR SEQ ID NO: 50:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 36 amino acids

;; TYPE: amino acid

;; TOPOLOGY: both

;; PCT-US94-04361-50

Query Match 33.3%; Score 32; DB 5; Length 36;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFDVTVT 11
| | | | |
Db 9 EHCSLNENIT 18

RESULT 15

US-10-038-612-55
;; Sequence 55, Application US/10038612
;; Patent No. 6723830
;; GENERAL INFORMATION:

;; APPLICANT: Ben-Sasson, Shmuel A.

;; TITLE OF INVENTION: Short Peptides Which Selectively

;; FILE REFERENCE: 1242.1029-000 (CMCC-679)

;; CURRENT APPLICATION NUMBER: US/10/038,612

;; PRIOR FILING DATE: 2002-01-08

;; PRIOR APPLICATION NUMBER: US 09/161,094

;; NUMBER OF SEQ ID NOS: 172

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 55

;; LENGTH: 40

;; TYPE: PRT

;; ORGANISM: unknown

;; FEATURE:

;; OTHER INFORMATION: PDGFR-a

;; US-10-038-612-55

Query Match 33.3%; Score 32; DB 2; Length 40;
Best Local Similarity 33.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 EHCNFDVTVTRLREN 16
| | | | |
Db 2 EYCFYGLVNLHKN 16

RESULT 16

US-08-165-038-12

;; Sequence 12, Application US/08165038

;; Patent No. 5639869

;; GENERAL INFORMATION:

;; APPLICANT: Cole, Barry C.

;; APPLICANT: Atkin, Curtis L.

;; APPLICANT: Poie, Ann

;; APPLICANT: Oliphant, Arnold

;; TITLE OF INVENTION: Mycoplasma Arthritis T-Cell

;; NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Thorpe, No. 5639869th & Western

;; STREET: 9035 South 700 East, Suite 200

;; CITY: Sandy

;; STATE: Utah

;; COUNTRY: USA

;; ZIP: 84070

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage

;; COMPUTER: AST Advantage NB-SX20

;; OPERATING SYSTEM: DOS 5.00

;; SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/165,038

;; FILING DATE:

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: M. Wayne Western

;; REGISTRATION NUMBER: 22,788

;; REFERENCE/DOCKET NUMBER: T676

TELECOMMUNICATION INFORMATION:

TELEPHONE: (801)566-6633
TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
CELL TYPE: unicellular organism
FEATURE:

NAME/KEY: staphylococcal enterotoxin C1 amino acid
NAME/KEY: sequence having sequence similarity to
NAME/KEY: MAM
LOCATION: residues 121 to 147
IDENTIFICATION METHOD: computer searching for
IDENTIFICATION METHOD: sequence similarities.
PUBLICATION INFORMATION:
AUTHORS: Bohach, G.A.
AUTHORS: Schlievert, P.M.
TITLE: Nucleotide sequence of the staphylococcal
TITLE: enterotoxin C1 gene and relatedness to
TITLE: other pyrogenic toxins
JOURNAL: Mol. Gen. Genet.
VOLUME: 209
PAGES: 15-20
DATE: 1987
US-08-165-038-12

Query Match 32.3%; Score 31; DB 1; Length 27;
Best Local Similarity 35.3%; Pred. No. 2.2e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTRENE 17

Db 3 FDNGNLQNVLRVYENK 19

RESULT 17

US-08-876-781-12
Sequence 12, Application US/08876781
Patent No. 5872233

GENERAL INFORMATION:

APPLICANT: Cole, Barry C.
APPLICANT: Atkin, Curtis L.
APPLICANT: Pole, Ann
APPLICANT: Oliphant, Arnold
TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
TITLE OF INVENTION: Mitogen
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5872233th & Western
STREET: 9035 South 700 East, Suite 200
CITY: Sandy
STATE: Utah
COUNTRY: USA
ZIP: 84070

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: AST Advantage NB-SX20
OPERATING SYSTEM: DOS 5.00
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,781
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: M. Wayne Western
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: T676
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801)566-6633
TELEFAX: (801)566-0750
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
CELL TYPE: unicellular organism
FEATURE:
NAME/KEY: staphylococcal enterotoxin C1 amino acid
NAME/KEY: sequence having sequence similarity to
NAME/KEY: MAM
LOCATION: residues 121 to 147
IDENTIFICATION METHOD: computer searching for
IDENTIFICATION METHOD: sequence similarities.
PUBLICATION INFORMATION:
AUTHORS: Bohach, G.A.
AUTHORS: Schlievert, P.M.
TITLE: Nucleotide sequence of the staphylococcal
TITLE: enterotoxin C1 gene and relatedness to
TITLE: other pyrogenic toxins
JOURNAL: Mol. Gen. Genet.
VOLUME: 209
PAGES: 15-20
DATE: 1987
US-08-876-781-12

Query Match 32.3%; Score 31; DB 1; Length 27;
Best Local Similarity 35.3%; Pred. No. 2.2e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTRENE 17

Db 3 FDNGNLQNVLRVYENK 19

RESULT 18

US-09-671-773C-37
Sequence 37, Application US/09671773C
Patent No. 6972319

GENERAL INFORMATION:

APPLICANT: Pan, Clark
APPLICANT: Tsutsumi, Manami
APPLICANT: Shanafelt, Armen B.
TITLE OF INVENTION: Piculicary Adenylate Cyclase Activating Peptide (PACAP) Receptor
FILE REFERENCE: MSB 7272P2
CURRENT APPLICATION NUMBER: US/09/671,773C
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/595,280
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/407,832
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn version 3.3
SEQ ID NO 37
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
NAME/KEY: PEPTIDE
LOCATION: (1)..(28)
US-09-671-773C-37

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Query Match      32.3%; Score 31; DB 2; Length 28;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
   | | | | |
Db 6 FTDNYTRLRE 15

RESULT 19
US-09-500-747-16
; Sequence 16, Application US/09500747
; Patent No. 6753173
; GENERAL INFORMATION:
; APPLICANT: Kosan Biosciences, Inc.
; APPLICANT: Gokhale, Rajesh
; APPLICANT: Tsuji, Stuart
; APPLICANT: Khosla, Chaitan
; TITLE OF INVENTION: METHODS TO MEDIATE POLYKETIDE SYNTHASE
; TITLE OF INVENTION: MODULE EFFECTIVENESS
; FILE REFERENCE: 30062-20046.00
; CURRENT APPLICATION NUMBER: US/09/500,747
; CURRENT FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/119,363
; PRIOR FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminal inter-polypeptide linker M8rif
US-09-500-747-16

Query Match      32.3%; Score 31; DB 2; Length 32;
Best Local Similarity 70.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 DVTTRLRENE 17
   | | | | |
Db 19 DARTLREVE 28

RESULT 20
US-10-091-244A-16
; Sequence 16, Application US/10091244A
; Patent No. 7001748
; GENERAL INFORMATION:
; APPLICANT: Gokhale, Rajesh
; APPLICANT: Tsuji, Stuart
; APPLICANT: Khosla, Chaitan
; TITLE OF INVENTION: METHODS TO MEDIATE POLYKETIDE SYNTHASE
; TITLE OF INVENTION: MODULE EFFECTIVENESS
; FILE REFERENCE: 300622004620
; CURRENT APPLICATION NUMBER: US/10/091,244A
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/500,747
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/119,363
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/272,985
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/272,987
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; OTHER INFORMATION: N-Terminal Inter-polypeptide linker
US-10-091-244A-16

Query Match      32.3%; Score 31; DB 3; Length 33;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 DVTTRLRENE 17
   | | | | |
Db 20 DARTLREVE 29

RESULT 21
US-09-201-227A-31
; Sequence 31, Application US/09201227A
; Patent No. 6468770
; GENERAL INFORMATION:
; APPLICANT: Keyes, Linda N.
; APPLICANT: Doberstein, Stephen K.
; APPLICANT: Buchman, Andrew R.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 7326-066
; CURRENT APPLICATION NUMBER: US/09/201,227A
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Freshwater Snail
US-09-201-227A-31

Query Match      32.3%; Score 31; DB 2; Length 38;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FEHCNFND 8
   | | | |
Db 2 FSACNIND 9

RESULT 22
US-09-084-303B-227
; Sequence 227, Application US/09084303B
; Patent No. 6627746
; GENERAL INFORMATION:
; APPLICANT: Doberstein, Stephen
; APPLICANT: Reddy, Bindu
; APPLICANT: Platt, Darren
; APPLICANT: Ferguson, Kimberly
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 7326-069-999
; CURRENT APPLICATION NUMBER: US/09/084,303B
; CURRENT FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Freshwater Snail
US-09-084-303B-227

Query Match      32.3%; Score 31; DB 2; Length 38;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FEHCNFND 8
   | | | |
Db 2 FSACNIND 9
```

RESULT 23
US-09-500-747-13
; Sequence 13, Application US/09500747
; Patent No. 6753173
; GENERAL INFORMATION:
; APPLICANT: Kosan Biosciences, Inc.
; APPLICANT: Gokhale, Rajesh
; APPLICANT: Tsuji, Stuart
; APPLICANT: Khosla, Chaitan
; TITLE OF INVENTION: METHODS TO MEDIATE POLYKETIDE SYNTHASE
; TITLE OF INVENTION: MODULE EFFECTIVENESS
; FILE REFERENCE: 30062-20046.00
; CURRENT APPLICATION NUMBER: US/09/500,747
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/119,363
; PRIOR FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminal inter-polypeptide linker M5ery
US-09-500-747-13

Query Match 32.3%; Score 31; DB 2; Length 38;
Best Local Similarity 63.6%; Pred. No. 3.2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 7 NDVTTLRRENE 17
: || |||||
Db 24 DSVTARLRVE 34

RESULT 24
US-10-091-244A-13
; Sequence 13, Application US/10091244A
; Patent No. 7001748
; GENERAL INFORMATION:
; APPLICANT: Gokhale, Rajesh
; APPLICANT: Tsuji, Stuart
; APPLICANT: Khosla, Chaitan
; TITLE OF INVENTION: METHODS TO MEDIATE POLYKETIDE SYNTHASE
; TITLE OF INVENTION: MODULE EFFECTIVENESS
; FILE REFERENCE: 300622004620
; CURRENT APPLICATION NUMBER: US/10/091,244A
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 09/500,747
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: 60/119,363
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/272,985
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/272,987
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-Terminal Inter-polypeptide linker
US-10-091-244A-13

Query Match 32.3%; Score 31; DB 3; Length 38;
Best Local Similarity 63.6%; Pred. No. 3.2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 7 NDVTTLRRENE 17
: || |||||
Db 24 DSVTARLRVE 34

RESULT 25
US-09-187-859-1594
; Sequence 1594, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1594
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-187-859-1594

Query Match 31.2%; Score 30; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CNFNDVT 10
: || |||||
Db 1 CQINDVT 7

RESULT 26
US-09-839-542B-1594
; Sequence 1594, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1594
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-839-542B-1594

Query Match 31.2%; Score 30; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 CNFNDVT 10
: || |||||
Db 1 CQINDVT 7

RESULT 27
US-10-006-869-1594
; Sequence 1594, Application US/10006869
; Patent No. 6962969
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.

```
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006.869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1594
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-10-006-869-1594

Query Match          31.2%; Score 30; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CNFNDVT 10
      | | | | |
Db      1 CQINDVT 7

RESULT 28
US-09-187-859-1597
; Sequence 1597, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187.859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1597
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-187-859-1597

Query Match          31.2%; Score 30; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CNFNDVT 10
      | | | | |
Db      1 CQINDVT 7

RESULT 29
US-09-839-542B-1597
; Sequence 1597, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839.542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1597
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-09-839-542B-1597

Query Match          31.2%; Score 30; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CNFNDVT 10
      | | | | |
Db      1 CQINDVT 7

RESULT 30
US-10-006-869-1597
; Sequence 1597, Application US/10006869
; Patent No. 6962969
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006.869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1597
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
US-10-006-869-1597

Query Match          31.2%; Score 30; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CNFNDVT 10
      | | | | |
Db      1 CQINDVT 7

RESULT 31
US-08-758-621-21
; Sequence 21, Application US/08758621
; Patent No. 5846821
; GENERAL INFORMATION:
; APPLICANT: Gueriot, Mary Lou, and Eide, David J.
; TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/758,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/018,578
; FILING DATE: 29-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Silveri, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: DCI-099CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-758-621-21

Query Match 31.2%; Score 30; DB 1; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDTVTRLRENE 17
||| :|:|:
Db 3 NDTVTLPIKEDD 13

RESULT 32

US-09-107-858-21
; Sequence 21, Application US/09107858
; Patent No. 6162900
; GENERAL INFORMATION:
; APPLICANT: Guerillot, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/107,858
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758,621
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-21

Query Match 31.2%; Score 30; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDTVTRLRENE 17
||| :|:|:
Db 3 NDTVTLPIKEDD 13

RESULT 33

US-09-579-174-21
; Sequence 21, Application US/09579174
; Patent No. 6590140
; GENERAL INFORMATION:
; APPLICANT: Guerillot, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/579,174
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/107,858
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 08/758,621
; PRIOR FILING DATE: 1996-11-27

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-579-174-21

Query Match 31.2%; Score 30; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDTVTRLRENE 17
||| :|:|:
Db 3 NDTVTLPIKEDD 13

RESULT 34

US-09-084-303B-240
; Sequence 240, Application US/09084303B
; Patent No. 6627746
; GENERAL INFORMATION:
; APPLICANT: Doberstein, Stephen
; APPLICANT: Reddy, Bindu
; APPLICANT: Platt, Darren
; APPLICANT: Ferguson, Kimberly
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF C. ELEGANS INSULIN-LIKE GENES AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 7326-069-999
; CURRENT APPLICATION NUMBER: US/09/084,303B
; CURRENT FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-084-303B-240

Query Match 31.2%; Score 30; DB 2; Length 27;
Best Local Similarity 44.4%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CNFNDVTTR 12
| :|:|:
Db 14 CTMEDITTK 22

RESULT 35

US-08-952-568-14
; Sequence 14, Application US/08952568
; Patent No. 6037321
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Vasoactive Intestinal Peptide
; NUMBER OF SEQUENCES: 43
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,568
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA96/00280
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

```
; MOLECULE TYPE: protein
US-08-952-568-14

Query Match      31.2%; Score 30; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
   ||| |||
Db 6 FDTYTRLRK 15

RESULT 36
US-09-623-548A-453
; Sequence 453, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 453
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-453

Query Match      31.2%; Score 30; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
   ||| |||
Db 6 FDTYTRLRK 15

RESULT 37
US-09-623-548A-453
; Sequence 453, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
```

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; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 453
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-453

Query Match      31.2%; Score 30; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
   ||| |||
Db 6 FDTYTRLRK 15

RESULT 38
5496552-8
; Patent No. 5496552
; APPLICANT: KUBERASAMPATH, THANGAVEL;RUEGER, DAVID C.
; TITLE OF INVENTION:OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,252
; FILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 103,604
; FILING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: 179,406
; FILING DATE: 08-APR-1988
; SEQ ID NO:8
; LENGTH: 11
5496552-8

Query Match      30.2%; Score 29; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FEHCNFD 8
   |||
Db 1 FLHCQFSE 8

RESULT 39
US-08-460-309-23
; Sequence 23, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
```



```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-460-309-23
;
; Query Match 30.2%; Score 29; DB 1; Length 14;
; Best Local Similarity 38.5%; Pred. No. 2.3e+02;
; Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
;
; QY 4 CNFNDVTTTLREN 16
; Db 1 CSIVDIDTQNEEN 13
;
; RESULT 40
; US-08-125-077-23
; Sequence 23, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
```

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-125-077-23
;
; Query Match 30.2%; Score 29; DB 1; Length 14;
; Best Local Similarity 38.5%; Pred. No. 2.3e+02;
; Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
;
; QY 4 CNFNDVTTTLREN 16
; Db 1 CSIVDIDTQNEEN 13
;
; RESULT 41
; 5444158-4
; Patent No. 5444158
; APPLICANT: ENGVALL, EVA;SAMES, JOSHUA
; TITLE OF INVENTION: MEROSIN, NUCLEIC ACIDS ENCODING,
; FRAGMENTS AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/87,642
; FILING DATE: 08-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 587,689
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 472,319
; FILING DATE: 30-JAN-1990
; SEQ ID NO:4:
; LENGTH: 14
; 5444158-4
;
; Query Match 30.2%; Score 29; DB 7; Length 14;
; Best Local Similarity 38.5%; Pred. No. 2.3e+02;
; Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
;
; QY 4 CNFNDVTTTLREN 16
; Db 1 CSIVDIDTQNEEN 13
;
; RESULT 42
; US-10-769-803-5
; Sequence 5, Application US/10769803
; Patent No. 6911430
; GENERAL INFORMATION:
; APPLICANT: Gandhi, Salil Atul
; TITLE OF INVENTION: Compositions and Methods for Treating Ileus
; FILE REFERENCE: 8041-4000
; CURRENT APPLICATION NUMBER: US/10/769,803
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/507,122
; PRIOR FILING DATE: 2003-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 18
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa is Diphenylalanine
US-10-769-803-5

Query Match      30.2%; Score 29; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      6 FNDVTRLRE 15
Db      1 FTDYTRLRK 10

RESULT 43
US-09-962-756-63
; Sequence 63, Application US/09962756
; Patent No. 6875741
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-40SLUS1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-63

Query Match      30.2%; Score 29; DB 2; Length 21;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 EHCNFND 8
Db      8 EDCNFYD 14

RESULT 44
US-10-769-803-6
; Sequence 6, Application US/10769803
; Patent No. 6911430
; GENERAL INFORMATION:
; APPLICANT: Gandhi, Salil Atul
; TITLE OF INVENTION: Compositions and Methods for Treating Ileus
; FILE REFERENCE: 8041-4000
; CURRENT APPLICATION NUMBER: US/10/769,803
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/507,122
; PRIOR FILING DATE: 2003-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa is Diphenylalanine
US-10-769-803-6

Query Match      30.2%; Score 29; DB 2; Length 23;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      6 FNDVTRLRE 15
Db      1 FTDYTRLRK 10

RESULT 45
US-08-952-736A-8
; Sequence 8, Application US/08952736A
; Patent No. 6320026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell Growth Inhibitory Factor
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,736A
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-952-736A-8

Query Match      30.2%; Score 29; DB 2; Length 26;
Best Local Similarity 41.7%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTR 12
Db      12 FERTHYPDVTR 23

RESULT 46
US-08-952-736A-9
; Sequence 9, Application US/08952736A
; Patent No. 6320026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell Growth Inhibitory Factor
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,736A
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-952-736A-9

Query Match      30.2%; Score 29; DB 2; Length 26;
Best Local Similarity 41.7%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 FEHCNFDVTVTR 12
      || :|: ||
Db      12 FERTHPDIYTR 23

RESULT 47
US-08-413-708B-2
; Sequence 2, Application US/08413708B
; Patent No. 5972883
; GENERAL INFORMATION:
; APPLICANT: GOZES, Iilana
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: VIP, OR ANALOGUES DERIVATIVES AND FRAGMENTS THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,708B
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,671
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 105061
; FILING DATE: 16-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GOZES-3A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-413-708B-2

Query Match      30.2%; Score 29; DB 1; Length 28;
Best Local Similarity 53.3%; Pred. No. 4.9e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY      3 HCN--FNDVTVTRLE 15
      ||| :|: |||
Db      1 HSNAXFTDNYTRLRK 15

RESULT 48
US-09-528-200-53

; Sequence 53, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARTSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-53

Query Match      30.2%; Score 29; DB 2; Length 28;
Best Local Similarity 46.7%; Pred. No. 4.9e+02;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      1 FEHCNFDVTVTRLE 15
      ||| :|: |||
Db      1 FSDAVFTDNYTRLRK 15

RESULT 49
US-09-528-200-112
; Sequence 112, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARTSEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-112

Query Match      30.2%; Score 29; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      6 FNDVTRLRENE 17
Db      6 FTDNYTRLRQQ 17

RESULT 50
US-08-416-709-2
; Sequence 2, Application US/08416709
; Patent No. 5695970
; GENERAL INFORMATION:
; APPLICANT: YU, Shukun
; APPLICANT: PEDERSEN, Marianne
; APPLICANT: KENNE, Lennart
; TITLE OF INVENTION: A new glucan lyase producing
; TITLE OF INVENTION: 1,5-anhydrofructose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - 4th Floor
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/416,709
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203084-0
; FILING DATE: 21-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard B
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF-DIAZ-MEC
; TELEPHONE: 703-683-0500
; TELEFAX: 703-683-1080
; TELEX: 89-9124 BATO AGTN
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Gracilariopsis lemaneiformis/Gracilaria
; ORGANISM: verrucosa
US-08-416-709-2

Query Match      30.2%; Score 29; DB 1; Length 30;
Best Local Similarity 50.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      8 DVTTRLRENE 17
Db      7 DITPFLRND 16

RESULT 51
US-10-144-929-117
; Sequence 117, Application US/10144929
; Patent No. 6881823
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2014P1

; CURRENT APPLICATION NUMBER: US/10/144,929
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: PCT/US98/17044
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals stop translation
US-10-144-929-117

Query Match      30.2%; Score 29; DB 2; Length 36;
Best Local Similarity 30.8%; Pred. No. 6.5e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 FEHCNFNDVTRL 13
Db      4 FNQCDYDPSLQL 16

RESULT 52
US-08-682-485A-4
; Sequence 4, Application US/08682485A
; Patent No. 5763568
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PLO722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax robustus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
; OTHER INFORMATION: /note= "this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
US-08-682-485A-4

Query Match 30.2%; Score 29; DB 1; Length 37;
Best Local Similarity 40.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 EHCNFDVTTLRLEN 16
Db 15 EHCCSGSCTYKENEN 29

RESULT 53
US-08-933-314-4
; Sequence 4, Application US/08933314
; Patent No. 5959182
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN B.H.
; APPLICANT: TYLER, MARGARET J
; APPLICANT: VONARY, EDWARD I
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,314
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU P0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax robustus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
; OTHER INFORMATION: /note= "this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
US-08-933-314-4

Query Match 30.2%; Score 29; DB 1; Length 37;
Best Local Similarity 40.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 EHCNFDVTTLRLEN 16
Db 15 EHCCSGSCTYKENEN 29

RESULT 54
US-09-605-703B-1458
; Sequence 1458, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habehauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1458
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1458

Query Match 30.2%; Score 29; DB 2; Length 40;
Best Local Similarity 35.7%; Pred. No. 7.3e+02;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 EHCNFDVTTLRLE 15
Db 3 EACDFRDSLSNLD 16

RESULT 55
US-08-493-235-12
; Sequence 12, Application US/08493235
; Patent No. 5840313
; GENERAL INFORMATION:
; APPLICANT: Vahlne, Anders
; APPLICANT: Svennerholm, Bo
; APPLICANT: Rymo, Lars
; APPLICANT: Jeansson, Stig
; APPLICANT: Horal, Peter
; TITLE OF INVENTION: PEPTIDES FOR USE IN VACCINATION AND
; TITLE OF INVENTION: INDUCTION OF NEUTRALIZING ANTIBODIES AGAINST HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
```

```

/ ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
/ STREET: 620 NEWPORT CENTER DRIVE 16TH FLOOR
/ CITY: NEWPORT BEACH
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/493,235
/ FILING DATE: 20/JUN/1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kaiser, AnneMarie
/ REGISTRATION NUMBER: 37,649
/ REFERENCE/DOCKET NUMBER: METRICS.12CPC1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-235-8550
/ TELEFAX: 619-235-0176
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 25 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ US-08-493-235-12

Query Match 29.7%; Score 28.5; DB 1;
Best Local Similarity 38.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 6; Mismatches 1;

QY 2 EHCNFNDVTVTLRL 14
   :|:||:||:|
DB 4 KNCSPN-ISTSIR 15

RESULT 56
US-08-468-011A-25
/ Sequence 25, Application US/08468011A
/ Patent No. 6030804
/ GENERAL INFORMATION:
/ APPLICANT: Soppet, Daniel R
/ APPLICANT: Yi, Li
/ APPLICANT: Rosen, Craig A
/ APPLICANT: Ruben, Steven
/ TITLE OF INVENTION: G-Protein Parathyroid Hormone
/ TITLE OF INVENTION: HLTDPG74
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Ce
/ ADDRESSEE: Stewart & Olstein
/ STREET: 6 Becker Farm Road
/ CITY: Roseland
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07068-1739
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 INCH DISKETTE
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WORD PERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,011A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:

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Query Match      29.7%; Score 28.5; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 3 HCNFNDVTTLRRENE 17
Db 12 HCLRLQD---KLEQEQ 23

RESULT 59
US-09-695-950-6
; Sequence 6, Application US/09695950
; Patent No. 6265378
; GENERAL INFORMATION:
; APPLICANT: Broze, George J., Jr.
; TITLE OF INVENTION: Protein Z-Dependent Protease Inhibitor
; FILE REFERENCE: WU-3110/1
; CURRENT APPLICATION NUMBER: US/09/695,950
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/271,608
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Word Perfect 5.0
; SEQ ID NO 6
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: /note="synthetic construct"
US-09-695-950-6

Query Match      29.7%; Score 28.5; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 3 HCNFNDVTTLRRENE 17
Db 12 HCLRLQD---KLEQEQ 23

RESULT 60
US-09-696-147-6
; Sequence 6, Application US/09696147
; Patent No. 6271367
; GENERAL INFORMATION:
; APPLICANT: Broze, George J., Jr.
; TITLE OF INVENTION: Protein Z-Dependent Protease Inhibitor
; FILE REFERENCE: WU-3110/1
; CURRENT APPLICATION NUMBER: US/09/696,147
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: 09/271,608
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Word Perfect 5.0
; SEQ ID NO 6
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: /note="synthetic construct"
US-09-696-147-6

Query Match      29.7%; Score 28.5; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 3 HCNFNDVTTLRRENE 17
Db 12 HCLRLQD---KLEQEQ 23

RESULT 61
US-08-908-371B-4
; Sequence 4, Application US/08908371B
; Patent No. 6331610
; GENERAL INFORMATION:
; APPLICANT: Bourinbalar, Aldar S.
```


;; TITLE OF INVENTION: A Method for Preventing and Treating
;; TITLE OF INVENTION: AIDS and HIV Infection Using Select Peptides From the
;; TITLE OF INVENTION: Beta Subunit of Human Chorionic Gonadotropin
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Metatron, Inc.
;; STREET: 367 Bay Shore Road
;; CITY: Deer Park
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 11729
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 in. diskette (1.44megabytes)
;; COMPUTER: IBM Compatible PC
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: WORD 6.0 ASCII TEXT CONVERSION ONLY
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/908,371B
;; FILING DATE: 07-AUG-1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/044,937
;; FILING DATE: 25-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: COLEMAN, HENRY D.
;; REGISTRATION NUMBER: 32,559
;; REFERENCE/DOCKET NUMBER: M31-013
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 679-9121
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acid units
;; TYPE: Amino Acid
;; STRANDEDNESS: Single Stranded
;; TOPOLOGY: N/A
;; MOLECULE TYPE: Protein Subunit
;; DESCRIPTION: 13 amino acids corresponding to amino
;; DESCRIPTION: acids 50-62 of the beta subunit of human chorionic
;; DESCRIPTION: gonadotropin
;; HYPOTHETICAL: No
;; ANTI-SENSE: No
;; IMMEDIATE SOURCE: Chemical Synthesis
;; POSITION IN GENOME: N/A
;; FEATURE:
;; NAME/KEY: Oligopeptide corresponding to Amino Acids 50-62
;; NAME/KEY: of Beta Subunit of Human Chorionic Gonadotropin
;; LOCATION: Beta subunit of Human Chorionic Gonadotropin
;; IDENTIFICATION METHOD: Chemical synthesis
;; PUBLICATION INFORMATION:
;; AUTHORS: STEVENS, Vernon C.
;; TITLE: ANTIGENIC MODIFICATION OF AMINO ACIDS
;; JOURNAL: UNITED STATES PATENT NUMBER 4,302,386
;; VOLUME: N/A
;; PAGES: N/A
;; DATE: No. 6331610ember 24, 1981

US-08-908-371B-4
Query Match 29.2%; Score 28; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CNFNVDV 9
Db 8 CNYRDV 13

RESULT 64

US-09-701-080C-23
; Sequence 23, Application US/09701080C
; Patent No. 6864054
; GENERAL INFORMATION:
; APPLICANT: THORPE, Alan
; APPLICANT: DUVE, Hanne
; APPLICANT: JOHNSEN, Anders Holten
; TITLE OF INVENTION: NEUROPEPTIDES AND THEIR USE AS
; INSECTICIDES

;; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
;; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 FC
;; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
;; FILE REFERENCE: N73477C GCW
;; CURRENT APPLICATION NUMBER: US/09/701,080C
;; CURRENT FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: GB 9811303.8
;; PRIOR FILING DATE: 1998-05-26
;; PRIOR APPLICATION NUMBER: GB 9900157.0
;; PRIOR FILING DATE: 1999-01-05
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 23
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:derived from E2F
US-09-701-080C-23

Query Match 29.2%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CNFNVDV 10
Db 3 CDFGDLT 9

RESULT 65

US-09-701-080C-28
; Sequence 28, Application US/09701080C
; Patent No. 6864054
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 FC
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from E2F
US-09-701-080C-28

Query Match 29.2%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CNFNVDV 10
Db 3 CDFGDLT 9

RESULT 66

US-08-522-326-6
; Sequence 6, Application US/08522326
; Patent No. 5753615
; GENERAL INFORMATION:
; APPLICANT: THORPE, Alan
; APPLICANT: DUVE, Hanne
; APPLICANT: JOHNSEN, Anders Holten
; TITLE OF INVENTION: NEUROPEPTIDES AND THEIR USE AS
; INSECTICIDES

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (SPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,326
FILING DATE: 12-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9305120.9
FILING DATE: 12-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUDWIG, STEVEN R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0623.0340000
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Manduca sexta
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "pyro-glutamic acid"
PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO 94/20530 A2
FILING DATE: 14-MAR-1994
PUBLICATION DATE: 15-SEP-1994
US-08-522-326-6

Query Match 29.2%; Score 28; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVDT 10
DB 4 FRQCYFNPIIS 13

RESULT 67
US-09-220-415-34
Sequence 34, Application US/09220415
Patent No. 6583109
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Ikandar, Yanto
TITLE OF INVENTION: Therapeutic Polypeptides from (-HCG and Derivatives
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Patent In
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,415
FILING DATE: 24-DEC-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Steven J. Hultquist
REGISTRATION NUMBER: 28,021
REFERENCE/DOCKET NUMBER: 4115-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-220-415-34

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNFNDDV 9
DB 12 CNYRDV 17

RESULT 68
US-09-675-776-34
Sequence 34, Application US/09675776
Patent No. 6596688
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Ikandar, Yanto
TITLE OF INVENTION: METHOD FOR PROMOTING HEMATOPOIESIS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Patent In
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675,776
FILING DATE: 29-SEP-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998

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; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Marianne Fuierer
; REGISTRATION NUMBER: 39,983
; REFERENCE/DOCKET NUMBER: 4115-116 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-676-739-34
Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNFNDV 9
DB 12 CNYRDV 17

; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Marianne Fuierer
; REGISTRATION NUMBER: 39,983
; REFERENCE/DOCKET NUMBER: 4115-116 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-675-362-34
Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNFNDV 9
DB 12 CNYRDV 17

; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Marianne Fuierer
; REGISTRATION NUMBER: 39,983
; REFERENCE/DOCKET NUMBER: 4115-116 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-675-362-34

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 4 CNFNDV 9
||: ||
DB 12 CNYRDV 17

RESULT 71

US-09-677-152-34
; Sequence 34, Application US/09677152
; Patent No. 6805882
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: Therapeutic Fractions of Sources of hCG
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/677,152
FILING DATE: 02-OCT-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: US98 09/220,415
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Steven J. Hultquist
REGISTRATION NUMBER: 28,021
REFERENCE/DOCKET NUMBER: 4115-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-677-152-34

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 4 CNFNDV 9
||: ||
DB 12 CNYRDV 17

RESULT 72

US-07-928-930A-9
; Sequence 9, Application US/07928930A
; Patent No. 534822
; GENERAL INFORMATION:
; APPLICANT: Levine, Daniel M.; Parker, Thomas S.;
; Rubinfeld, Albert L.
; TITLE OF INVENTION: Methods Useful in Endotoxin
; TITLE OF INVENTION: Prophylaxis and Therapy
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,930A
FILING DATE: 19920812
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5344822man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: ROGO 206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

US-07-928-930A-9

Query Match 29.2%; Score 28; DB 1; Length 22;
Best Local Similarity 55.6%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 DVTTLREN 16
||: ||: ||
DB 5 DLQTKLNN 13

RESULT 73

US-08-288-568-9
; Sequence 9, Application US/08288568
; Patent No. 5506218
; GENERAL INFORMATION:
; APPLICANT: Parker, Thomas S.; Levine, Daniel M.;
; Rubinfeld, Albert L.; Gordon, Bruce R.; Saal, Stuart D.
; TITLE OF INVENTION: Methods Useful in Endotoxin Based
; TITLE OF INVENTION: Prophylaxis and Therapy
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS

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; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,568
; FILING DATE: 10-AUGUST-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07453
; FILING DATE: 9-AUGUST-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,930
; FILING DATE: 12-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5506218man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: ROGO 211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-288-568-9

Query Match          29.2%; Score 28; DB 1; Length 22;
Best Local Similarity 55.6%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      8 DVVTRLREN 16
Db      5 DLQTKLNEN 13

RESULT 74
US-08-487-461-9
; Sequence 9, Application US/08487461
; Patent No. 5587366
; GENERAL INFORMATION:
; APPLICANT: Parker, Thomas S.; Levine, Daniel M.;
; APPLICANT: Rubin, Albert L; Gordon, Bruce R; Saal, Stuart D.
; TITLE OF INVENTION: Methods Useful in Endotoxin Based
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb
; MEDIUM TYPE: storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,461
; FILING DATE: June 7, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07453
; FILING DATE: 9-AUGUST-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5587366man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: ROGO 211.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

Qy      8 DVVTRLREN 16
Db      5 DLQTKLNEN 13

RESULT 75
US-08-432-691-9
; Sequence 9, Application US/08432691
; Patent No. 5614507
; GENERAL INFORMATION:
; APPLICANT: Parker, Thomas S.; Levine, Daniel M.;
; APPLICANT: Rubin, Albert L; Gordon, Bruce R; Saal, Stuart D.
; TITLE OF INVENTION: Methods Useful in Endotoxin Based
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb
; MEDIUM TYPE: storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,691
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/288,568
; FILING DATE: 10-AUGUST-1994
; APPLICATION NUMBER: PCT/US93/07453
; FILING DATE: 9-AUGUST-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,930
; FILING DATE: 12-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5614507man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: ROGO 211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-432-691-9

Query Match          29.2%; Score 28; DB 1; Length 22;
Best Local Similarity 55.6%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      8 DVVTRLREN 16
Db      5 DLQTKLNEN 13

RESULT 76
US-08-487-461-9
; Sequence 9, Application US/08487461
; Patent No. 5587366
; GENERAL INFORMATION:
; APPLICANT: Parker, Thomas S.; Levine, Daniel M.;
; APPLICANT: Rubin, Albert L; Gordon, Bruce R; Saal, Stuart D.
; TITLE OF INVENTION: Methods Useful in Endotoxin Based
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb
; MEDIUM TYPE: storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,461
; FILING DATE: June 7, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07453
; FILING DATE: 9-AUGUST-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5587366man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: ROGO 211.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

Qy      8 DVVTRLREN 16
Db      5 DLQTKLNEN 13
```

RESULT 76
US-08-487-459-9
; Sequence 9, Application US/08487459
; Patent No. 5674855
; GENERAL INFORMATION:
; APPLICANT: Levine, Daniel M.; Parker, Thomas S.;
; APPLICANT: Rubin, Albert L.; Gordon, Bruce R.; Saal, Stuart D.
; TITLE OF INVENTION: Methods Useful in Endotoxin Based
; TITLE OF INVENTION: Prophylaxis and Therapy
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb
; MEDIUM TYPE: storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,459
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07453
; FILING DATE: 9-AUGUST-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/928,930
; FILING DATE: 12-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5674855man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: ROGO 211.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-487-459-9
Query Match 29.2%; Score 28; DB 1; Length 22;
Best Local Similarity 55.6%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 8 DVTTTLREN 16
Db 5 DLQTKLNN 13
RESULT 77
US-08-029-402-5
; Sequence 5, Application US/08029402
; Patent No. 5516657
; GENERAL INFORMATION:
; APPLICANT: Murphy, Cheryl I.
; APPLICANT: Young, Elihu
; TITLE OF INVENTION: Baculovirus Vectors For Expression of
; TITLE OF INVENTION: Secretory and Membrane-Bound Proteins
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.

COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,402
FILING DATE: 19930305
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0614.0860001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-029-402-5
Query Match 29.2%; Score 28; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EHCN 5
Db 22 EHCN 25
RESULT 78
US-08-484-635-105
; Sequence 105, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-105

Query Match 29.2%; Score 28; DB 1; Length 25;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CNFNDVT 10
Db 4 CNFGPIT 10

RESULT 79
US-08-484-631-105
; Sequence 105, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-105

Query Match 29.2%; Score 28; DB 1; Length 25;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CNFNDVT 10
Db 4 CNFGPIT 10

RESULT 81
US-08-029-402-7
; Sequence 7, Application US/08029402
; Patent No. 5516657
; GENERAL INFORMATION:
```


APPLICANT: Murphy, Cheryl I.
APPLICANT: Young, Elihu
TITLE OF INVENTION: Baculovirus Vectors For Expression of
TITLE OF INVENTION: Secretory and Membrane-Bound Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,402
FILING DATE: 19930305
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0614.0860001
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-029-402-7

Query Match 29.2%; Score 28; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHCN 5
DB 22 EHCN 25

RESULT 82
US-08-029-402-9
Sequence 9, Application US/08029402
Patent No. 5516657
GENERAL INFORMATION:
APPLICANT: Murphy, Cheryl I.
APPLICANT: Young, Elihu
TITLE OF INVENTION: Baculovirus Vectors For Expression of
TITLE OF INVENTION: Secretory and Membrane-Bound Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,402
FILING DATE: 19930305
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.

REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0614.0860001
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-029-402-9

Query Match 29.2%; Score 28; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHCN 5
DB 22 EHCN 25

RESULT 83
US-08-208-264A-23
Sequence 23, Application US/08208264A
Patent No. 6057287
GENERAL INFORMATION:
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C.
TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"
TITLE OF INVENTION: PROTEINS AND ANALOGUES THEREOF
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,264A
FILING DATE: 10-MAR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,964
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: DYX-006.1 US
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-208-264A-23

Query Match 29.2%; Score 28; DB 2; Length 27;
Best Local Similarity 66.7%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CNFNDVTR 12
| | | | |

Db 8 CCFDVTTR 16

RESULT 84

US-09-421-097-23

Sequence 23, Application US/09421097

Patent No. 6333402

GENERAL INFORMATION:

APPLICANT: MARKLAND, William

APPLICANT: LADNER, Robert C.

TITLE OF INVENTION: KALLIKREIN-BINDING "KUNITZ DOMAIN"

TITLE OF INVENTION: PROTEINS AND ANALOGUES THEREOF

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yankwich & Associates

STREET: 130 Bishop Allen Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02139

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5-inch diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Microsoft Windows 98

SOFTWARE: Microsoft Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421.097

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/208,264

FILING DATE: 10-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/179,964

FILING DATE: 11-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Leon R. Yankwich

REGISTRATION NUMBER: 30,237

REFERENCE/DOCKET NUMBER: DYX-006.1 US-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-491-4343

TELEFAX: 617-491-8801

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-421-097-23

Query Match 29.2%; Score 28; DB 2; Length 27;

Best Local Similarity 66.7%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCFDVTTR 12

Db 8 CCFDVTTR 16

RESULT 85

US-09-288-143-140

Sequence 140, Application US/09288143

Patent No. 6433139

GENERAL INFORMATION:

APPLICANT: Brewer et al.

TITLE OF INVENTION: 53 Human Secreted Proteins

FILE REFERENCE: P2018P1

CURRENT APPLICATION NUMBER: US/09/288,143

CURRENT FILING DATE: 1999-04-08

EARLIER APPLICATION NUMBER: PCT/US98/21142

EARLIER FILING DATE: 1998-10-08

EARLIER APPLICATION NUMBER: 60/061,463

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,529

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/071,498

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,527

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,536

; EARLIER FILING DATE: 1997-10-09

; EARLIER APPLICATION NUMBER: 60/061,532

; EARLIER FILING DATE: 1997-10-09

NUMBER OF SEQ ID NOS: 219

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 140

LENGTH: 28

TYPE: PRT

ORGANISM: Homo sapiens

US-09-288-143-140

Query Match 29.2%; Score 28; DB 2; Length 28;

Best Local Similarity 50.0%; Pred. No. 7.3e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 FNDVTTTLRENE 17

Db 7 FSDKTGTLTENK 18

RESULT 86

US-09-528-200-110

Sequence 110, Application US/09528200

Patent No. 6630570

GENERAL INFORMATION:

APPLICANT: BECKER, ANDREAS

APPLICANT: SEMMLER, WOLFHARD

APPLICANT: WEIDENMANN, BERTRAM

APPLICANT: HESSNIUS, CARSTEN

APPLICANT: VOLKMER-ENGERT, RUDOLF

APPLICANT: SCHNEIDER-MERGENER, JENS

APPLICANT: BHARGAVA, SARAH

TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA

FILE REFERENCE: SCH-1731

CURRENT APPLICATION NUMBER: US/09/528,200

CURRENT FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: DE 199 17 713.9

PRIOR FILING DATE: 1999-09-04

NUMBER OF SEQ ID NOS: 196

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 110

LENGTH: 28

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-09-528-200-110

Query Match 29.2%; Score 28; DB 2; Length 28;

Best Local Similarity 50.0%; Pred. No. 7.3e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 FNDVTTTLRENE 17

Db 6 FTDNYTLRLKQK 17

RESULT 87

US-09-984-429-140

Sequence 140, Application US/09984429

Patent No. 7026447

GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,591
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR FILING DATE: 1999-04-08
PRIOR APPLICATION NUMBER: PCT/US98/21142
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/071,498
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,532
PRIOR FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 140
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-429-140

Query Match 29.2%; Score 28; DB 3; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 FNDVTRLRENE 17
|:|:|:|:|:
DB 7 FSDKTGTLTENK 18

RESULT 88
US-08-029-402-19
Sequence 19, Application US/08029402
Patent No. 5516657
GENERAL INFORMATION:
APPLICANT: Murphy, Cheryl I.
APPLICANT: Young, Elihu
TITLE OF INVENTION: Baculovirus Vectors For Expression of
TITLE OF INVENTION: Secretory and Membrane-Bound Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSES: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,402
FILING DATE: 19930305
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0614.0860001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-029-402-19

Query Match 29.2%; Score 28; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHCN 5
|:|:|:
DB 22 EHCN 25

RESULT 89
US-09-092-297A-19
Sequence 19, Application US/09092297A
Patent No. 6949357
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Stephen D.
APPLICANT: Yu, Hong
TITLE OF INVENTION: Reagents And Methods Useful For
TITLE OF INVENTION: Detecting Diseases Of The Urinary Tract
FILE REFERENCE: 6107.US.P1
CURRENT APPLICATION NUMBER: US/09/092,297A
CURRENT FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 08/869,579
PRIOR FILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-09-092-297A-19

Query Match 29.2%; Score 28; DB 2; Length 30;
Best Local Similarity 33.3%; Pred. No. 7.8e+02;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 EHCNFNDVTRL 13
|:|:|:|:
DB 17 QHCYDDAVVPL 28

RESULT 90
US-09-671-773C-77
Sequence 77, Application US/09671773C
Patent No. 6972319
GENERAL INFORMATION:
APPLICANT: Pan, Clark
APPLICANT: Tsutsumi, Manami
APPLICANT: Shanafelt, Armen B.
TITLE OF INVENTION: Pituitary Adenylate Cyclase Activating Peptide (PACAP) Receptor
TITLE OF INVENTION: (R3) Agonists an Their Pharmacological Methods of Use
FILE REFERENCE: MSB 7272P2

; CURRENT APPLICATION NUMBER: US/09/671,773C
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/595,280
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/407,832
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(31)
US-09-671-773C-77

Query Match 29.2%; Score 28; DB 2; Length 31;
Best Local Similarity 60.0%; Pred. No. 8.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
| | | | |
Db 6 FTDQYTRLRK 15

RESULT 91

US-09-671-773C-78
; Sequence 78, Application US/09671773C
; Patent No. 6972319
; GENERAL INFORMATION:
; APPLICANT: Pan, Clark
; APPLICANT: Teutsumi, Manami
; APPLICANT: Shanafelt, Armen B.
; TITLE OF INVENTION: Pituitary Adenylate Cyclase Activating Peptide (PACAP) Receptor 3
; FILE REFERENCE: MSB 7272P2
; CURRENT APPLICATION NUMBER: US/09/671,773C
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/595,280
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/407,832
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(31)
US-09-671-773C-78

Query Match 29.2%; Score 28; DB 2; Length 31;
Best Local Similarity 60.0%; Pred. No. 8.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
| | | | |
Db 6 FTDQYTRLRK 15

RESULT 92

US-09-671-773C-81
; Sequence 81, Application US/09671773C
; Patent No. 6972319
; GENERAL INFORMATION:
; APPLICANT: Pan, Clark

; APPLICANT: Teutsumi, Manami
; APPLICANT: Shanafelt, Armen B.
; TITLE OF INVENTION: Pituitary Adenylate Cyclase Activating Peptide (PACAP) Receptor 3
; FILE REFERENCE: MSB 7272P2
; CURRENT APPLICATION NUMBER: US/09/671,773C
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/595,280
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/407,832
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(31)
US-09-671-773C-81

Query Match 29.2%; Score 28; DB 2; Length 31;
Best Local Similarity 60.0%; Pred. No. 8.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
| | | | |
Db 6 FTDQYTRLRK 15

RESULT 93

US-09-671-773C-82
; Sequence 82, Application US/09671773C
; Patent No. 6972319
; GENERAL INFORMATION:
; APPLICANT: Pan, Clark
; APPLICANT: Teutsumi, Manami
; APPLICANT: Shanafelt, Armen B.
; TITLE OF INVENTION: Pituitary Adenylate Cyclase Activating Peptide (PACAP) Receptor 3
; FILE REFERENCE: MSB 7272P2
; CURRENT APPLICATION NUMBER: US/09/671,773C
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/595,280
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/407,832
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(31)
US-09-671-773C-82

Query Match 29.2%; Score 28; DB 2; Length 31;
Best Local Similarity 60.0%; Pred. No. 8.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTRLRE 15
| | | | |
Db 6 FTDQYTRLRK 15

RESULT 94

US-08-867-087B-63
; Sequence 63, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-63

Query Match 29.2%; Score 28; DB 1; Length 33;
Best Local Similarity 42.9%; Pred. No. 8.7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFN 7
: : : : :
Db 12 YOHCCYN 18

RESULT 95
US-09-471-276-1544
; Sequence 1544, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712

; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1544
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1544

Query Match 29.2%; Score 28; DB 2; Length 33;
Best Local Similarity 80.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCN 5
: : : : :
Db 28 PAHCN 32

RESULT 96
US-08-867-087B-64
; Sequence 64, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-64

Query Match 29.2%; Score 28; DB 1; Length 34;
Best Local Similarity 42.9%; Pred. No. 9e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFN 7
: : : : :
Db 12 YOHCCYN 18

RESULT 97
US-08-867-087B-57
; Sequence 57, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 228-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-867-087B-57

Query Match 29.2%; Score 28; DB 1; Length 40;
Best Local Similarity 42.9%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FEHCNFN 7
; : : : :
; 15 YQKCNYN 21

RESULT 98
US-08-556-597-133
; Sequence 133, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA

ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-556-597-133

Query Match 28.6%; Score 27.5; DB 1; Length 10;
Best Local Similarity 46.2%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

Qy 2 EHCNFNDVTRLR 14
; : : : :
; 1 KHGS---IHTRLR 10

RESULT 99
US-08-218-025A-43
; Sequence 43, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-218-025A-43

Query Match 28.6%; Score 27.5; DB 1; Length 20;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2 EHCNFNDVTTRL 13
:::|:|:|:
Db 10 KNCSEF-ITTSI 20

RESULT 100

US-08-306-116A-6
Sequence 6, Application US/08306116A
Patent No. 5691135
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Goodglick, Lee A.
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERANTIGEN BINDING TO GP120
TITLE OF INVENTION: FROM HIV
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,116A
FILING DATE: 14-SEP-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/259,669
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: UCLA004.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-306-116A-6

Query Match 28.6%; Score 27.5; DB 1; Length 20;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 2 EHCNFNDVTTRL 13
:::|:|:|:
Db 10 KNCSEF-ITTSI 20

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Title: US-09-020-393B-3_COPY_42_58
 Perfect score: 96
 Sequence: 1 FEHCNFNDVTRLRENE 17

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
 587501

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- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	23	5	US-10-870-342A-14
2	96	100.0	26	5	US-10-870-342A-20
3	96	100.0	30	5	US-10-870-342A-15
4	96	100.0	36	6	US-11-006-031-44
5	96	100.0	36	6	US-11-194-110-44
6	91	94.8	18	5	US-10-870-342A-13
7	80	83.3	18	5	US-10-870-342A-19
8	77	80.2	25	5	US-10-870-342A-41
9	62	64.6	21	5	US-10-870-342A-45
10	52	54.2	13	5	US-10-870-342A-4
11	52	54.2	16	5	US-10-870-342A-16
12	52	54.2	14	5	US-10-870-342A-22
13	48	50.0	14	5	US-10-870-342A-23
14	46	47.9	18	5	US-10-870-342A-24
15	44	45.8	21	5	US-10-870-342A-44
16	43	44.8	14	5	US-10-870-342A-3
17	43	44.8	14	5	US-10-870-342A-10
18	43	44.8	15	3	US-09-835-752-1
19	43	44.8	15	5	US-10-833-581-1
20	40	41.7	13	5	US-10-870-342A-21
21	40	41.7	17	5	US-10-870-342A-17
22	40	41.7	19	5	US-10-870-342A-43
23	39	40.6	18	4	US-10-206-699-264
24	39	40.6	22	4	US-10-206-699-270
25	36	37.5	14	5	US-10-813-638-1248
26	36	37.5	40	4	US-10-424-599-175430
27	35	36.5	29	5	US-10-656-894-20

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30	35	36.5	35	5	US-10-656-894-15	Sequence 15, Appl
31	35	36.5	38	4	US-10-437-963-195917	Sequence 195917,
32	34.5	35.9	34	4	US-10-038-407-2	Sequence 2, Appli
33	34	35.4	18	4	US-10-206-699-260	Sequence 260, App
34	34	35.4	20	4	US-10-449-548-11	Sequence 11, Appl
35	34	35.4	22	4	US-10-206-699-266	Sequence 266, App
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37	34	35.4	25	5	US-10-775-204-1704	Sequence 1704, Ap
38	34	35.4	25	5	US-10-775-204-1706	Sequence 1706, Ap
39	34	35.4	25	5	US-10-775-204-1766	Sequence 1766, Ap
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42	34	35.4	27	5	US-10-775-204-1707	Sequence 1707, Ap
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44	34	35.4	40	4	US-10-038-612-56	Sequence 56, Appl
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47	33	34.4	28	3	US-09-929-818-106	Sequence 106, App
48	33	34.4	28	3	US-09-929-818-123	Sequence 123, App
49	33	34.4	28	6	US-11-262-067-106	Sequence 106, App
50	33	34.4	28	6	US-11-262-067-123	Sequence 123, App
51	33	34.4	30	4	US-10-600-070-28	Sequence 28, Appl
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57	32	33.3	14	4	US-10-206-699-7	Sequence 7, Appli
58	32	33.3	15	5	US-10-522-297-19	Sequence 19, Appl
59	32	33.3	15	5	US-10-522-297-20	Sequence 20, Appl
60	32	33.3	15	5	US-10-530-061-1759	Sequence 1759, Ap
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66	32	33.3	18	6	US-11-152-974A-117	Sequence 117, App
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79	32	33.3	36	6	US-11-004-399-851	Sequence 3346, Ap
80	32	33.3	36	6	US-11-004-399-3346	Sequence 3625, Ap
81	32	33.3	36	6	US-11-004-399-3625	Sequence 538, App
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86	32	33.3	15	5	US-09-989-919-123	Sequence 18, Appl
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91	31	32.3	21	5	US-10-895-226-31	Sequence 806, App
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94	31	32.3	21	5	US-10-522-297-5	Sequence 267, App
95	31	32.3	22	4	US-10-206-699-267	Sequence 38, Appl
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97	31	32.3	26	3	US-09-833-245-695	Sequence 695, App
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106	31	32.3	33	4	US-10-425-115-228642	Sequence 16, Appl	179	29	30.2	22	5	US-10-769-803-6	Sequence 6, Appl
107	31	32.3	34	4	US-10-091-244A-16	Sequence 210, App	180	29	30.2	22	5	US-10-626-719-53	Sequence 53, Appl
108	31	32.3	34	4	US-10-218-102-210	Sequence 210, App	181	29	30.2	28	5	US-10-626-719-112	Sequence 112, App
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139	30	31.2	28	6	US-11-262-067-11	Sequence 11, Appl	212	28.5	29.7	16	4	US-10-062-710-39	Sequence 39, Appl
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157	29	30.2	12	4	US-10-462-262-202	Sequence 202, App	230	28	29.2	15	4	US-10-213-821-184	Sequence 184, App
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257	28	29.2	28	5	US-10-626-719-110	Sequence 110, App	330	28	29.2	31	4	US-10-618-126A-1	Sequence 1, Appl
258	28	29.2	28	6	US-11-262-067-103	Sequence 103, App	331	28	29.2	31	4	US-10-618-126A-2	Sequence 2, Appl
259	28	29.2	28	6	US-11-262-067-109	Sequence 109, App	332	28	29.2	31	4	US-10-618-126A-3	Sequence 3, Appl
260	28	29.2	28	6	US-11-262-067-110	Sequence 110, App	333	28	29.2	31	4	US-10-618-126A-5	Sequence 5, Appl
261	28	29.2	28	6	US-11-262-067-112	Sequence 112, App	334	28	29.2	31	4	US-10-618-126A-6	Sequence 6, Appl
262	28	29.2	28	6	US-11-262-067-120	Sequence 120, App	335	28	29.2	31	4	US-10-618-126A-8	Sequence 8, Appl
263	28	29.2	28	6	US-11-262-067-156	Sequence 156, App	336	28	29.2	31	4	US-10-618-126A-9	Sequence 9, Appl
264	28	29.2	28	6	US-11-262-067-162	Sequence 162, App	337	28	29.2	31	4	US-10-618-126A-9	Sequence 9, Appl
265	28	29.2	28	6	US-11-262-067-182	Sequence 182, App	338	28	29.2	31	4	US-10-618-126A-11	Sequence 11, Appl
266	28	29.2	28	9	US-10-211-088-136	Sequence 136, App	339	28	29.2	31	4	US-10-618-126A-77	Sequence 77, Appl
267	28	29.2	28	4	US-10-264-049-4079	Sequence 4079, App	340	28	29.2	31	4	US-10-618-126A-78	Sequence 78, Appl
268	28	29.2	28	4	US-10-618-126A-4	Sequence 4, Appl	341	28	29.2	31	4	US-10-618-126A-79	Sequence 79, Appl
269	28	29.2	28	4	US-10-437-963-201159	Sequence 201159, App	342	28	29.2	31	4	US-10-618-126A-81	Sequence 81, Appl
270	28	29.2	28	3	US-09-092-297-19	Sequence 19, Appl	343	28	29.2	31	4	US-10-618-126A-82	Sequence 82, Appl
271	28	29.2	30	3	US-10-618-126A-7	Sequence 7, Appl	344	28	29.2	31	4	US-10-618-126A-84	Sequence 84, Appl
272	28	29.2	30	4	US-10-618-126A-12	Sequence 12, Appl	345	28	29.2	31	4	US-10-618-126A-85	Sequence 85, Appl
273	28	29.2	30	4	US-10-618-126A-13	Sequence 13, Appl	346	28	29.2	31	4	US-10-618-126A-86	Sequence 86, Appl
274	28	29.2	30	4	US-10-618-126A-14	Sequence 14, Appl	347	28	29.2	31	4	US-10-618-126A-87	Sequence 87, Appl
275	28	29.2	30	4	US-10-618-126A-15	Sequence 15, Appl	348	28	29.2	31	4	US-10-618-126A-121	Sequence 121, App
276	28	29.2	30	4	US-10-618-126A-16	Sequence 16, Appl	349	28	29.2	31	4	US-10-618-126A-126	Sequence 126, App
277	28	29.2	30	4	US-10-618-126A-17	Sequence 17, Appl	350	28	29.2	31	4	US-10-618-126A-127	Sequence 127, App
278	28	29.2	30	4	US-10-618-126A-18	Sequence 18, Appl	351	28	29.2	31	4	US-10-618-126A-128	Sequence 128, App
279	28	29.2	30	4	US-10-618-126A-19	Sequence 19, Appl	352	28	29.2	31	4	US-10-618-126A-129	Sequence 129, App
280	28	29.2	30	4	US-10-618-126A-20	Sequence 20, Appl	353	28	29.2	31	4	US-10-618-126A-130	Sequence 130, App
281	28	29.2	30	4	US-10-618-126A-21	Sequence 21, Appl	354	28	29.2	31	4	US-10-618-126A-131	Sequence 131, App
282	28	29.2	30	4	US-10-618-126A-22	Sequence 22, Appl	355	28	29.2	31	4	US-10-618-126A-132	Sequence 132, App
283	28	29.2	30	4	US-10-618-126A-23	Sequence 23, Appl	356	28	29.2	31	4	US-10-618-126A-133	Sequence 133, App
284	28	29.2	30	4	US-10-618-126A-24	Sequence 24, Appl	357	28	29.2	31	4	US-10-618-126A-134	Sequence 134, App
285	28	29.2	30	4	US-10-618-126A-25	Sequence 25, Appl	358	28	29.2	31	4	US-10-618-126A-135	Sequence 135, App
286	28	29.2	30	4	US-10-618-126A-26	Sequence 26, Appl	359	28	29.2	31	4	US-10-618-126A-136	Sequence 136, App
287	28	29.2	30	4	US-10-618-126A-27	Sequence 27, Appl	360	28	29.2	31	4	US-10-618-126A-137	Sequence 137, App
288	28	29.2	30	4	US-10-618-126A-28	Sequence 28, Appl	361	28	29.2	31	4	US-10-618-126A-138	Sequence 138, App
289	28	29.2	30	4	US-10-618-126A-29	Sequence 29, Appl	362	28	29.2	31	4	US-10-618-126A-139	Sequence 139, App
290	28	29.2	30	4	US-10-618-126A-30	Sequence 30, Appl	363	28	29.2	31	4	US-10-618-126A-140	Sequence 140, App
291	28	29.2	30	4	US-10-618-126A-31	Sequence 31, Appl	364	28	29.2	31	4	US-10-618-126A-141	Sequence 141, App
292	28	29.2	30	4	US-10-618-126A-32	Sequence 32, Appl	365	28	29.2	31	4	US-10-618-126A-142	Sequence 142, App
293	28	29.2	30	4	US-10-618-126A-33	Sequence 33, Appl	366	28	29.2	31	4	US-10-618-126A-143	Sequence 143, App
294	28	29.2	30	4	US-10-618-126A-34	Sequence 34, Appl	367	28	29.2	31	4	US-10-618-126A-144	Sequence 144, App
295	28	29.2	30	4	US-10-618-126A-35	Sequence 35, Appl	368	28	29.2	31	4	US-10-618-126A-145	Sequence 145, App
296	28	29.2	30	4	US-10-618-126A-36	Sequence 36, Appl	369	28	29.2	31	4	US-10-618-126A-146	Sequence 146, App
297	28	29.2	30	4	US-10-618-126A-37	Sequence 37, Appl	370	28	29.2	31	4	US-10-618-126A-147	Sequence 147, App
298	28	29.2	30	4	US-10-618-126A-38	Sequence 38, Appl	371	28	29.2	31	4	US-10-618-126A-148	Sequence 148, App
299	28	29.2	30	4	US-10-618-126A-83	Sequence 83, Appl	372	28	29.2	31	4	US-10-618-126A-149	Sequence 149, App
300	28	29.2	30	4	US-10-618-126A-88	Sequence 88, Appl	373	28	29.2	31	4	US-10-618-126A-150	Sequence 150, App
301	28	29.2	30	4	US-10-618-126A-89	Sequence 89, Appl	374	28	29.2	31	4	US-10-618-126A-151	Sequence 151, App
302	28	29.2	30	4	US-10-618-126A-90	Sequence 90, Appl	375	28	29.2	31	4	US-10-618-126A-152	Sequence 152, App
303	28	29.2	30	4	US-10-618-126A-91	Sequence 91, Appl	376	28	29.2	31	4	US-10-425-115-286559	Sequence 286559, App
304	28	29.2	30	4	US-10-618-126A-92	Sequence 92, Appl	377	28	29.2	31	5	US-10-851-691-74	Sequence 74, Appl
305	28	29.2	30	4	US-10-618-126A-93	Sequence 93, Appl	378	28	29.2	31	5	US-10-851-691-75	Sequence 75, Appl
306	28	29.2	30	4	US-10-618-126A-94	Sequence 94, Appl	379	28	29.2	31	5	US-10-851-691-78	Sequence 78, Appl
307	28	29.2	30	4	US-10-618-126A-95	Sequence 95, Appl	380	28	29.2	31	5	US-10-851-691-79	Sequence 79, Appl
308	28	29.2	30	4	US-10-618-126A-96	Sequence 96, Appl	381	28	29.2	31	5	US-10-892-981A-77	Sequence 77, Appl
309	28	29.2	30	4	US-10-618-126A-97	Sequence 97, Appl	382	28	29.2	31	5	US-10-892-981A-78	Sequence 78, Appl
310	28	29.2	30	4	US-10-618-126A-98	Sequence 98, Appl	383	28	29.2	31	5	US-10-892-981A-81	Sequence 81, Appl
311	28	29.2	30	4	US-10-618-126A-99	Sequence 99, Appl	384	28	29.2	31	5	US-10-892-981A-82	Sequence 82, Appl
312	28	29.2	30	4	US-10-618-126A-100	Sequence 100, App	385	28	29.2	32	4	US-10-084-994-21	Sequence 21, Appl
313	28	29.2	30	4	US-10-618-126A-101	Sequence 101, App	386	28	29.2	32	4	US-10-193-409-21	Sequence 21, Appl
314	28	29.2	30	4	US-10-618-126A-102	Sequence 102, App	387	28	29.2	32	4	US-10-193-409-21	Sequence 21, Appl
315	28	29.2	30	4	US-10-618-126A-103	Sequence 103, App	388	28	29.2	32	4	US-10-424-599-209957	Sequence 209957, App
316	28	29.2	30	4	US-10-618-126A-104	Sequence 104, App	389	28	29.2	32	4	US-10-455-822-126	Sequence 126, App
317	28	29.2	30	4	US-10-618-126A-105	Sequence 105, App	390	28	29.2	32	4	US-10-618-126A-115	Sequence 115, App
318	28	29.2	30	4	US-10-618-126A-106	Sequence 106, App	391	28	29.2	32	4	US-10-618-126A-116	Sequence 116, App
319	28	29.2	30	4	US-10-618-126A-107	Sequence 107, App	392	28	29.2	32	4	US-10-618-126A-117	Sequence 117, App

393	28	29.2	32	4	US-10-618-126A-119	Sequence 119, App	466	27	28.1	13	4	US-10-158-847-129	Sequence 129, App
394	28	29.2	32	4	US-10-618-126A-120	Sequence 120, App	467	27	28.1	13	4	US-10-158-825-129	Sequence 129, App
395	28	29.2	32	4	US-10-618-126A-121	Sequence 121, App	468	27	28.1	13	4	US-10-158-825-129	Sequence 129, App
396	28	29.2	32	4	US-10-618-126A-122	Sequence 122, App	469	27	28.1	13	6	US-11-011-523-17	Sequence 17, Appl
397	28	29.2	32	4	US-10-618-126A-123	Sequence 123, App	470	27	28.1	14	3	US-09-833-245-729	Sequence 729, App
398	28	29.2	32	4	US-10-618-126A-124	Sequence 124, App	471	27	28.1	14	4	US-10-098-093-45	Sequence 45, Appl
399	28	29.2	32	4	US-10-618-126A-125	Sequence 125, App	472	27	28.1	14	4	US-10-098-093-45	Sequence 45, Appl
400	28	29.2	32	6	US-10-407-484-126	Sequence 126, App	473	27	28.1	14	5	US-10-206-699-6	Sequence 6, Appl
401	28	29.2	33	3	US-11-068-859-126	Sequence 126, App	474	27	28.1	14	5	US-10-794-514A-606	Sequence 606, App
402	28	29.2	33	3	US-09-864-761-33307	Sequence 33307, A	475	27	28.1	14	5	US-10-472-533-606	Sequence 549, App
403	28	29.2	33	4	US-10-455-822-127	Sequence 127, App	476	27	28.1	14	6	US-11-264-096-729	Sequence 729, App
404	28	29.2	33	4	US-10-437-963-108618	Sequence 108618, App	477	27	28.1	15	3	US-09-819-308-18	Sequence 18, Appl
405	28	29.2	33	5	US-10-407-484-127	Sequence 127, App	478	27	28.1	15	3	US-09-733-416A-4	Sequence 4, Appl
406	28	29.2	33	5	US-10-926-683-1544	Sequence 1544, App	479	27	28.1	15	4	US-10-105-774-16	Sequence 16, Appl
407	28	29.2	33	6	US-11-068-859-127	Sequence 127, App	480	27	28.1	15	6	US-11-011-523-16	Sequence 16, Appl
408	28	29.2	34	4	US-10-218-102-50	Sequence 50, Appl	481	27	28.1	16	4	US-10-038-612-16	Sequence 16, Appl
409	28	29.2	34	4	US-10-218-102-66	Sequence 66, Appl	482	27	28.1	17	4	US-10-038-612-114	Sequence 114, App
410	28	29.2	34	4	US-10-218-102-109	Sequence 109, App	483	27	28.1	17	4	US-10-422-571-96	Sequence 96, Appl
411	28	29.2	34	4	US-10-252-734-62	Sequence 62, Appl	484	27	28.1	18	3	US-09-834-240-28	Sequence 28, Appl
412	28	29.2	34	6	US-11-121-301-62	Sequence 62, Appl	485	27	28.1	18	4	US-10-142-238A-36	Sequence 36, Appl
413	28	29.2	35	3	US-09-764-887-205	Sequence 205, App	486	27	28.1	18	4	US-10-206-699-257	Sequence 257, App
414	28	29.2	35	4	US-10-073-961-205	Sequence 205, App	487	27	28.1	18	4	US-10-206-699-262	Sequence 262, App
415	28	29.2	35	4	US-10-028-075B-169	Sequence 169, App	488	27	28.1	18	4	US-10-125-869A-31	Sequence 31, Appl
416	28	29.2	35	4	US-10-029-206A-169	Sequence 169, App	489	27	28.1	18	4	US-10-462-262-255	Sequence 255, App
417	28	29.2	35	4	US-10-437-963-133573	Sequence 133573, App	490	27	28.1	19	3	US-09-771-209-54	Sequence 54, Appl
418	28	29.2	35	5	US-10-753-510-169	Sequence 169, App	491	27	28.1	19	5	US-10-958-216-1090	Sequence 1090, Ap
419	28	29.2	35	5	US-10-821-240A-169	Sequence 169, App	492	27	28.1	20	3	US-09-974-026-65	Sequence 65, Appl
420	28	29.2	35	5	US-10-817-756A-200	Sequence 200, App	493	27	28.1	20	4	US-10-206-699-292	Sequence 292, App
421	28	29.2	36	4	US-10-333-900-29	Sequence 29, Appl	494	27	28.1	20	5	US-10-721-553-20	Sequence 20, Appl
422	28	29.2	37	4	US-10-437-963-152649	Sequence 152649, App	495	27	28.1	21	5	US-10-622-675-41	Sequence 41, Appl
423	28	29.2	38	4	US-10-028-075B-35	Sequence 35, Appl	496	27	28.1	21	5	US-10-895-226-41	Sequence 41, Appl
424	28	29.2	38	4	US-10-029-206A-35	Sequence 35, Appl	497	27	28.1	22	4	US-10-206-699-268	Sequence 268, App
425	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	498	27	28.1	22	5	US-10-792-582-391	Sequence 391, App
426	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	499	27	28.1	22	5	US-10-792-582-395	Sequence 395, App
427	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	500	27	28.1	23	4	US-10-043-487-436	Sequence 436, App
428	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	501	27	28.1	23	4	US-10-612-090-17	Sequence 17, Appl
429	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	502	27	28.1	23	4	US-10-416-822-6	Sequence 6, Appl
430	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	503	27	28.1	23	4	US-10-416-822-9	Sequence 9, Appl
431	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	504	27	28.1	23	5	US-10-467-059-31	Sequence 31, Appl
432	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	505	27	28.1	23	5	US-10-494-634-15	Sequence 15, Appl
433	28	29.2	38	4	US-10-455-822-128	Sequence 128, App	506	27	28.1	23	5	US-10-898-143-8	Sequence 8, Appl
434	28	29.2	38	4	US-10-437-963-130024	Sequence 130024, App	507	27	28.1	23	5	US-10-898-143-11	Sequence 11, Appl
435	28	29.2	38	4	US-10-407-484-128	Sequence 128, App	508	27	28.1	23	5	US-10-895-064-1725	Sequence 1725, Ap
436	28	29.2	38	4	US-10-409-630-24	Sequence 24, Appl	509	27	28.1	23	6	US-11-066-697-460	Sequence 460, App
437	28	29.2	38	4	US-10-753-510-35	Sequence 35, Appl	510	27	28.1	23	6	US-11-129-741-1725	Sequence 1725, Ap
438	28	29.2	38	5	US-10-808-187-1742	Sequence 1742, Ap	511	27	28.1	24	4	US-10-145-206-18	Sequence 18, Appl
439	28	29.2	38	5	US-10-821-240A-35	Sequence 35, Appl	512	27	28.1	24	4	US-10-424-599-255616	Sequence 255616, App
440	28	29.2	38	5	US-10-807-807-1742	Sequence 1742, Ap	513	27	28.1	24	4	US-10-467-059-33	Sequence 33, Appl
441	28	29.2	38	5	US-10-817-756A-47	Sequence 47, Appl	514	27	28.1	24	5	US-10-494-634-11	Sequence 11, Appl
442	28	29.2	38	6	US-11-068-859-128	Sequence 128, App	515	27	28.1	24	5	US-10-494-634-14	Sequence 14, Appl
443	28	29.2	38	6	US-11-004-399-2435	Sequence 2435, Ap	516	27	28.1	25	4	US-10-467-059-34	Sequence 34, Appl
444	28	29.2	39	4	US-10-424-599-258450	Sequence 258450, App	517	27	28.1	25	5	US-10-494-634-10	Sequence 10, Appl
445	28	29.2	39	4	US-10-425-115-331830	Sequence 331830, App	518	27	28.1	25	5	US-10-494-634-13	Sequence 13, Appl
446	28	29.2	40	4	US-10-424-599-253104	Sequence 253104, App	519	27	28.1	25	5	US-10-768-974-27	Sequence 27, Appl
447	28	29.2	40	4	US-10-437-963-140290	Sequence 140290, App	520	27	28.1	25	5	US-10-240-392-1	Sequence 1, Appl
448	28	29.2	40	5	US-10-472-928-2960	Sequence 2960, Ap	521	27	28.1	25	5	US-10-240-392-2	Sequence 2, Appl
449	27.5	28.6	10	6	US-11-003-951-133	Sequence 133, App	522	27	28.1	26	4	US-10-029-386-34195	Sequence 34195, A
450	27.5	28.6	20	4	US-10-038-612-37	Sequence 37, Appl	523	27	28.1	26	4	US-10-424-599-197655	Sequence 197655, App
451	27.5	28.6	20	4	US-10-422-571-97	Sequence 97, Appl	524	27	28.1	26	4	US-10-424-599-283992	Sequence 283992, App
452	27.5	28.6	21	4	US-10-038-612-110	Sequence 110, App	525	27	28.1	26	4	US-10-467-059-35	Sequence 35, Appl
453	27.5	28.6	31	5	US-10-742-669-97	Sequence 87, Appl	526	27	28.1	26	5	US-10-494-634-9	Sequence 9, Appl
454	27.5	28.6	33	4	US-10-282-122A-44224	Sequence 44224, A	527	27	28.1	26	5	US-10-768-974-41	Sequence 41, Appl
455	27.5	28.6	34	4	US-10-218-102-194	Sequence 194, App	528	27	28.1	27	5	US-10-467-059-36	Sequence 36, Appl
456	27.5	28.6	37	4	US-10-425-115-280435	Sequence 280435, App	529	27	28.1	27	5	US-10-494-634-8	Sequence 8, Appl
457	27	28.1	11	4	US-10-468-543-12	Sequence 12, Appl	530	27	28.1	27	5	US-10-851-691-50	Sequence 50, Appl
458	27	28.1	12	3	US-09-978-309A-72	Sequence 72, Appl	531	27	28.1	27	5	US-10-770-712-30	Sequence 30, Appl
459	27	28.1	12	3	US-09-965-738-260	Sequence 260, App	532	27	28.1	27	5	US-10-496-905-369	Sequence 369, App
460	27	28.1	12	4	US-10-105-774-2	Sequence 2, Appl	533	27	28.1	27	5	US-10-496-905-393	Sequence 393, App
461	27	28.1	12	4	US-10-680-670-1	Sequence 1, Appl	534	27	28.1	28	3	US-09-929-818-1	Sequence 1, Appl
462	27	28.1	12	5	US-10-898-675-72	Sequence 72, Appl	535	27	28.1	28	3	US-09-929-818-8	Sequence 8, Appl
463	27	28.1	12	5	US-10-892-831-72	Sequence 72, Appl	536	27	28.1	28	3	US-09-929-818-9	Sequence 9, Appl
464	27	28.1	12	6	US-11-011-523-2	Sequence 2, Appl	537	27	28.1	28	3	US-09-929-818-13	Sequence 13, Appl
465	27	28.1	13	4	US-10-105-774-17	Sequence 17, Appl	538	27	28.1	28	3	US-09-929-818-15	Sequence 15, Appl

539	27	28.1	28	3	US-09-929-818-16	Sequence 16, Appl	612	27	28.1	28	4	US-10-254-569A-1	Sequence 1, Appl
540	27	28.1	28	3	US-09-929-818-38	Sequence 38, Appl	613	27	28.1	28	4	US-10-254-569A-5	Sequence 5, Appl
541	27	28.1	28	3	US-09-929-818-99	Sequence 99, Appl	614	27	28.1	28	4	US-10-254-569A-6	Sequence 6, Appl
542	27	28.1	28	3	US-09-929-818-100	Sequence 100, Appl	615	27	28.1	28	4	US-10-254-569A-7	Sequence 7, Appl
543	27	28.1	28	3	US-09-929-818-102	Sequence 102, Appl	616	27	28.1	28	4	US-10-254-569A-8	Sequence 8, Appl
544	27	28.1	28	3	US-09-929-818-104	Sequence 104, Appl	617	27	28.1	28	4	US-10-254-569A-9	Sequence 9, Appl
545	27	28.1	28	3	US-09-929-818-105	Sequence 105, Appl	618	27	28.1	28	4	US-10-254-569A-11	Sequence 11, Appl
546	27	28.1	28	3	US-09-929-818-107	Sequence 107, Appl	619	27	28.1	28	4	US-10-254-569A-12	Sequence 12, Appl
547	27	28.1	28	3	US-09-929-818-108	Sequence 108, Appl	620	27	28.1	28	4	US-10-201-288-31	Sequence 31, Appl
548	27	28.1	28	3	US-09-929-818-119	Sequence 119, Appl	621	27	28.1	28	4	US-10-343-654-22	Sequence 22, Appl
549	27	28.1	28	3	US-09-929-818-121	Sequence 121, Appl	622	27	28.1	28	4	US-10-416-822-1	Sequence 1, Appl
550	27	28.1	28	3	US-09-929-818-122	Sequence 122, Appl	623	27	28.1	28	4	US-10-332-765-14	Sequence 14, Appl
551	27	28.1	28	3	US-09-929-818-124	Sequence 124, Appl	624	27	28.1	28	4	US-10-467-059-14	Sequence 14, Appl
552	27	28.1	28	3	US-09-929-818-125	Sequence 125, Appl	625	27	28.1	28	4	US-10-467-059-20	Sequence 20, Appl
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554	27	28.1	28	3	US-09-929-818-127	Sequence 127, Appl	627	27	28.1	28	5	US-10-718-071-36	Sequence 36, Appl
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556	27	28.1	28	3	US-09-929-818-129	Sequence 129, Appl	629	27	28.1	28	5	US-10-851-691-16	Sequence 16, Appl
557	27	28.1	28	3	US-09-929-818-131	Sequence 131, Appl	630	27	28.1	28	5	US-10-851-691-29	Sequence 29, Appl
558	27	28.1	28	3	US-09-929-818-132	Sequence 132, Appl	631	27	28.1	28	5	US-10-851-691-33	Sequence 33, Appl
559	27	28.1	28	3	US-09-929-818-133	Sequence 133, Appl	632	27	28.1	28	5	US-10-851-691-34	Sequence 34, Appl
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561	27	28.1	28	3	US-09-929-818-135	Sequence 135, Appl	634	27	28.1	28	5	US-10-851-691-38	Sequence 38, Appl
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563	27	28.1	28	3	US-09-929-818-138	Sequence 138, Appl	636	27	28.1	28	5	US-10-851-691-40	Sequence 40, Appl
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566	27	28.1	28	3	US-09-929-818-143	Sequence 143, Appl	639	27	28.1	28	5	US-10-851-691-43	Sequence 43, Appl
567	27	28.1	28	3	US-09-929-818-145	Sequence 145, Appl	640	27	28.1	28	5	US-10-851-691-52	Sequence 52, Appl
568	27	28.1	28	3	US-09-929-818-146	Sequence 146, Appl	641	27	28.1	28	5	US-10-851-691-53	Sequence 53, Appl
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572	27	28.1	28	3	US-09-929-818-153	Sequence 153, Appl	645	27	28.1	28	5	US-10-892-981A-1	Sequence 1, Appl
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589	27	28.1	28	3	US-09-929-818-177	Sequence 177, Appl	662	27	28.1	28	5	US-10-769-803-4	Sequence 4, Appl
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598	27	28.1	28	3	US-09-929-818-196	Sequence 196, Appl	671	27	28.1	28	5	US-10-626-719-55	Sequence 55, Appl
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607	27	28.1	28	4	US-10-004-530A-17	Sequence 17, Appl	680	27	28.1	28	5	US-10-626-719-64	Sequence 64, Appl
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609	27	28.1	28	4	US-10-211-994-1	Sequence 1, Appl	682	27	28.1	28	5	US-10-626-719-66	Sequence 66, Appl
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833	27	28.1	29	4	US-10-131-543-11	Sequence 11, App	906	27	28.1	30	5	US-10-851-691-97	Sequence 97, Appl
834	27	28.1	29	4	US-10-131-546-11	Sequence 11, App	907	27	28.1	30	5	US-10-851-691-98	Sequence 98, Appl
835	27	28.1	29	4	US-10-131-346-11	Sequence 11, App	908	27	28.1	30	5	US-10-851-691-99	Sequence 99, Appl
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839	27	28.1	29	5	US-10-851-691-30	Sequence 30, App	912	27	28.1	30	5	US-10-851-691-103	Sequence 103, App
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846	27	28.1	29	5	US-10-892-981A-28	Sequence 28, App	919	27	28.1	30	5	US-10-851-691-110	Sequence 110, App
847	27	28.1	29	5	US-10-892-981A-30	Sequence 30, App	920	27	28.1	30	5	US-10-851-691-111	Sequence 111, App
848	27	28.1	29	5	US-10-892-981A-46	Sequence 46, App	921	27	28.1	30	5	US-10-851-691-112	Sequence 112, App
849	27	28.1	29	5	US-10-892-981A-50	Sequence 50, App	922	27	28.1	30	5	US-10-851-691-113	Sequence 113, App
850	27	28.1	29	5	US-10-892-981A-87	Sequence 87, App	923	27	28.1	30	5	US-10-851-691-114	Sequence 114, App
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852	27	28.1	29	5	US-10-892-981A-92	Sequence 92, App	925	27	28.1	30	5	US-10-851-691-116	Sequence 116, App
853	27	28.1	29	5	US-10-892-981A-95	Sequence 95, App	926	27	28.1	30	5	US-10-851-691-117	Sequence 117, App
854	27	28.1	29	5	US-10-892-981A-96	Sequence 96, App	927	27	28.1	30	5	US-10-851-691-118	Sequence 118, App
855	27	28.1	29	5	US-10-892-981A-99	Sequence 99, App	928	27	28.1	30	5	US-10-851-691-119	Sequence 119, App
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863	27	28.1	30	4	US-10-147-603-232	Sequence 232, App	936	27	28.1	30	5	US-10-851-691-127	Sequence 127, App
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878	27	28.1	30	4	US-10-618-126A-62	Sequence 62, App	951	27	28.1	30	5	US-10-851-691-142	Sequence 142, App
879	27	28.1	30	4	US-10-618-126A-63	Sequence 63, App	952	27	28.1	30	5	US-10-851-691-143	Sequence 143, App
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982 27 28.1 30 5 US-10-851-691-202 Sequence 202, App
983 27 28.1 30 5 US-10-851-691-203 Sequence 203, App
984 27 28.1 30 5 US-10-851-691-204 Sequence 204, App
985 27 28.1 30 5 US-10-851-691-205 Sequence 205, App
986 27 28.1 30 5 US-10-851-691-206 Sequence 206, App
987 27 28.1 30 5 US-10-851-691-207 Sequence 207, App
988 27 28.1 30 5 US-10-851-691-208 Sequence 208, App
989 27 28.1 30 5 US-10-851-691-209 Sequence 209, App
990 27 28.1 30 5 US-10-851-691-210 Sequence 210, App
991 27 28.1 30 5 US-10-851-691-211 Sequence 211, App
992 27 28.1 30 5 US-10-851-691-212 Sequence 212, App
993 27 28.1 30 5 US-10-851-691-213 Sequence 213, App
994 27 28.1 30 5 US-10-851-691-214 Sequence 214, App
995 27 28.1 30 5 US-10-851-691-215 Sequence 215, App
996 27 28.1 30 5 US-10-851-691-216 Sequence 216, App
997 27 28.1 30 5 US-10-851-691-217 Sequence 217, App
998 27 28.1 30 5 US-10-851-691-218 Sequence 218, App
999 27 28.1 30 5 US-10-851-691A-27 Sequence 27, Appl
1000 27 28.1 30 5 US-10-852-981A-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-870-342A-14
; Sequence 14, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-14

Query Match 100.0%; Score 96; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | |
Db 4 FEHCNFNDVTTTLRENE 20

RESULT 2
US-10-870-342A-20
; Sequence 20, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-20

Query Match 100.0%; Score 96; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 96; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | |
Db 5 FEHCNFNDVTTTLRENE 21

RESULT 3
US-10-870-342A-15
; Sequence 15, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-15

Query Match 100.0%; Score 96; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | |
Db 12 FEHCNFNDVTTTLRENE 28

RESULT 4
US-11-006-031-44
; Sequence 44, Application US/11006031
; Publication No. US20050272114A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Keith V.
; APPLICANT: Klaubert, Dieter
; APPLICANT: Los, Georgyi V.
; APPLICANT: Bulleit, Robert F.
; APPLICANT: McDougall, Mark
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Substrates for Covalent Tethering to Proteins
; FILE REFERENCE: 341.035US1
; CURRENT APPLICATION NUMBER: US/11/006,031
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 10/768,976
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,094
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/474,659
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/592,499
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-006-031-44

Query Match 100.0%; Score 96; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 1 FEHCNFDVTTTLRENE 17

RESULT 5

US-11-194-110-44

; Sequence 44, Application US/11194110
; Publication No. US2006002480A1
; GENERAL INFORMATION:

; APPLICANT: Encells, Al

; APPLICANT: Klaubert, Dieter

; APPLICANT: Los, Georgyi V.

; APPLICANT: McDougall, Mark

; APPLICANT: Wood, Keith V.

; APPLICANT: Wood, Monika G.

; APPLICANT: Zimprich, Chad

; APPLICANT: Promega Corporation

; TITLE OF INVENTION: Covalent Tethering of Functional Groups to Proteins and Substrate

; FILE OF INVENTION: Therefor

; FILE REFERENCE: 341.032US1

; CURRENT APPLICATION NUMBER: US/11/194,110

; CURRENT FILING DATE: 2005-07-29

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-194-110-44

Query Match

Best Local Similarity 100.0%; Score 96; DB 6; Length 36;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||||
Db 1 FEHCNFDVTTTLRENE 17

RESULT 6

US-10-870-342A-13

; Sequence 13, Application US/10870342A

; Publication No. US20050032128A1

; GENERAL INFORMATION:

; APPLICANT: Halperin, Jose

; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF

; FILE REFERENCE: H0498.70223US00

; CURRENT APPLICATION NUMBER: US/10/870,342A

; CURRENT FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-870-342A-13

Query Match

Best Local Similarity 94.8%; Score 91; DB 5; Length 18;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLREN 16
|||||
Db 3 FEHCNFDVTTTLREN 18

RESULT 7

US-10-870-342A-19

; Sequence 19, Application US/10870342A

; Publication No. US20050032128A1

; GENERAL INFORMATION:

; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-19

Query Match

Best Local Similarity 83.3%; Score 80; DB 5; Length 18;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRL 14
|||||
Db 5 FEHCNFDVTTTLRL 18

RESULT 8

US-10-870-342A-41

; Sequence 41, Application US/10870342A

; Publication No. US20050032128A1

; GENERAL INFORMATION:

; APPLICANT: Halperin, Jose

; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF

; FILE REFERENCE: H0498.70223US00

; CURRENT APPLICATION NUMBER: US/10/870,342A

; CURRENT FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 41

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-870-342A-41

Query Match

Best Local Similarity 80.2%; Score 77; DB 5; Length 25;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CNFNFDVTTTLRENE 17
|||||
Db 1 CNFNFDVTTTLRENE 14

RESULT 9

US-10-870-342A-45

; Sequence 45, Application US/10870342A

; Publication No. US20050032128A1

; GENERAL INFORMATION:

; APPLICANT: Halperin, Jose

; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF

; FILE REFERENCE: H0498.70223US00

; CURRENT APPLICATION NUMBER: US/10/870,342A

; CURRENT FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 45

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-870-342A-45

Query Match

Best Local Similarity 64.6%; Score 62; DB 5; Length 21;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FNDVTTTLRENE 17
|||||

```
Db      1 FNDVTRLRENE 12

RESULT 10
US-10-870-342A-4
; Sequence 4, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-4

Query Match      54.2%; Score 52; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FEHCNFND 8
      |||||
Db      6 FEHCNFND 13

RESULT 11
US-10-870-342A-16
; Sequence 16, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-16

Query Match      54.2%; Score 52; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FEHCNFND 8
      |||||
Db      9 FEHCNFND 16

RESULT 12
US-10-870-342A-22
; Sequence 22, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-22

Query Match      54.2%; Score 52; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FEHCNFND 8
      |||||
Db     11 FEHCNFND 18

RESULT 13
US-10-870-342A-23
; Sequence 23, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-23

Query Match      50.0%; Score 48; DB 5; Length 14;
Best Local Similarity 87.5%; Pred. No. 0.81;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FEHCNFND 8
      |||||
Db      7 FEHCNFNE 14

RESULT 14
US-10-870-342A-24
; Sequence 24, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-24

Query Match      47.9%; Score 46; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FEHCNFN 7
      |||||
Db     12 FEHCNFN 18

RESULT 15
US-10-870-342A-44
; Sequence 44, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
```

; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-44

Query Match 45.8%; Score 44; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTTRLRENE 17
|||||

Db 1 VTTRLRENE 9

RESULT 16
US-10-870-342A-3
; Sequence 3, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Lys is glycosylated
US-10-870-342A-3

Query Match 44.8%; Score 43; DB 5; Length 14;
Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FEHCNFND 8
|||||

Db 6 FEHCNFND 13

RESULT 17
US-10-870-342A-10
; Sequence 10, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-10

Query Match 44.8%; Score 43; DB 5; Length 14;
Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FEHCNFND 8

Db 6 FEHCNFND 13
|||||

RESULT 18
US-09-835-752-1
; Sequence 1, Application US/09835752
; Publication No. US20040166531A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
; FILE REFERENCE: H0498/7137(ERG)
; CURRENT APPLICATION NUMBER: US/09/835,752
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 06/203,254
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-752-1

Query Match 44.8%; Score 43; DB 3; Length 15;
Best Local Similarity 87.5%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
|||||

Db 7 FEHCNFND 14

RESULT 19
US-10-833-581-1
; Sequence 1, Application US/10833581
; Publication No. US20040219606A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
; FILE REFERENCE: H0498/7137(ERG)
; CURRENT APPLICATION NUMBER: US/10/833,581
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/835,752
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 06/203,254
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-833-581-1

Query Match 44.8%; Score 43; DB 5; Length 15;
Best Local Similarity 87.5%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
|||||

Db 7 FEHCNFND 14

RESULT 20
US-10-870-342A-21
; Sequence 21, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A

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US-10-206-699-264
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-21
Query Match 41.7%; Score 40; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FEHCNF 6
Db 8 FEHCNF 13
RESULT 21
US-10-870-342A-17
; Sequence 17, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-17
Query Match 41.7%; Score 40; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FEHCNF 6
Db 12 FEHCNF 17
RESULT 22
US-10-870-342A-43
; Sequence 43, Application US/10870342A
; Publication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: H0498.70223US00
; CURRENT APPLICATION NUMBER: US/10/870,342A
; CURRENT FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-43
Query Match 41.7%; Score 40; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 TTRLRENE 17
Db 1 TTRLRENE 8
RESULT 23
US-10-870-699-264
; Sequence 264, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 264
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-264
Query Match 40.6%; Score 39; DB 4; Length 18;
Best Local Similarity 41.2%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 1 FEHCNFVTVTLRENE 17
Db 2 FYICNINEVCHYARRND 18
RESULT 24
US-10-206-699-270
; Sequence 270, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 270
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-270
Query Match 40.6%; Score 39; DB 4; Length 22;
Best Local Similarity 41.2%; Pred. No. 38;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 1 FEHCNFVTVTLRENE 17
Db 6 FYICNINEVCHYARRND 22
RESULT 25
US-10-813-638-1248

```

; Sequence 1248, Application US/10813638
; Publication No. US20040235026A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/10/813,638
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: 60/163,783
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 1248
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)...(0)
; OTHER INFORMATION: cSNP translation
US-10-813-638-1248

Query Match 37.5%; Score 36; DB 5; Length 14;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTTTL 13
:|:|:|:|:|
DB 3 QHCSRNFMTWL 14

RESULT 26
US-10-424-599-175430
; Sequence 175430, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 175430
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT3847_129431C.1.pep
US-10-424-599-175430

Query Match 37.5%; Score 36; DB 4; Length 40;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCNFNDV 9
||:|:|:|
DB 26 HCHYNDI 32

RESULT 27
US-10-656-894-20
; Sequence 20, Application US/10656894
; Publication No. US20050260601A1
; GENERAL INFORMATION:
; APPLICANT: Whitt, Michael
; TITLE OF INVENTION: RECOMBINANT MUTANTS OF RHABDOVIRUS AND METHODS OF USE THEREO
; FILE REFERENCE: P-3558-US

; CURRENT APPLICATION NUMBER: US/10/656,894
; CURRENT FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-10-656-894-20

Query Match 36.5%; Score 35; DB 5; Length 29;
Best Local Similarity 35.3%; Pred. No. 2.3e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||:|:|:|:|:|
DB 1 FEHPHIQDAASQLPDDE 17

RESULT 28
US-10-656-894-16
; Sequence 16, Application US/10656894
; Publication No. US20050260601A1
; GENERAL INFORMATION:
; APPLICANT: Whitt, Michael
; TITLE OF INVENTION: RECOMBINANT MUTANTS OF RHABDOVIRUS AND METHODS OF USE THEREO
; FILE REFERENCE: P-3558-US
; CURRENT APPLICATION NUMBER: US/10/656,894
; CURRENT FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-10-656-894-16

Query Match 36.5%; Score 35; DB 5; Length 32;
Best Local Similarity 35.3%; Pred. No. 2.5e+02;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTTLRENE 17
|||:|:|:|:|:|
DB 1 FEHPHIQDAASQLPDDE 17

RESULT 29
US-09-864-761-44741
; Sequence 44741, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44741
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL21931.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85
; OTHER INFORMATION: EST_HUMAN HIT: AW836842.1, EVALUE 1.10e+00
```

US-09-864-761-44741

```
Query Match 36.5%; Score 35; DB 3; Length 33;
Best Local Similarity 46.7%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 3 HCNFNDVTRLRENE 17
Db 7 HDNFTASTIRIPENQ 21
```

```
RESULT 30
US-10-656-894-15
; Sequence 15, Application US/10656894
; Publication No. US20050260601A1
; GENERAL INFORMATION:
; APPLICANT: Whitt, Michael
; TITLE OF INVENTION: RECOMBINANT MUTANTS OF RHABDOVIRUS AND METHODS OF USE THEREOF
; FILE REFERENCE: P-3558-US
; CURRENT APPLICATION NUMBER: US/10/656,894
; CURRENT FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-10-656-894-15
```

```
Query Match 36.5%; Score 35; DB 5; Length 35;
Best Local Similarity 35.3%; Pred. No. 2.8e+02;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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```
Qy 1 FEHCNFDVTRLRENE 17
Db 1 FEHPHIQDAASQLPDDE 17
```

```
RESULT 31
US-10-437-963-195917
; Sequence 195917, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 195917
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91819C.1.pep
US-10-437-963-195917
```

```
Query Match 36.5%; Score 35; DB 4; Length 38;
Best Local Similarity 70.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 7 NDVTTLRLEN 16
Db 24 NDVTTLRLEN 33
```

```
RESULT 32
US-10-038-407-2
; Sequence 2, Application US/10038407
; Publication No. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 VL/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-2
```

```
Query Match 35.9%; Score 34.5; DB 4; Length 34;
Best Local Similarity 42.9%; Pred. No. 3.3e+02;
Matches 6; Conservative 6; Mismatches 1; Indels 1; Gaps 1;
```

```
Qy 2 EHCNFDVTRLRE 15
Db 4 KNCSFN-ITTSIRD 16
```

```
RESULT 33
US-10-206-699-260
```

; Sequence 260, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 260
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-260

Query Match 35.4%; Score 34; DB 4; Length 18;
Best Local Similarity 41.2%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTLRENE 17
| | | | |
DB 2 FLFCNVNDVCNFSRND 18

RESULT 34
US-10-449-548-11
; Sequence 11, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRocheville, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062

; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Domain
US-10-449-548-11

Query Match 35.4%; Score 34; DB 4; Length 20;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDVTVTLRENE 17
| | | | |
DB 2 NDISTPLPDNE 12

RESULT 35
US-10-206-699-266
; Sequence 266, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 266
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-266

Query Match 35.4%; Score 34; DB 4; Length 22;
Best Local Similarity 41.2%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTLRENE 17
| | | | |
DB 6 FLFCNVNDVCNFSRND 22

RESULT 36
US-10-032-221B-37
; Sequence 37, Application US/10032221B
; Publication No. US20030144481A1
; GENERAL INFORMATION:
; APPLICANT: Kalluri, Raghuram
; TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE THEREOF.
; FILE REFERENCE: 2312/2082B (formerly 1440.1027-016)
; CURRENT APPLICATION NUMBER: US/10/032,221B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/00565
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/625,191
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/543,371
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: US 09/479,118

```
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/335,224
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/126,175
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/089,689
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 (amino acids 73-97 of SEQ ID NO:10)
US-10-032-221B-37

Query Match          35.4%; Score 34; DB 4; Length 25;
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTLRENE 17
Db 4 FLFCNVNDVCFASRND 20

RESULT 37
US-10-775-204-1704
; Sequence 1704, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1706

Query Match          35.4%; Score 34; DB 5; Length 25;
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTLRENE 17
Db 4 FLFCNVNDVCFASRND 20

RESULT 39
US-10-775-204-1766
; Sequence 1766, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1704

Query Match          35.4%; Score 34; DB 5; Length 25;
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTLRENE 17
```

```
Db 4 FLFCNVNDVCFASRND 20

RESULT 38
US-10-775-204-1706
; Sequence 1706, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1706
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1706

Query Match          35.4%; Score 34; DB 5; Length 25;
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTLRENE 17
Db 4 FLFCNVNDVCFASRND 20

RESULT 39
US-10-775-204-1766
; Sequence 1766, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1706
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1706

Query Match          35.4%; Score 34; DB 5; Length 25;
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTLRENE 17
Db 4 FLFCNVNDVCFASRND 20

RESULT 39
US-10-775-204-1766
; Sequence 1766, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1706
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1706

Query Match          35.4%; Score 34; DB 5; Length 25;
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTLRENE 17
```


;; PRIOR FILING DATE: 2002-05-10
;; PRIOR APPLICATION NUMBER: 60/398,008
;; PRIOR FILING DATE: 2002-07-24
;; PRIOR APPLICATION NUMBER: 60/411,355
;; PRIOR FILING DATE: 2002-09-18
;; PRIOR APPLICATION NUMBER: 60/414,984
;; PRIOR FILING DATE: 2002-10-02
;; PRIOR APPLICATION NUMBER: 60/417,611
;; PRIOR FILING DATE: 2002-10-11
;; PRIOR APPLICATION NUMBER: 60/420,246
;; PRIOR FILING DATE: 2002-10-23
;; PRIOR APPLICATION NUMBER: 60/423,623
;; PRIOR FILING DATE: 2002-11-05
;; PRIOR APPLICATION NUMBER: 60/351,360
;; PRIOR FILING DATE: 2002-01-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 222
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1766
;; LENGTH: 25
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-775-204-1766

Query Match 35.4%; Score 34; DB 5; Length 25;
Best Local Similarity 41.2%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNPNVDVTRLRENE 17
Db 4 FLFCNVNDVCNFSRND 20

RESULT 40

US-10-032-221B-39
;; Sequence 39, Application US/10032221B
;; Publication No. US20030144491A1
;; GENERAL INFORMATION:
;; APPLICANT: Kalluri, Raghuram
;; TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE THEREOF
;; FILE REFERENCE: 2312/2082B (formerly 1440.1027-016)
;; CURRENT APPLICATION NUMBER: US/10/032,221B
;; CURRENT FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: PCT/US01/00565
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: US 09/625,191
;; PRIOR FILING DATE: 2000-07-21
;; PRIOR APPLICATION NUMBER: US 09/543,371
;; PRIOR FILING DATE: 2000-04-04
;; PRIOR APPLICATION NUMBER: US 09/479,118
;; PRIOR FILING DATE: 2000-01-07
;; PRIOR APPLICATION NUMBER: US 09/335,224
;; PRIOR FILING DATE: 1999-06-17
;; PRIOR APPLICATION NUMBER: US 60/126,175
;; PRIOR FILING DATE: 1999-03-25
;; PRIOR APPLICATION NUMBER: US 60/089,689
;; PRIOR FILING DATE: 1998-06-17
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 39
;; LENGTH: 27
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: T8 (amino acids 68-94 of SEQ ID NO:10; lysine has been substituted
;; OTHER INFORMATION: d for the leucine residue at position 68 of the full-length Tumb
;; OTHER INFORMATION: atin molecule)
US-10-032-221B-39

Query Match 35.4%; Score 34; DB 4; Length 27;
Best Local Similarity 41.2%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNPNVDVTRLRENE 17
Db 9 FLFCNVNDVCNFSRND 25

RESULT 41

US-10-775-204-1705
;; Sequence 1705, Application US/10775204
;; Publication No. US20050186664A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Haseltine, William A.
;; APPLICANT: Balance, David J.
;; APPLICANT: Turner, Andrew J.
;; TITLE OF INVENTION: Albumin Fusion Proteins
;; FILE REFERENCE: PF564
;; CURRENT APPLICATION NUMBER: US/10/775,204
;; CURRENT FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/341,811
;; PRIOR FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 60/360,000
;; PRIOR FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: 60/378,950
;; PRIOR FILING DATE: 2002-05-10
;; PRIOR APPLICATION NUMBER: 60/398,008
;; PRIOR FILING DATE: 2002-07-24
;; PRIOR APPLICATION NUMBER: 60/411,355
;; PRIOR FILING DATE: 2002-09-18
;; PRIOR APPLICATION NUMBER: 60/414,984
;; PRIOR FILING DATE: 2002-10-02
;; PRIOR APPLICATION NUMBER: 60/417,611
;; PRIOR FILING DATE: 2002-10-11
;; PRIOR APPLICATION NUMBER: 60/420,246
;; PRIOR FILING DATE: 2002-10-23
;; PRIOR APPLICATION NUMBER: 60/423,623
;; PRIOR FILING DATE: 2002-11-05
;; PRIOR APPLICATION NUMBER: 60/351,360
;; PRIOR FILING DATE: 2002-01-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 222
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1705
;; LENGTH: 27
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-775-204-1705

Query Match 35.4%; Score 34; DB 5; Length 27;
Best Local Similarity 41.2%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNPNVDVTRLRENE 17
Db 9 FLFCNVNDVCNFSRND 25

RESULT 42

US-10-775-204-1707
;; Sequence 1707, Application US/10775204
;; Publication No. US20050186664A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Haseltine, William A.
;; APPLICANT: Balance, David J.
;; APPLICANT: Turner, Andrew J.
;; TITLE OF INVENTION: Albumin Fusion Proteins
;; FILE REFERENCE: PF564
;; CURRENT APPLICATION NUMBER: US/10/775,204
;; CURRENT FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/341,811
;; PRIOR FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 60/360,000
;; PRIOR FILING DATE: 2002-02-28

```

US-10-038-812-36

Query Match      35.4%; Score 34; DB 4; Length 40;
Best Local Similarity 31.2%; Pred. NO. 4.7e+02;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy      2 EHCNFNDVTTRLRENE 17
| | : | : | : | :
Db      2 EYCRYGDLVDYLHRNK 17

RESULT 45
US-10-225-567A-1174
; Sequence 1174, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1174
; LENGTH: 16
; TYPE: PRI
; ORGANISM: Homo sapiens
US-10-225-567A-1174

Query Match      34.4%; Score 33; DB 4; Length 16;
Best Local Similarity 42.9%; Pred. NO. 2.5e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy      4 CNFNDVTTLRLENE 17
| | : | : | : | :

```

Db 1 CGLSNKENRLBENB 14

RESULT 46

```

US-10-704-363--47
; Sequence 47, Application US/10704363
; Publication No. US20040249145A1
; GENERAL INFORMATION:
; APPLICANT: Stark, Karen A.
; APPLICANT: Weaver, Alix
; APPLICANT: Hoffmann, Heidi M.
; APPLICANT: Krauss, Raul
; APPLICANT: Saini, Kulvinder S.
; APPLICANT: Valenzuela, Dario B.
; TITLE OF INVENTION: Cell Adhesion-Mediating Proteins and
; POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 1966.1014003
; CURRENT APPLICATION NUMBER: US/10/704,363
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: PCT/US02/14457
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,179
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 60/315,736
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 20
; TYPE: PR1
; ORGANISM: Homo Sapiens
US-10-704-363--47

```

Query Match 34.4%; Score 33; DB 5; Length 20;
Best Local Similarity 38.5%; Pred. NO. 3.2e+02;
Matches 5; Conservative 4; Mismatches 4; Indels

QY 2 EHCNFDVTTLR 14
 | : | : | : |
Dd 5 EYCNISQLGRIR 17

RESIT.T 47

```

000001 4)
US-09-929-818-106
; Sequence 106, Application US/09929818
; Patent No. US20020099003A1
; GENERAL INFORMATION:
; APPLICANT: WILSON, LELAND P.
; APPLICANT: PLACES, VIRGIL A.
; TITLE OF INVENTION: TREATMENT OF FEMALE SEXUAL DYSFUNCTION WITH VASOACTIVE
; TITLE OF INVENTION: AGENTS, PARTICULARLY VASOACTIVE INTESTINAL POLYPEPTIDE
; TITLE OF INVENTION: AND AGONISTS THEREOF
; FILE REFERENCE: 9050-0013.24
; CURRENT APPLICATION NUMBER: US/09/929,818
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/498,522
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 09/181,316
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 08/959,064
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 08/959,057
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VIP
; OTHER INFORMATION: analog
US-09-929-818-106

```

Query Match 34.4%; Score 33; DB 3; Length 28;
Best Local Similarity 70.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FNDVTTRLRE 15
||| |||:
Db 6 FNDNYTRLRK 15

RESULT 48

```

US-09-929-818-123
; Sequence 123, Application US/09929818
; Patent No. US2002099003A1
; GENERAL INFORMATION:
; APPLICANT: WILSON, LELAND F.
; APPLICANT: PLACE, VIRGIL A.
; TITLE OF INVENTION: TREATMENT OF FEMALE SEXUAL DYSFUNCTION WITH VASOACTIVE
; TITLE OF INVENTION: AGENTS, PARTICULARLY VASOACTIVE INTESTINAL POLYPEPTIDE
; TITLE OF INVENTION: AND AGONISTS THEREOF
; FILE REFERENCE: 9050-0013.24
; CURRENT APPLICATION NUMBER: US/09/929,818
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/498,522
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 09/181,316
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 08/959,064
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 08/959,057
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VIP
; OTHER INFORMATION: analog
US-09-929-818-123

```

```

Query Match          34.4%; Score 33; DB 3; Length 28;
Best Local Similarity 63.6%; Pred. No. 4.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

Qy 6 FNDVTTLRKN 16
| | | | | : |
Db 6 FTDNYTTLRKN 16

RESULT 49

RESUMI 43
US-11-262-067-106
; Sequence 106, Application US/11262067
; Publication No. US20060041021A1
; GENERAL INFORMATION:
; APPLICANT: WILSON, LELAND F.
; APPLICANT: PLACE, VIRGIL A.
; TITLE OF INVENTION: TREATMENT OF FEMALE SEXUAL DYSFUNCTION WITH VASOACTIVE
; TITLE OF INVENTION: AGENTS, PARTICULARLY VASOACTIVE INTESTINAL POLYPEPTIDE
; TITLE OF INVENTION: AND AGONISTS THEREOF
; FILE REFERENCE: 9050-0013.24
; CURRENT APPLICATION NUMBER: US/11/262,067
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 09/496,522
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 09/181,316
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 08/959,064
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 08/959,057
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 207

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VIP
US-11-262-067-106

Query Match      34.4%; Score 33; DB 6; Length 28;
Best Local Similarity 70.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      6 FNDVTTLRLE 15
      |||||
Db      6 FNDNYTRLRK 15

RESULT 50
US-11-262-067-123
; Sequence 123, Application US/11262067
; Publication No. US20060041021A1
; GENERAL INFORMATION:
; APPLICANT: WILSON, LELAND F.
; APPLICANT: PLACE, VIRGIL A.
; TITLE OF INVENTION: TREATMENT OF FEMALE SEXUAL DYSFUNCTION WITH VASOACTIVE
; TITLE OF INVENTION: AGENTS, PARTICULARLY VASOACTIVE INTESTINAL POLYPEPTIDE
; TITLE OF INVENTION: AND AGONISTS THEREOF
; FILE REFERENCE: 9050-0013.24
; CURRENT APPLICATION NUMBER: US/11/262,067
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 09/498,522
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 09/181,316
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 08/959,064
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 08/959,057
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic VIP
US-11-262-067-123

Query Match      34.4%; Score 33; DB 6; Length 28;
Best Local Similarity 63.6%; Pred. No. 4.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      6 FNDVTTLRLEN 16
      |||||
Db      6 FTDNYTRLRKN 16

RESULT 51
US-10-600-070-28
; Sequence 28, Application US/10600070
; Publication No. US20040139500A1
; GENERAL INFORMATION:
; APPLICANT: Oosteryoung, Katherine W.
; APPLICANT: Vitha, Stanislaw
; APPLICANT: Koksharova, Olga A.
; APPLICANT: Gao, Hongo
; TITLE OF INVENTION: Plasmid Division and Related Genes and Proteins, and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: MSU-08153
; CURRENT APPLICATION NUMBER: US/10/600,070
```

```
; CURRENT FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; TYPE: PRT
; LENGTH: 30
; ORGANISM: Arabidopsis thaliana
US-10-600-070-28

Query Match      34.4%; Score 33; DB 4; Length 30;
Best Local Similarity 37.5%; Pred. No. 5e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTRLREN 16
      |::|
Db      14 FQLCRLLPPATTKURRS 29

RESULT 52
US-10-106-698-6745
; Sequence 6745, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6745
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (11)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (16)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (21)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (22)_
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6745

Query Match      34.4%; Score 33; DB 4; Length 32;
Best Local Similarity 44.4%; Pred. No. 5.3e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FEHCNFNDV 9
      |::|
Db      24 FDHCDPEEL 32

RESULT 53
US-10-424-599-144297
; Sequence 144297, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
```

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 144297
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101313C.1.pep
US-10-424-599-144297

Query Match 34.4%; Score 33; DB 4; Length 33;
Best Local Similarity 28.6%; Pred. No. 5.5e+02;
Matches 4; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 3 HCNFNDVTRLREN 16
:|:|::|:|:
Db 17 YCHQNNISTNLQDH 30

RESULT 54

US-10-218-102-260
; Sequence 260, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:

; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahlyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 260
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-260

Query Match 34.4%; Score 33; DB 4; Length 34;
Best Local Similarity 41.7%; Pred. No. 5.7e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 FNDVTRLRENE 17
||| |::|:
Db 20 FNDATNTMQESQ 31

RESULT 55

US-10-425-115-368852
; Sequence 368852, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 368852
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_99567C.1.pep
US-10-425-115-368852

Query Match 34.4%; Score 33; DB 4; Length 37;
Best Local Similarity 72.7%; Pred. No. 6.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 4 CNFNDVTRLR 14
||| |::|:
Db 8 CNF--VNTLR 16

RESULT 56

US-10-206-699-3
; Sequence 3, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:

; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-3

Query Match 33.3%; Score 32; DB 4; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FEHCNFDV 9
| | | | |
Db 2 FLFCNVDV 10

RESULT 57

US-10-206-699-7
; Sequence 7, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:

; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523

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; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-7

Query Match      33.3%; Score 32; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FEHCNFDV 9
Db 2 FYCNIINEV 10

RESULT 58
US-10-522-297-19
; Sequence 19, Application US/10522297
; Publication No. US20060035322A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: T-CELL EPITOPES IN ERYTHROPOIETIN
; FILE REFERENCE: MER-137
; CURRENT APPLICATION NUMBER: US/10/522,297
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: PCT/EP2003/008725
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: EP02017914.9
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential epitope sequences
US-10-522-297-19

Query Match      33.3%; Score 32; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFDVTT 11
Db 4 EHCNLNENIT 13

RESULT 59
US-10-522-297-20
; Sequence 20, Application US/10522297
; Publication No. US20060035322A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: T-CELL EPITOPES IN ERYTHROPOIETIN
; FILE REFERENCE: MER-137
; CURRENT APPLICATION NUMBER: US/10/522,297
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: PCT/EP2003/008725
; PRIOR FILING DATE: 2003-08-07

; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: EP02017914.9
; PRIOR FILING DATE: 2002-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential epitope sequences
US-10-522-297-20

Query Match      33.3%; Score 32; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFDVTT 11
Db 1 EHCNLNENIT 10

RESULT 60
US-10-530-061-1759
; Sequence 1759, Application US/10530061
; Publication No. US20060079453A1
; GENERAL INFORMATION:
; APPLICANT: SIDNEY, JOHN
; APPLICANT: SOUTHWOOD, SCOTT
; APPLICANT: SETTE, ALESSANDRO
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; FILE REFERENCE: 2060.033US02/EKS/M-M
; CURRENT APPLICATION NUMBER: US/10/530,061
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31308
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/416,207
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/417,269
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 2503
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1759
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Potential epitope sequences
US-10-530-061-1759

Query Match      33.3%; Score 32; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFDVTT 11
Db 1 EHCNLNENIT 10

RESULT 61
US-10-455-697-3
; Sequence 3, Application US/10455697
; Publication No. US20040018978A1
; GENERAL INFORMATION:
; APPLICANT: Campana, Wendy Marie
; APPLICANT: Myers, Robert R
; TITLE OF INVENTION: Use of erythropoietin and erythropoietin mimetics for the
; FILE REFERENCE: 6627-PA1090
; CURRENT APPLICATION NUMBER: US/10/455,697
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,286
; PRIOR FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
```

```
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: modified human sequence
US-10-455-697-3

Query Match      33.3%; Score 32; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
Db 1 EHCSLNENIT 10

RESULT 62
US-10-746-442-16
; Sequence 16, Application US/10746442
; Publication No. US20040121958A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; FILE REFERENCE: 07256/024001
; CURRENT APPLICATION NUMBER: US/10/746,442
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/08/928,074
; PRIOR FILING DATE: FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 08/611,307
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US97/04143
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Peptide Sequence (hEP0)
US-10-746-442-16

Query Match      33.3%; Score 32; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
Db 2 EHCSLNENIT 11

RESULT 63
US-11-036-867-16
; Sequence 16, Application US/11036867
; Publication No. US20050164948A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/11/036,867
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,074
; FILING DATE: 11-SEP-1997
; APPLICATION NUMBER: 08/611,307
; FILING DATE: 05-MAR-1996
; APPLICATION NUMBER: PCT/US97/04143
; FILING DATE: 05-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07256/024001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-036-867-16

Query Match      33.3%; Score 32; DB 6; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
Db 2 EHCSLNENIT 11

RESULT 64
US-10-206-699-254
; Sequence 254, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 254
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-254

Query Match      33.3%; Score 32; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FEHCNFDV 9
Db 6 FLFCNVNDV 14

RESULT 65
US-10-206-699-258
; Sequence 258, Application US/10206699
```

```
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-206-699-258

Query Match      33.3%; Score 32; DB 4; Length 18;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 FEHCNFDV 9
      | : | | : |
Db      6 FIYCINIEV 14

RESULT 66
US-11-152-974A-117
; Sequence 117, Application US/11152974A
; Publication No. US20060051395A1
; GENERAL INFORMATION:
; APPLICANT: Wayne F. Beyer, Jr.
; APPLICANT: Robin Hyde-DeRuyscher
; APPLICANT: Paul T. Hamilton
; APPLICANT: Ray Edward Benson
; TITLE OF INVENTION: IFMBs to Promote the Specific Attachment of Target Analytes to th
; TITLE OF INVENTION: of Orthopedic Implants
; FILE REFERENCE: AFF006
; CURRENT APPLICATION NUMBER: US/11/152,974A
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: 60/580,019
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/651,338
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/651,747
; PRIOR FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 558
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated from phage display libraries
US-11-152-974A-117

Query Match      33.3%; Score 32; DB 6; Length 18;
Best Local Similarity 53.3%; Pred. No. 4.1e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy      4 CNFN--DVTTFLREN 16
      | | | | | | | |
Db      1 CNNNHRDVMNLRDN 15

RESULT 67
```

```
US-11-153-143A-117
; Sequence 117, Application US/11153143A
; Publication No. US20060051396A1
; GENERAL INFORMATION:
; APPLICANT: Paul T. Hamilton
; APPLICANT: Mark W. Grinstaff
; APPLICANT: Daniel J. Kenan
; APPLICANT: Dale J. Christensen
; TITLE OF INVENTION: Biofunctional Coatings
; FILE REFERENCE: AFF005
; CURRENT APPLICATION NUMBER: US/11/153,143A
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: 60/580,019
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/651,338
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/651,747
; PRIOR FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 558
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated from phage display libraries
US-11-153-143A-117

Query Match      33.3%; Score 32; DB 6; Length 18;
Best Local Similarity 53.3%; Pred. No. 4.1e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy      4 CNFN--DVTTFLREN 16
      | | | | | | | |
Db      1 CNNNHRDVMNLRDN 15

RESULT 68
US-10-206-699-289
; Sequence 289, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 289
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-206-699-289

Query Match      33.3%; Score 32; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FEHCNFDV 9
      | | | | |
Db      9 FLFCNVNDV 17
```



```
RESULT 69
US-10-206-699-293
; Sequence 293, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 293
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-293

Query Match      33.3%; Score 32; DB 4; Length 20;
Best Local Similarity 55.6%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 FEHCNFDV 9
      | | | | |
Db      9 FIVCINEV 17

RESULT 70
US-10-032-221B-29
; Sequence 29, Application US/10032221B
; Publication No. US20030144481A1
; GENERAL INFORMATION:
; APPLICANT: Kalluri, Raghuram
; TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE THEREOF
; FILE REFERENCE: 2312/2082B (formerly 1440.1027-016)
; CURRENT APPLICATION NUMBER: US/10/032,221B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/00565
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/625,191
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/543,371
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: US 09/479,118
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/335,224
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/126,175
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/089,689
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T3 (amino acids 68-87 of SEQ ID NO:10)
US-10-032-221B-29

Query Match      33.3%; Score 32; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FEHCNFDV 9
      | | | | |
Db      9 FIVCINEV 17

RESULT 71
US-11-145-861-11
; Sequence 11, Application US/11145861
; Publication No. US20060014138A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul
; APPLICANT: Wang, Xiaoju
; TITLE OF INVENTION: Phage Microarray Profiling of the Humoral Response to Disease
; FILE REFERENCE: UM-09899
; CURRENT APPLICATION NUMBER: US/11/145,861
; CURRENT FILING DATE: 2005-06-06
; NUMBER OF SEQ ID NOS: 464
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-861-11

Query Match      33.3%; Score 32; DB 6; Length 20;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 EHCNFN 7
      : | | | |
Db      15 QHCDFN 20

RESULT 72
US-10-626-719-69
; Sequence 69, Application US/10626719
; Publication No. US20060036072A1
; GENERAL INFORMATION:
; APPLICANT: LICHA, KAI
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/10/626,719
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/528,200
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-626-719-69

Query Match      33.3%; Score 32; DB 5; Length 28;
Best Local Similarity 53.8%; Pred. No. 6.7e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      3 HCNFNDVTTLRE 15
      | | | | |
```

```
Db      3 HAVFTDNYTRLRK 15

RESULT 73
US-10-522-297-2
; Sequence 2, Application US/10522297
; Publication No. US20060035322A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: T-CELL EPITOPES IN ERYTHROPOIETIN
; FILE REFERENCE: MER-137
; CURRENT APPLICATION NUMBER: US/10/522,297
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: PCT/EP2003/008725
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: EP02017914.9
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-522-297-2

Query Match      33.3%; Score 32; DB 5; Length 33;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 3; Gaps 0;

QY      2 EHCNFDVTT 11
      |||:|:|
Db      22 EHCSLNNIT 31

RESULT 74
US-10-437-963-149572
; Sequence 149572, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 149572
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(34)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_49892C.1.pep
US-10-437-963-149572

Query Match      33.3%; Score 32; DB 4; Length 34;
Best Local Similarity 62.5%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY      4 CNFNDVTT 11
      |||:|:|

Db      26 CNYNTVNT 33

RESULT 75
US-10-424-599-206856
; Sequence 206856, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206856
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28818C.1.pep
US-10-424-599-206856

Query Match      33.3%; Score 32; DB 4; Length 35;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FEHCNFDV 9
      |||||
Db      20 FYPCNFNGV 28

RESULT 76
US-10-808-187-158
; Sequence 158, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 158
; LENGTH: 36
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; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-158

Query Match 33.3%; Score 32; DB 5; Length 36;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 11
: || | |||
Db 11 YEHVTLNCVTT 21

RESULT 77

US-10-807-807-158
; Sequence 158, Application US/10807807
; Publication No. US20050181357A1

; GENERAL INFORMATION:

; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG

; APPLICANT: NICHOLLS, JOHN M.

; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; TITLE OF INVENTION: CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)

; FILE REFERENCE: V9661.0077

; CURRENT APPLICATION NUMBER: US/10/807,807

; CURRENT FILING DATE: 2004-03-24

; PRIOR APPLICATION NUMBER: 60/457,031

; PRIOR FILING DATE: 2003-03-24

; PRIOR APPLICATION NUMBER: 60/457,730

; PRIOR FILING DATE: 2003-03-26

; PRIOR APPLICATION NUMBER: 60/459,931

; PRIOR FILING DATE: 2003-04-02

; PRIOR APPLICATION NUMBER: 60/460,357

; PRIOR FILING DATE: 2003-04-03

; PRIOR APPLICATION NUMBER: 60/461,265

; PRIOR FILING DATE: 2003-04-08

; PRIOR APPLICATION NUMBER: 60/462,805

; PRIOR FILING DATE: 2003-04-14

; PRIOR APPLICATION NUMBER: 60/464,886

; PRIOR FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: 60/465,738

; PRIOR FILING DATE: 2003-04-25

; PRIOR APPLICATION NUMBER: 60/470,935

; PRIOR FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 2487

; SOFTWARE: PatentIn ver. 3.2

; SEQ ID NO 158

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-158

Query Match 33.3%; Score 32; DB 5; Length 36;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 11
: || | |||
Db 11 YEHVTLNCVTT 21

RESULT 78

US-11-004-399-33

; Sequence 33, Application US/11004399

; Publication No. US20060053516A1

; GENERAL INFORMATION:

; APPLICANT: Chye, Mee Lee

; APPLICANT: Li, Hong Ye

; APPLICANT: Ramalingam, Sathiskumar

; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S:
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399

; CURRENT FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: US 60/527,637

; PRIOR FILING DATE: 2003-12-03

; NUMBER OF SEQ ID NOS: 4043

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 33

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: pCV1

US-11-004-399-33

Query Match 33.3%; Score 32; DB 6; Length 36;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 11
: || | |||
Db 11 YEHVTLNCVTT 21

RESULT 79

US-11-004-399-851

; Sequence 851, Application US/11004399

; Publication No. US20060053516A1

; GENERAL INFORMATION:

; APPLICANT: Chye, Mee Lee

; APPLICANT: Li, Hong Ye

; APPLICANT: Ramalingam, Sathiskumar

; APPLICANT: Poon, Leo Lit Man

; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide

; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S:

; FILE REFERENCE: 2587/73166/RDK

; CURRENT APPLICATION NUMBER: US/11/004,399

; CURRENT FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: US 60/527,637

; PRIOR FILING DATE: 2003-12-03

; NUMBER OF SEQ ID NOS: 4043

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 851

; LENGTH: 36

; TYPE: PRT

; ORGANISM: SARS-CoV Virus

US-11-004-399-851

Query Match 33.3%; Score 32; DB 6; Length 36;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 11
: || | |||
Db 11 YEHVTLNCVTT 21

RESULT 80

US-11-004-399-3346

; Sequence 3346, Application US/11004399

; Publication No. US20060053516A1

; GENERAL INFORMATION:

; APPLICANT: Chye, Mee Lee

; APPLICANT: Li, Hong Ye

; APPLICANT: Ramalingam, Sathiskumar

; APPLICANT: Poon, Leo Lit Man

; APPLICANT: Peiris, Joseph Sriyal Malik

; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide

```
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SARS
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3346
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCV2
US-11-004-399-3346

Query Match          33.3%; Score 32; DB 6; Length 36;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 11
   :||| |
Db 11 YEVTLNCVTT 21

RESULT 81
US-11-004-399-3625
; Sequence 3625, Application US/11004399
; Publication No. US20050053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3625
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCV6
US-11-004-399-3625

Query Match          33.3%; Score 32; DB 6; Length 36;
Best Local Similarity 54.5%; Pred. No. 8.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 11
   :||| |
Db 11 YEVTLNCVTT 21

RESULT 82
US-11-127-877-538
; Sequence 538, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. P.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: Amyloid-Beta Protein Production
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
```

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; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 538
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-538

Query Match          33.3%; Score 32; DB 6; Length 38;
Best Local Similarity 35.3%; Pred. No. 9.4e+02;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 FEHCNFDVTT 17
   :||| |
Db 16 FMECNISHSADLPVND 32

RESULT 83
US-09-462-713-8
; Sequence 8, Application US/09462713
; Publication No. US20030054012A1
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Mreny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
; FILE REFERENCE: 015280-361100US
; CURRENT APPLICATION NUMBER: US/09/462,713
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ib loop region
; OTHER INFORMATION: of ntPE-V3MN26 protein
US-09-462-713-8

Query Match          33.3%; Score 32; DB 3; Length 40;
Best Local Similarity 80.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCNFN 7
   :||| |
Db 6 HCNYN 10

RESULT 84
US-10-038-612-55
; Sequence 55, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
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; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 40
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: PDGFR-a
US-10-038-612-55

Query Match 33.3%; Score 32; DB 4; Length 40;
Best Local Similarity 33.3%; Pred. No. 9.9e+02;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 EHCNPNVTRLREN 16
|.:|.:|.:|.:|.:|.:|
Db 2 EYCFYGDLYNLYLKN 16

RESULT 85
US-10-424-599-244557
; Sequence 244557, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 244557
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_62862C.1.pap
US-10-424-599-244557

Query Match 33.3%; Score 32; DB 4; Length 40;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNP 6
|.:|.:|.:|
Db 11 FDHCSF 16

RESULT 86
US-10-659-036-8
; Sequence 8, Application US/10659036
; Publication No. US20050079171A1
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Mrsny, Randall J.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens for
; FILE REFERENCE: 015280-361200US
; CURRENT APPLICATION NUMBER: US/10/659,036
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US 60/056,924
; PRIOR FILING DATE: 1997-07-11
; PRIOR APPLICATION NUMBER: WO PCT/US98/14336
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 09/462,713

; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:1b loop region
; OTHER INFORMATION: of ntPE-V3MN26
US-10-659-036-8

Query Match 33.3%; Score 32; DB 5; Length 40;
Best Local Similarity 80.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCNFN 7
|.:|.:|.:|
Db 6 HCNYN 10

RESULT 87
US-09-989-919-123
; Sequence 123, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pri
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-919-123

Query Match 32.3%; Score 31; DB 3; Length 15;
Best Local Similarity 30.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNPNVDVT 10
|.:|.:|.:|.:|.:|
Db 4 YKHCHNNLS 13

RESULT 88
US-10-522-297-18
; Sequence 18, Application US/10522297
; Publication No. US20060035322A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: T-CELL EPITOPES IN ERYTHROPOIETIN
; FILE REFERENCE: MER-137
; CURRENT APPLICATION NUMBER: US/10/522,297
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: PCT/EP2003/008725
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: EP02017914.9
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential epitope sequences
US-10-522-297-18

Query Match      32.3%; Score 31; DB 5; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 EHCNFND 8
Db      7 EHCSLNE 13

RESULT 89
US-10-206-699-261
; Sequence 261, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MBHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 261
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-261

Query Match      32.3%; Score 31; DB 4; Length 18;
Best Local Similarity 35.3%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTRLRENE 17
Db      2 FMFCNINNVCFASND 18

RESULT 90
US-10-007-280A-185
; Sequence 185, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DBX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 185
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-185

Query Match      32.3%; Score 31; DB 4; Length 21;
Best Local Similarity 25.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy      2 EHCNFNDVTRLRENE 17
Db      4 QQLGFSEIISRLQSNQ 19

RESULT 91
US-10-622-675-31
; Sequence 31, Application US/10622675
; Publication No. US20050026215A1
; GENERAL INFORMATION:
; APPLICANT: Predki, Paul F.
; APPLICANT: Guo, Hong
; TITLE OF INVENTION: METHOD FOR THE PREDICTION OF AN EPITOPE
; FILE REFERENCE: 10959-013-999
; CURRENT APPLICATION NUMBER: US/10/622,675
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Yeast
US-10-622-675-31

Query Match      32.3%; Score 31; DB 5; Length 21;
Best Local Similarity 40.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTRLRE 15
Db      7 FLELNNEVTDLIRD 21

RESULT 92
US-10-895-226-31
; Sequence 31, Application US/10895226
; Publication No. US20050129678A1
; GENERAL INFORMATION:
; APPLICANT: Predki, Paul F.
; APPLICANT: Guo, Hong
; TITLE OF INVENTION: METHOD FOR THE PREDICTION OF AN EPITOPE
; FILE REFERENCE: 10959-019
; CURRENT APPLICATION NUMBER: US/10/895,226
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 10/622,675
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Yeast
US-10-895-226-31

Query Match      32.3%; Score 31; DB 5; Length 21;
Best Local Similarity 40.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTRLRE 15
Db      7 FLELNNEVTDLIRD 21

RESULT 93
US-10-946-647-806
; Sequence 806, Application US/10946647
```

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RESULT 97
US-10-032-221B-38
; Sequence 38, Application US/10032221B
; Publication No. US20030144481A1
; GENERAL INFORMATION:
; APPLICANT: kalluri, raghuram
; TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEIN
; FILE REFERENCE: 2312/2082B (formerly 1440.
; CURRENT APPLICATION NUMBER: US/10/032,221B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/00565
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/625,191
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/543,371
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: US 09/479,118
; PRIOR FILING DATE: 2000-01-07

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OM protein - protein search, using sw model

Run on: July 15, 2006, 00:36:31 ; Search time 27 Seconds
(without alignments)
36.020 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58

Perfect score: 96
Sequence: 1 FEHCNFDVTRLRENE 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 36205

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	34.4	31	7	US-11-134-871-3344
2	32	33.3	25	7	US-11-178-155-14
3	32	33.3	33	7	US-11-134-871-1716
4	32	33.3	39	7	US-11-178-155-34
5	31.5	32.8	26	7	US-11-178-155-2
6	31	32.3	19	7	US-11-134-871-7
7	31	32.3	19	7	US-11-134-871-3070
8	31	32.3	33	6	US-10-506-630A-31
9	31	32.3	38	6	US-10-506-630A-28
10	30	31.2	38	6	US-10-449-902-29052
11	29.5	30.7	25	7	US-11-134-871-3063
12	28.5	29.7	36	6	US-10-471-571A-686
13	28	29.2	24	6	US-10-560-723-184
14	28	29.2	38	7	US-11-243-438-24
15	27.5	28.6	18	7	US-11-134-871-2426
16	27	28.1	14	7	US-11-346-079-45
17	27	28.1	16	7	US-11-255-634-4
18	27	28.1	18	7	US-11-338-681-28
19	27	28.1	20	7	US-11-134-871-2246
20	27	28.1	20	7	US-11-134-871-2754
21	27	28.1	24	7	US-11-272-521-18
22	27	28.1	25	7	US-11-134-871-2274
23	27	28.1	28	7	US-11-334-622-37
24	27	28.1	29	7	US-11-134-871-2816
25	27	28.1	30	7	US-11-055-093-283
26	27	28.1	31	7	US-11-134-871-3344
27	27	28.1	32	7	US-11-178-155-14
28	27	28.1	33	7	US-11-134-871-1716
29	27	28.1	39	7	US-11-178-155-34
30	27	28.1	26	7	US-11-178-155-2
31	27	28.1	19	7	US-11-134-871-7
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33	27	28.1	33	6	US-10-506-630A-31
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36	27	28.1	25	7	US-11-134-871-3063
37	27	28.1	36	6	US-10-471-571A-686
38	27	28.1	24	6	US-10-560-723-184
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40	27	28.1	18	7	US-11-134-871-2426
41	27	28.1	14	7	US-11-346-079-45
42	27	28.1	16	7	US-11-255-634-4
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50	27	28.1	30	7	US-11-055-093-283
51	27	28.1	31	7	US-11-134-871-3344
52	27	28.1	32	7	US-11-178-155-14
53	27	28.1	33	7	US-11-134-871-1716
54	27	28.1	39	7	US-11-178-155-34
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101	24	25.0	22	6	US-10-953-613C-948	Sequence 948, App	174	23	24.0	26	6	US-10-449-902-42353	Sequence 42353, A
102	24	25.0	24	7	US-11-134-871-1897	Sequence 1897, Ap	175	23	24.0	27	7	US-11-134-871-2747	Sequence 2747, Ap
103	24	25.0	27	7	US-11-366-462-12	Sequence 12, Appl	176	23	24.0	27	7	US-11-366-462-10	Sequence 10, Appl
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105	24	25.0	29	7	US-11-134-871-1023	Sequence 1023, Ap	178	23	24.0	28	7	US-11-134-871-3521	Sequence 3521, Ap
106	24	25.0	31	6	US-10-953-613C-944	Sequence 944, App	179	23	24.0	30	7	US-11-056-355B-3319	Sequence 339, App
107	24	25.0	31	7	US-11-134-871-1415	Sequence 1415, App	180	23	24.0	31	7	US-11-343-583-313	Sequence 313, App
108	24	25.0	33	7	US-11-368-086-108	Sequence 108, App	181	23	24.0	31	7	US-11-343-583-354	Sequence 354, App
109	24	25.0	33	7	US-11-254-500-91	Sequence 91, Appl	182	23	24.0	32	7	US-11-134-871-1187	Sequence 1187, Ap
110	24	25.0	34	6	US-10-953-613C-949	Sequence 949, App	183	23	24.0	33	7	US-11-274-682-38	Sequence 38, Appl
111	24	25.0	34	7	US-11-134-871-1097	Sequence 1097, Ap	184	23	24.0	35	6	US-10-953-349-13974	Sequence 13974, A
112	24	25.0	36	6	US-10-449-902-44950	Sequence 44950, A	185	23	24.0	36	7	US-11-134-871-892	Sequence 892, App
113	24	25.0	37	7	US-11-134-871-452	Sequence 452, App	186	23	24.0	37	6	US-10-449-902-43795	Sequence 43795, A
114	24	25.0	38	6	US-10-471-571A-4448	Sequence 4448, App	187	23	24.0	37	6	US-10-449-902-47439	Sequence 47439, A
115	23.5	24.5	13	7	US-11-005-836-51	Sequence 51, Appl	188	23	24.0	37	7	US-11-055-093-188	Sequence 188, App
116	23.5	24.5	25	7	US-11-134-871-2617	Sequence 2617, Ap	189	23	24.0	38	7	US-11-134-871-2024	Sequence 2024, Ap
117	23.5	24.5	27	7	US-11-134-871-3151	Sequence 3151, Ap	190	23	24.0	40	7	US-11-366-001-140	Sequence 140, App
118	23.5	24.5	27	7	US-11-187-891-39	Sequence 39, Appl	191	22.5	23.4	17	7	US-11-134-871-641	Sequence 641, App
119	23	24.0	9	7	US-11-061-841-217	Sequence 217, App	192	22.5	23.4	18	7	US-11-272-521-37	Sequence 37, Appl
120	23	24.0	10	7	US-11-134-871-626	Sequence 626, App	193	22.5	23.4	18	7	US-11-234-731-518	Sequence 518, App
121	23	24.0	10	7	US-11-134-871-2832	Sequence 2832, Ap	194	22.5	23.4	19	7	US-11-134-871-2367	Sequence 2367, Ap
122	23	24.0	11	6	US-10-953-613C-25	Sequence 25, Appl	195	22.5	23.4	19	7	US-11-234-731-341	Sequence 341, App
123	23	24.0	11	6	US-10-953-613C-40	Sequence 40, Appl	196	22.5	23.4	22	7	US-11-259-950-22	Sequence 22, Appl
124	23	24.0	11	7	US-11-134-871-711	Sequence 711, App	197	22.5	23.4	24	7	US-11-272-521-20	Sequence 20, Appl
125	23	24.0	11	7	US-11-234-731-15	Sequence 15, Appl	198	22	22.9	9	7	US-11-340-431-124	Sequence 124, App
126	23	24.0	11	7	US-11-234-731-26	Sequence 26, Appl	199	22	22.9	9	7	US-11-340-431-162	Sequence 162, App
127	23	24.0	14	6	US-10-449-902-28668	Sequence 28668, A	200	22	22.9	10	7	US-11-061-841-232	Sequence 232, App
128	23	24.0	14	6	US-10-953-613C-950	Sequence 950, App	201	22	22.9	10	7	US-11-099-283B-607	Sequence 607, App
129	23	24.0	15	6	US-10-468-182-4	Sequence 4, Appli	202	22	22.9	11	7	US-11-054-072-7140	Sequence 7140, Ap
130	23	24.0	15	7	US-11-295-192A-547	Sequence 547, App	203	22	22.9	11	7	US-11-054-072-7141	Sequence 7141, Ap
131	23	24.0	15	7	US-11-295-192A-548	Sequence 548, App	204	22	22.9	11	7	US-11-054-072-7142	Sequence 7142, Ap
132	23	24.0	15	7	US-11-295-192A-549	Sequence 549, App	205	22	22.9	11	7	US-11-054-072-7143	Sequence 7143, Ap
133	23	24.0	15	7	US-11-295-192A-550	Sequence 550, App	206	22	22.9	11	7	US-11-054-072-7144	Sequence 7144, Ap
134	23	24.0	15	7	US-11-295-192A-551	Sequence 551, App	207	22	22.9	11	7	US-11-054-072-7145	Sequence 7145, Ap
135	23	24.0	15	7	US-11-295-192A-552	Sequence 552, App	208	22	22.9	11	7	US-11-054-072-7146	Sequence 7146, Ap
136	23	24.0	15	7	US-11-295-192A-553	Sequence 553, App	209	22	22.9	11	7	US-11-054-072-7147	Sequence 7147, Ap
137	23	24.0	15	7	US-11-295-192A-554	Sequence 554, App	210	22	22.9	11	7	US-11-054-072-7148	Sequence 7148, Ap
138	23	24.0	15	7	US-11-295-192A-555	Sequence 555, App	211	22	22.9	11	7	US-11-054-072-7149	Sequence 7149, Ap
139	23	24.0	15	7	US-11-295-192A-556	Sequence 556, App	212	22	22.9	11	7	US-11-054-072-7150	Sequence 7150, Ap
140	23	24.0	15	7	US-11-295-192A-622	Sequence 622, App	213	22	22.9	11	7	US-11-054-072-7151	Sequence 7151, Ap
141	23	24.0	15	7	US-11-295-192A-623	Sequence 623, App	214	22	22.9	11	7	US-11-054-072-7152	Sequence 7152, Ap
142	23	24.0	15	7	US-11-295-192A-628	Sequence 628, App	215	22	22.9	11	7	US-11-054-072-7153	Sequence 7153, Ap
143	23	24.0	15	7	US-11-295-192A-629	Sequence 629, App	216	22	22.9	11	7	US-11-054-072-7154	Sequence 7154, Ap
144	23	24.0	15	7	US-11-295-192A-630	Sequence 630, App	217	22	22.9	11	7	US-11-054-072-7155	Sequence 7155, Ap
145	23	24.0	16	7	US-11-134-871-1793	Sequence 1793, Ap	218	22	22.9	11	7	US-11-054-072-7156	Sequence 7156, Ap
146	23	24.0	18	7	US-11-253-223-13	Sequence 13, Appl	219	22	22.9	11	7	US-11-054-072-7157	Sequence 7157, Ap
147	23	24.0	18	7	US-11-253-223-32	Sequence 32, Appl	220	22	22.9	11	7	US-11-054-072-7158	Sequence 7158, Ap
148	23	24.0	18	7	US-11-134-871-179	Sequence 179, App	221	22	22.9	11	7	US-11-054-072-7159	Sequence 7159, Ap
149	23	24.0	18	7	US-11-134-871-1536	Sequence 1536, Ap	222	22	22.9	11	7	US-11-054-072-7160	Sequence 7160, Ap
150	23	24.0	19	7	US-11-234-731-317	Sequence 317, App	223	22	22.9	11	7	US-11-054-072-7161	Sequence 7161, Ap
151	23	24.0	20	6	US-10-953-613C-8	Sequence 8, Appli	224	22	22.9	11	7	US-11-054-072-7162	Sequence 7162, Ap
152	23	24.0	20	6	US-10-953-613C-9	Sequence 9, Appli	225	22	22.9	11	7	US-11-054-072-7163	Sequence 7163, Ap
153	23	24.0	20	6	US-10-953-613C-30	Sequence 30, Appl	226	22	22.9	12	7	US-11-054-072-5220	Sequence 5220, Ap
154	23	24.0	20	6	US-10-953-613C-33	Sequence 33, Appl	227	22	22.9	12	7	US-11-054-072-5221	Sequence 5221, Ap
155	23	24.0	20	7	US-11-176-182-108	Sequence 108, App	228	22	22.9	12	7	US-11-054-072-5222	Sequence 5222, Ap
156	23	24.0	20	7	US-11-268-959-44	Sequence 44, Appl	229	22	22.9	12	7	US-11-054-072-5223	Sequence 5223, Ap
157	23	24.0	20	7	US-11-343-583-149	Sequence 149, App	230	22	22.9	12	7	US-11-054-072-5224	Sequence 5224, Ap
158	23	24.0	20	7	US-11-134-871-857	Sequence 857, App	231	22	22.9	12	7	US-11-054-072-5225	Sequence 5225, Ap
159	23	24.0	20	7	US-11-234-731-5	Sequence 5, Appli	232	22	22.9	12	7	US-11-054-072-5226	Sequence 5226, Ap
160	23	24.0	20	7	US-11-234-731-6	Sequence 6, Appli	233	22	22.9	12	7	US-11-054-072-5227	Sequence 5227, Ap
161	23	24.0	20	7	US-11-234-731-16	Sequence 16, Appl	234	22	22.9	12	7	US-11-054-072-5228	Sequence 5228, Ap
162	23	24.0	20	7	US-11-234-731-19	Sequence 19, Appl	235	22	22.9	12	7	US-11-054-072-5229	Sequence 5229, Ap
163	23	24.0	20	7	US-11-234-731-180	Sequence 180, App	236	22	22.9	12	7	US-11-054-072-5230	Sequence 5230, Ap
164	23	24.0	20	7	US-11-234-731-198	Sequence 198, App	237	22	22.9	12	7	US-11-054-072-5231	Sequence 5231, Ap
165	23	24.0	21	7	US-11-251-465-56	Sequence 56, Appl	238	22	22.9	12	7	US-11-054-072-5232	Sequence 5232, Ap
166	23	24.0	21	7	US-11-134-871-2391	Sequence 2391, Ap	239	22	22.9	12	7	US-11-054-072-5233	Sequence 5233, Ap
167	23	24.0	22	6	US-10-953-613C-947	Sequence 947, App	240	22	22.9	12	7	US-11-054-072-5234	Sequence 5234, Ap
168	23	24.0	22	7	US-11-142-051-15	Sequence 15, Appl	241	22	22.9	12	7	US-11-054-072-5235	Sequence 5235, Ap
169	23	24.0	22	7	US-11-134-871-2769	Sequence 2769, Ap	242	22	22.9	12	7	US-11-054-072-5236	Sequence 5236, Ap
170	23	24.0	23	7	US-11-134-871-3153	Sequence 3153, Ap	243	22	22.9	12	7	US-11-054-072-5237	Sequence 5237, Ap
171	23	24.0	23	7	US-11-134-871-3450	Sequence 3450, Ap	244	22	22.9	12	7	US-11-054-072-5238	Sequence 5238, Ap

245	22	22.9	12	7	US-11-054-072-5339	Sequence 5239, Ap	318	22	22.9	20	7	US-11-301-554-2157	Sequence 2157, Ap
246	22	22.9	12	7	US-11-054-072-5240	Sequence 5240, Ap	319	22	22.9	20	7	US-11-134-871-2708	Sequence 2708, Ap
247	22	22.9	12	7	US-11-054-072-5241	Sequence 5241, Ap	320	22	22.9	20	7	US-11-150-871A-7	Sequence 7, Appl
248	22	22.9	12	7	US-11-054-072-5242	Sequence 5242, Ap	321	22	22.9	20	7	US-11-234-731-3	Sequence 3, Appl
249	22	22.9	12	7	US-11-054-072-5243	Sequence 5243, Ap	322	22	22.9	20	7	US-11-234-731-18	Sequence 18, Appl
250	22	22.9	12	7	US-11-054-072-6732	Sequence 6732, Ap	323	22	22.9	20	7	US-11-234-731-363	Sequence 363, App
251	22	22.9	12	7	US-11-054-072-6733	Sequence 6733, Ap	324	22	22.9	20	7	US-11-122-986-704	Sequence 704, App
252	22	22.9	12	7	US-11-054-072-6734	Sequence 6734, Ap	325	22	22.9	21	7	US-11-134-871-617	Sequence 617, App
253	22	22.9	12	7	US-11-054-072-6735	Sequence 6735, Ap	326	22	22.9	21	7	US-11-134-871-1153	Sequence 1153, Ap
254	22	22.9	12	7	US-11-054-072-6736	Sequence 6736, Ap	327	22	22.9	21	7	US-11-134-871-2284	Sequence 2284, Ap
255	22	22.9	12	7	US-11-054-072-6737	Sequence 6737, Ap	328	22	22.9	21	7	US-11-134-871-2578	Sequence 2578, Ap
256	22	22.9	12	7	US-11-054-072-6738	Sequence 6738, Ap	329	22	22.9	21	7	US-11-134-871-2911	Sequence 2911, Ap
257	22	22.9	12	7	US-11-054-072-6739	Sequence 6739, Ap	330	22	22.9	22	7	US-11-134-871-2924	Sequence 2924, Ap
258	22	22.9	12	7	US-11-054-072-6740	Sequence 6740, Ap	331	22	22.9	22	7	US-11-134-871-2995	Sequence 2995, Ap
259	22	22.9	12	7	US-11-054-072-6741	Sequence 6741, Ap	332	22	22.9	22	7	US-11-134-871-3473	Sequence 3473, Ap
260	22	22.9	12	7	US-11-054-072-6742	Sequence 6742, Ap	333	22	22.9	22	7	US-11-234-731-490	Sequence 490, App
261	22	22.9	12	7	US-11-054-072-6743	Sequence 6743, Ap	334	22	22.9	23	7	US-11-134-871-990	Sequence 990, App
262	22	22.9	12	7	US-11-054-072-6744	Sequence 6744, Ap	335	22	22.9	23	7	US-11-134-871-2876	Sequence 2876, Ap
263	22	22.9	12	7	US-11-054-072-6745	Sequence 6745, Ap	336	22	22.9	24	7	US-11-134-871-274	Sequence 274, App
264	22	22.9	12	7	US-11-054-072-6746	Sequence 6746, Ap	337	22	22.9	24	7	US-11-134-871-774	Sequence 774, App
265	22	22.9	12	7	US-11-054-072-6747	Sequence 6747, Ap	338	22	22.9	25	6	US-10-541-920-14	Sequence 14, Appl
266	22	22.9	12	7	US-11-054-072-6748	Sequence 6748, Ap	339	22	22.9	25	7	US-11-134-871-2981	Sequence 2981, Ap
267	22	22.9	12	7	US-11-054-072-6749	Sequence 6749, Ap	340	22	22.9	26	7	US-11-134-871-281	Sequence 281, App
268	22	22.9	12	7	US-11-054-072-6750	Sequence 6750, Ap	341	22	22.9	26	7	US-11-134-871-1895	Sequence 1895, Ap
269	22	22.9	12	7	US-11-054-072-6751	Sequence 6751, Ap	342	22	22.9	26	7	US-11-134-871-2513	Sequence 2513, Ap
270	22	22.9	12	7	US-11-054-072-6752	Sequence 6752, Ap	343	22	22.9	26	7	US-11-134-871-2687	Sequence 2687, Ap
271	22	22.9	12	7	US-11-054-072-6753	Sequence 6753, Ap	344	22	22.9	26	7	US-11-134-871-3180	Sequence 3180, Ap
272	22	22.9	12	7	US-11-054-072-6754	Sequence 6754, Ap	345	22	22.9	26	7	US-11-134-871-3514	Sequence 3514, Ap
273	22	22.9	12	7	US-11-054-072-6755	Sequence 6755, Ap	346	22	22.9	27	6	US-10-541-920-15	Sequence 15, Appl
274	22	22.9	13	7	US-11-054-072-4812	Sequence 4812, Ap	347	22	22.9	27	7	US-11-350-752-25	Sequence 25, Appl
275	22	22.9	13	7	US-11-054-072-4813	Sequence 4813, Ap	348	22	22.9	27	7	US-11-350-749-25	Sequence 25, Appl
276	22	22.9	13	7	US-11-054-072-4814	Sequence 4814, Ap	349	22	22.9	27	7	US-11-134-871-2221	Sequence 2221, Ap
277	22	22.9	13	7	US-11-054-072-4815	Sequence 4815, Ap	350	22	22.9	28	7	US-11-134-871-1359	Sequence 1359, Ap
278	22	22.9	13	7	US-11-054-072-4816	Sequence 4816, Ap	351	22	22.9	28	7	US-11-356-373-22	Sequence 22, Appl
279	22	22.9	13	7	US-11-054-072-4817	Sequence 4817, Ap	352	22	22.9	29	7	US-11-216-721-24	Sequence 24, Appl
280	22	22.9	13	7	US-11-054-072-4818	Sequence 4818, Ap	353	22	22.9	29	7	US-11-216-721-25	Sequence 25, Appl
281	22	22.9	13	7	US-11-054-072-4819	Sequence 4819, Ap	354	22	22.9	29	7	US-11-216-721-29	Sequence 29, Appl
282	22	22.9	13	7	US-11-054-072-4820	Sequence 4820, Ap	355	22	22.9	30	7	US-11-301-554-2009	Sequence 2009, Ap
283	22	22.9	13	7	US-11-054-072-4821	Sequence 4821, Ap	356	22	22.9	32	6	US-10-953-349-12581	Sequence 12581, A
284	22	22.9	13	7	US-11-054-072-4822	Sequence 4822, Ap	357	22	22.9	32	7	US-11-134-871-985	Sequence 985, App
285	22	22.9	13	7	US-11-054-072-4823	Sequence 4823, Ap	358	22	22.9	32	7	US-11-055-098-424	Sequence 424, App
286	22	22.9	13	7	US-11-054-072-4824	Sequence 4824, Ap	359	22	22.9	34	7	US-11-301-744-434	Sequence 424, App
287	22	22.9	13	7	US-11-054-072-4825	Sequence 4825, Ap	360	22	22.9	35	6	US-10-471-502-56693	Sequence 234, App
288	22	22.9	13	7	US-11-054-072-4826	Sequence 4826, Ap	361	22	22.9	35	6	US-10-449-902-56693	Sequence 56693, A
289	22	22.9	13	7	US-11-054-072-4827	Sequence 4827, Ap	362	22	22.9	36	7	US-11-134-871-2424	Sequence 2424, Ap
290	22	22.9	13	7	US-11-054-072-4828	Sequence 4828, Ap	363	22	22.9	36	6	US-10-953-349-12580	Sequence 12580, A
291	22	22.9	13	7	US-11-054-072-4829	Sequence 4829, Ap	364	22	22.9	38	6	US-10-953-349-10330	Sequence 10330, A
292	22	22.9	13	7	US-11-054-072-4830	Sequence 4830, Ap	365	22	22.9	38	6	US-10-471-571A-8	Sequence 8, Appl
293	22	22.9	13	7	US-11-054-072-4831	Sequence 4831, Ap	366	22	22.9	38	6	US-10-449-902-28666	Sequence 28666, A
294	22	22.9	13	7	US-11-054-072-4832	Sequence 4832, Ap	367	22	22.9	38	7	US-11-056-355B-20389	Sequence 20389, A
295	22	22.9	13	7	US-11-054-072-4833	Sequence 4833, Ap	368	22	22.9	40	6	US-10-449-902-29143	Sequence 29143, A
296	22	22.9	13	7	US-11-054-072-4834	Sequence 4834, Ap	369	22	22.9	40	6	US-10-449-902-36195	Sequence 36195, A
297	22	22.9	13	7	US-11-054-072-4835	Sequence 4835, Ap	370	21.5	22.4	20	7	US-11-134-871-1110	Sequence 1110, App
298	22	22.9	14	6	US-10-342-232-33	Sequence 33, Appl	371	21.5	22.4	21	7	US-11-366-001-102	Sequence 102, App
299	22	22.9	16	7	US-11-122-986-700	Sequence 700, App	372	21.5	22.4	28	6	US-10-890-071-53	Sequence 53, Appl
300	22	22.9	16	7	US-11-350-752-74	Sequence 74, Appl	373	21.5	22.4	28	7	US-11-366-001-217	Sequence 217, App
301	22	22.9	16	7	US-11-350-749-74	Sequence 74, Appl	374	21.5	22.4	35	6	US-10-953-349-25416	Sequence 25416, A
302	22	22.9	17	7	US-11-134-871-855	Sequence 855, App	375	21.5	22.4	36	7	US-11-134-871-2736	Sequence 2736, Ap
303	22	22.9	17	7	US-11-134-871-2452	Sequence 2452, Ap	376	21.5	22.4	39	6	US-10-449-902-31263	Sequence 31263, A
304	22	22.9	17	7	US-11-249-692-42	Sequence 42, Appl	377	21	21.9	9	7	US-11-140-487A-800	Sequence 800, App
305	22	22.9	17	7	US-11-061-841-257	Sequence 257, App	378	21	21.9	9	7	US-11-332-378-13	Sequence 1035, Ap
306	22	22.9	18	7	US-11-234-731-294	Sequence 294, App	379	21	21.9	9	7	US-11-332-378-14	Sequence 14, Appl
307	22	22.9	19	6	US-10-530-584-9	Sequence 9, Appl	380	21	21.9	9	7	US-11-332-378-15	Sequence 15, Appl
308	22	22.9	19	6	US-10-530-584-11	Sequence 11, Appl	381	21	21.9	9	7	US-11-332-378-16	Sequence 16, Appl
309	22	22.9	19	7	US-11-134-871-2433	Sequence 2433, Ap	382	21	21.9	10	7	US-11-134-871-1047	Sequence 8, Appl
310	22	22.9	20	6	US-10-953-613C-6	Sequence 6, Appl	383	21	21.9	12	7	US-09-784-950-8	Sequence 8, Appl
311	22	22.9	20	6	US-10-953-613C-32	Sequence 32, Appl	384	21	21.9	12	6	US-10-953-613C-41	Sequence 41, Appl
312	22	22.9	20	6	US-10-953-613C-959	Sequence 959, App	385	21	21.9	12	7	US-11-280-988-14	Sequence 14, Appl
313	22	22.9	20	7	US-11-301-554-1959	Sequence 1929, Ap	386	21	21.9	12	7	US-11-234-731-27	Sequence 27, Appl
314	22	22.9	20	7	US-11-301-554-1971	Sequence 1971, Ap	387	21	21.9	13	6	US-10-953-613C-24	Sequence 24, Appl
315	22	22.9	20	7	US-11-301-554-1972	Sequence 1972, Ap	388	21	21.9	13	6	US-10-953-613C-39	Sequence 39, Appl
316	22	22.9	20	7	US-11-301-554-1973	Sequence 1973, Ap	389	21	21.9	13	7	US-11-274-634-28	Sequence 28, Appl
317	22	22.9	20	7	US-11-301-554-2156	Sequence 2156, Ap	390	21	21.9	13	7		

391	21	21.9	13	7	US-11-234-731-14	Sequence 14, Appl	464	21	21.9	23	7	US-11-134-871-17	Sequence 17, Appl
392	21	21.9	13	7	US-11-234-731-25	Sequence 25, Appl	465	21	21.9	23	7	US-11-134-871-2595	Sequence 2595, Ap
393	21	21.9	14	7	US-11-234-731-267	Sequence 267, Appl	466	21	21.9	23	7	US-11-234-731-7	Sequence 7, Appl
394	21	21.9	15	6	US-10-430-949-26	Sequence 26, Appl	467	21	21.9	25	7	US-11-332-378-29	Sequence 29, Appl
395	21	21.9	15	7	US-11-295-192A-155	Sequence 155, Appl	468	21	21.9	25	7	US-11-134-871-655	Sequence 655, App
396	21	21.9	15	7	US-11-295-192A-156	Sequence 156, Appl	469	21	21.9	25	7	US-11-134-871-894	Sequence 894, App
397	21	21.9	15	7	US-11-295-192A-157	Sequence 157, Appl	470	21	21.9	25	7	US-11-134-871-921	Sequence 921, App
398	21	21.9	15	7	US-11-295-192A-158	Sequence 158, Appl	471	21	21.9	25	7	US-11-134-871-1917	Sequence 1917, Ap
399	21	21.9	15	7	US-11-295-192A-159	Sequence 159, Appl	472	21	21.9	25	7	US-11-134-871-2638	Sequence 2638, Ap
400	21	21.9	15	7	US-11-295-192A-160	Sequence 160, Appl	473	21	21.9	25	7	US-11-134-871-3166	Sequence 3166, Ap
401	21	21.9	15	7	US-11-295-192A-161	Sequence 161, Appl	474	21	21.9	26	6	US-10-787-734-70	Sequence 70, Appl
402	21	21.9	15	7	US-11-295-192A-162	Sequence 162, Appl	475	21	21.9	26	6	US-10-787-734-73	Sequence 73, Appl
403	21	21.9	15	7	US-11-295-192A-163	Sequence 163, Appl	476	21	21.9	26	6	US-10-787-734-79	Sequence 79, Appl
404	21	21.9	15	7	US-11-295-192A-164	Sequence 164, Appl	477	21	21.9	26	7	US-11-121-282-74	Sequence 74, Appl
405	21	21.9	15	7	US-11-295-192A-165	Sequence 165, Appl	478	21	21.9	26	7	US-11-134-871-158	Sequence 158, App
406	21	21.9	15	7	US-11-295-192A-166	Sequence 166, Appl	479	21	21.9	27	6	US-10-525-126-243	Sequence 243, App
407	21	21.9	15	7	US-11-295-192A-167	Sequence 167, Appl	480	21	21.9	27	6	US-10-787-734-107	Sequence 107, App
408	21	21.9	15	7	US-11-295-192A-627	Sequence 627, Appl	481	21	21.9	27	6	US-10-787-734-110	Sequence 110, App
409	21	21.9	15	7	US-11-295-192A-933	Sequence 933, Appl	482	21	21.9	27	7	US-11-334-622-36	Sequence 36, Appl
410	21	21.9	15	7	US-11-295-192A-934	Sequence 934, Appl	483	21	21.9	27	7	US-11-134-871-2899	Sequence 2899, Ap
411	21	21.9	15	7	US-11-295-192A-935	Sequence 935, Appl	484	21	21.9	27	7	US-11-366-462-11	Sequence 11, Appl
412	21	21.9	15	7	US-11-295-192A-937	Sequence 937, Appl	485	21	21.9	28	7	US-11-134-871-556	Sequence 556, App
413	21	21.9	15	7	US-11-295-192A-937	Sequence 937, Appl	486	21	21.9	28	7	US-11-134-871-2599	Sequence 2599, Ap
414	21	21.9	15	7	US-11-295-192A-1178	Sequence 1178, Ap	487	21	21.9	29	7	US-11-216-721-23	Sequence 23, Appl
415	21	21.9	15	7	US-11-295-192A-1179	Sequence 1179, Ap	488	21	21.9	29	7	US-11-134-871-1928	Sequence 1928, Ap
416	21	21.9	15	7	US-11-295-192A-1180	Sequence 1180, Ap	489	21	21.9	29	7	US-11-134-871-2518	Sequence 2518, Ap
417	21	21.9	15	7	US-11-295-192A-1181	Sequence 1181, Ap	490	21	21.9	29	7	US-11-134-871-3173	Sequence 3173, Ap
418	21	21.9	15	7	US-11-295-192A-1182	Sequence 1182, Ap	491	21	21.9	30	6	US-10-449-902-30861	Sequence 30861, A
419	21	21.9	15	7	US-11-295-192A-1183	Sequence 1183, Ap	492	21	21.9	30	7	US-11-134-871-533	Sequence 533, App
420	21	21.9	15	7	US-11-134-871-216	Sequence 216, App	493	21	21.9	30	7	US-11-134-871-759	Sequence 759, App
421	21	21.9	15	7	US-11-134-871-327	Sequence 327, App	494	21	21.9	31	6	US-10-953-349-17746	Sequence 17746, A
422	21	21.9	15	7	US-11-134-871-3377	Sequence 3377, Ap	495	21	21.9	31	7	US-11-343-583-315	Sequence 315, App
423	21	21.9	16	6	US-10-526-062-15	Sequence 15, Appl	496	21	21.9	32	6	US-10-449-902-44042	Sequence 44042, A
424	21	21.9	16	7	US-11-332-378-2	Sequence 2, Appl	497	21	21.9	32	7	US-11-134-871-2126	Sequence 2126, Ap
425	21	21.9	16	7	US-11-295-192A-1262	Sequence 1262, Ap	498	21	21.9	33	7	US-11-134-871-1637	Sequence 1637, Ap
426	21	21.9	16	7	US-11-134-871-307	Sequence 307, App	499	21	21.9	33	7	US-11-134-871-2173	Sequence 2173, Ap
427	21	21.9	16	7	US-11-134-871-2705	Sequence 2705, Ap	500	21	21.9	33	7	US-11-134-871-2935	Sequence 2935, Ap
428	21	21.9	16	7	US-11-368-660-6	Sequence 6, Appl	501	21	21.9	33	7	US-11-056-358-51057	Sequence 51057, A
429	21	21.9	17	6	US-10-787-734-38	Sequence 38, Appl	502	21	21.9	34	7	US-11-055-098-171	Sequence 171, App
430	21	21.9	17	7	US-11-134-871-50	Sequence 50, Appl	503	21	21.9	34	7	US-11-301-744-171	Sequence 171, App
431	21	21.9	17	7	US-11-134-871-2587	Sequence 2587, Ap	504	21	21.9	35	6	US-10-787-734-21	Sequence 21, Appl
432	21	21.9	17	7	US-11-249-692-41	Sequence 41, Appl	505	21	21.9	36	7	US-11-134-871-2840	Sequence 2840, Ap
433	21	21.9	18	6	US-10-953-613C-21	Sequence 21, Appl	506	21	21.9	36	7	US-11-368-086-115	Sequence 115, App
434	21	21.9	18	6	US-10-953-613C-36	Sequence 36, Appl	507	21	21.9	38	6	US-10-787-734-105	Sequence 105, App
435	21	21.9	18	7	US-11-134-871-795	Sequence 795, App	508	21	21.9	39	6	US-10-953-349-25806	Sequence 25806, A
436	21	21.9	18	7	US-11-134-871-2203	Sequence 2203, Ap	509	21	21.9	39	6	US-10-449-902-33738	Sequence 33738, A
437	21	21.9	18	7	US-11-234-731-11	Sequence 11, Appl	510	20.5	21.4	10	7	US-11-262-484-3	Sequence 3, Appl
438	21	21.9	18	7	US-11-234-731-22	Sequence 22, Appl	511	20.5	21.4	12	7	US-11-054-072-6972	Sequence 6972, Ap
439	21	21.9	18	7	US-11-234-731-297	Sequence 297, App	512	20.5	21.4	12	7	US-11-054-072-6973	Sequence 6973, Ap
440	21	21.9	18	7	US-11-234-731-315	Sequence 315, App	513	20.5	21.4	12	7	US-11-054-072-6978	Sequence 6978, Ap
441	21	21.9	20	6	US-10-515-429-11	Sequence 11, Appl	514	20.5	21.4	12	7	US-11-054-072-6979	Sequence 6979, Ap
442	21	21.9	20	6	US-10-515-429-25	Sequence 25, Appl	515	20.5	21.4	12	7	US-11-054-072-6984	Sequence 6984, Ap
443	21	21.9	20	6	US-10-953-613C-5	Sequence 5, Appl	516	20.5	21.4	12	7	US-11-054-072-6985	Sequence 6985, Ap
444	21	21.9	20	6	US-10-953-613C-10	Sequence 10, Appl	517	20.5	21.4	12	7	US-11-054-072-6990	Sequence 6990, Ap
445	21	21.9	20	6	US-10-953-613C-11	Sequence 11, Appl	518	20.5	21.4	12	7	US-11-054-072-6991	Sequence 6991, Ap
446	21	21.9	20	6	US-10-953-613C-31	Sequence 31, Appl	519	20.5	21.4	13	7	US-11-054-072-5052	Sequence 5052, Ap
447	21	21.9	20	7	US-11-262-044-10	Sequence 10, Appl	520	20.5	21.4	13	7	US-11-054-072-5053	Sequence 5053, Ap
448	21	21.9	20	7	US-11-262-044-25	Sequence 25, Appl	521	20.5	21.4	13	7	US-11-054-072-5058	Sequence 5058, Ap
449	21	21.9	20	7	US-11-041-207-2	Sequence 2, Appl	522	20.5	21.4	13	7	US-11-054-072-5059	Sequence 5059, Ap
450	21	21.9	20	7	US-11-041-207-4	Sequence 4, Appl	523	20.5	21.4	13	7	US-11-054-072-5064	Sequence 5064, Ap
451	21	21.9	20	7	US-11-041-207-10	Sequence 10, Appl	524	20.5	21.4	13	7	US-11-054-072-5065	Sequence 5065, Ap
452	21	21.9	20	7	US-11-041-207-12	Sequence 12, Appl	525	20.5	21.4	13	7	US-11-054-072-5070	Sequence 5070, Ap
453	21	21.9	20	7	US-11-234-731-17	Sequence 17, Appl	526	20.5	21.4	13	7	US-11-054-072-5071	Sequence 5071, Ap
454	21	21.9	20	7	US-11-234-731-17	Sequence 17, Appl	527	20.5	21.4	27	7	US-11-134-871-643	Sequence 643, App
455	21	21.9	21	7	US-11-122-986-378	Sequence 378, App	528	20.5	21.4	29	7	US-11-134-871-2101	Sequence 2101, Ap
456	21	21.9	22	6	US-10-449-902-36001	Sequence 36001, A	529	20.5	21.4	39	6	US-10-449-902-36142	Sequence 36142, A
457	21	21.9	22	6	US-10-953-613C-15	Sequence 15, Appl	530	20	20.8	5	7	US-11-263-230-369	Sequence 369, App
458	21	21.9	22	7	US-11-209-206-5	Sequence 5, Appl	531	20	20.8	7	7	US-11-263-230-574	Sequence 574, App
459	21	21.9	22	7	US-11-134-871-3391	Sequence 3391, Ap	532	20	20.8	9	6	US-10-538-066-62	Sequence 62, Appl
460	21	21.9	23	6	US-10-953-613C-12	Sequence 12, Appl	533	20	20.8	9	7	US-11-140-487A-2	Sequence 2, Appl
461	21	21.9	23	6	US-10-953-613C-13	Sequence 13, Appl	534	20	20.8	9	7	US-11-140-487A-363	Sequence 363, App
462	21	21.9	23	6	US-10-953-613C-14	Sequence 14, Appl	535	20	20.8	9	7	US-11-140-487A-558	Sequence 558, App
463	21	21.9	23	6	US-10-953-613C-16	Sequence 16, Appl	536	20	20.8	9	7	US-11-140-487A-618	Sequence 618, App

537	20	20.8	9	7	US-11-332-378-12	Sequence 12, Appl	610	20	20.8	19	7	US-11-234-731-588	Sequence 588, App
538	20	20.8	7	7	US-11-099-283B-53	Sequence 53, Appl	611	20	20.8	6	6	US-10-505-848-40	Sequence 40, Appl
539	20	20.8	9	7	US-11-099-283B-515	Sequence 515, App	612	20	20.8	20	7	US-11-295-192A-1257	Sequence 1257, Ap
540	20	20.8	10	7	US-11-140-487A-988	Sequence 988, App	613	20	20.8	20	7	US-11-343-583-79	Sequence 79, Appl
541	20	20.8	10	7	US-11-140-487A-1815	Sequence 1815, Ap	614	20	20.8	20	7	US-11-343-583-106	Sequence 106, App
542	20	20.8	11	6	US-10-492-108-4	Sequence 4, Appli	615	20	20.8	20	7	US-11-041-207-5	Sequence 5, Appli
543	20	20.8	11	7	US-11-140-487A-1465	Sequence 1465, Ap	616	20	20.8	20	7	US-11-041-207-6	Sequence 6, Appli
544	20	20.8	11	7	US-11-134-871-2302	Sequence 2302, Ap	617	20	20.8	20	7	US-11-134-871-1092	Sequence 1092, Ap
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546	20	20.8	13	7	US-11-245-628-39	Sequence 693, App	619	20	20.8	20	7	US-11-234-731-107	Sequence 107, App
547	20	20.8	13	7	US-11-261-429-5	Sequence 5, Appli	620	20	20.8	20	7	US-11-234-731-134	Sequence 134, App
548	20	20.8	13	7	US-11-134-871-3202	Sequence 3202, Ap	621	20	20.8	21	7	US-11-134-871-836	Sequence 836, App
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552	20	20.8	15	7	US-11-140-487A-2226	Sequence 2226, Ap	625	20	20.8	22	7	US-11-356-373-5	Sequence 5, Appli
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563	20	20.8	15	7	US-11-295-192A-824	Sequence 824, App	636	20	20.8	27	7	US-11-134-871-480	Sequence 480, App
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567	20	20.8	15	7	US-11-295-192A-828	Sequence 828, App	640	20	20.8	28	7	US-11-134-871-3358	Sequence 3358, App
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571	20	20.8	15	7	US-11-295-192A-832	Sequence 832, App	644	20	20.8	29	7	US-11-216-721-19	Sequence 19, Appl
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574	20	20.8	15	7	US-11-295-192A-979	Sequence 979, App	647	20	20.8	31	7	US-11-343-583-262	Sequence 262, App
575	20	20.8	15	7	US-11-295-192A-1177	Sequence 1177, App	648	20	20.8	31	7	US-11-343-583-289	Sequence 289, App
576	20	20.8	16	7	US-11-134-871-2373	Sequence 2373, Ap	649	20	20.8	31	7	US-11-343-583-309	Sequence 309, App
577	20	20.8	16	7	US-11-264-509A-67	Sequence 67, Appl	650	20	20.8	31	7	US-11-343-583-312	Sequence 312, App
578	20	20.8	16	7	US-11-266-957-17	Sequence 17, Appl	651	20	20.8	31	7	US-11-343-583-314	Sequence 314, App
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829	19	19.8	13	7	US-11-134-871-2624	Sequence 2624, Ap	902	19	19.8	18	7	US-11-134-871-1271	Sequence 1271, Ap
830	19	19.8	13	7	US-11-187-891-30	Sequence 30, Appl	903	19	19.8	18	7	US-11-134-871-2428	Sequence 2428, Ap
831	19	19.8	14	7	US-11-122-986-734	Sequence 734, Ap	904	19	19.8	18	7	US-11-134-871-3400	Sequence 3400, Ap
832	19	19.8	14	7	US-11-122-986-735	Sequence 735, Ap	905	19	19.8	18	7	US-11-234-731-189	Sequence 189, Ap
833	19	19.8	14	7	US-11-122-986-736	Sequence 736, Ap	906	19	19.8	18	7	US-10-839-442A-15	Sequence 15, Appl
834	19	19.8	14	7	US-11-343-583-1	Sequence 1, Appl	907	19	19.8	19	7	US-11-122-986-458	Sequence 458, Ap
835	19	19.8	14	7	US-11-134-871-462	Sequence 462, Ap	908	19	19.8	19	7	US-11-134-871-352	Sequence 352, Ap
836	19	19.8	14	7	US-11-134-871-572	Sequence 572, Ap	909	19	19.8	19	7	US-11-234-731-533	Sequence 533, Ap
837	19	19.8	14	7	US-11-134-871-1090	Sequence 1090, Ap	910	19	19.8	19	7	US-11-234-731-579	Sequence 579, Ap
838	19	19.8	14	7	US-11-134-871-2906	Sequence 2906, Ap	911	19	19.8	20	6	US-10-505-848-9	Sequence 9, Appl
839	19	19.8	14	7	US-11-234-731-235	Sequence 235, Ap	912	19	19.8	20	6	US-10-706-435A-17	Sequence 17, Appl
840	19	19.8	15	1	US-09-784-950-12	Sequence 12, Appl	913	19	19.8	20	6	US-10-539-677-29	Sequence 29, Appl
841	19	19.8	15	6	US-10-506-877-48	Sequence 48, Appl	914	19	19.8	20	6	US-10-792-640-29	Sequence 29, Appl
842	19	19.8	15	7	US-11-140-487A-2248	Sequence 2248, Ap	915	19	19.8	20	6	US-10-792-640-30	Sequence 30, Appl
843	19	19.8	15	7	US-11-251-340-34	Sequence 34, Appl	916	19	19.8	20	7	US-11-301-554-1848	Sequence 1848, Ap
844	19	19.8	15	7	US-11-295-192A-342	Sequence 342, Ap	917	19	19.8	20	7	US-11-301-554-2099	Sequence 2099, Ap
845	19	19.8	15	7	US-11-295-192A-343	Sequence 343, Ap	918	19	19.8	20	7	US-11-301-554-2100	Sequence 2100, Ap
846	19	19.8	15	7	US-11-295-192A-344	Sequence 344, Ap	919	19	19.8	20	7	US-11-343-583-96	Sequence 96, Appl
847	19	19.8	15	7	US-11-295-192A-345	Sequence 345, Ap	920	19	19.8	20	7	US-11-041-207-11	Sequence 11, Appl
848	19	19.8	15	7	US-11-295-192A-347	Sequence 347, Ap	921	19	19.8	20	7	US-11-134-871-3499	Sequence 3499, Ap
849	19	19.8	15	7	US-11-295-192A-348	Sequence 348, Ap	922	19	19.8	20	7	US-11-234-731-134	Sequence 124, Ap
850	19	19.8	15	7	US-11-295-192A-347	Sequence 347, Ap	923	19	19.8	20	7	US-11-234-731-342	Sequence 342, Ap
851	19	19.8	15	7	US-11-295-192A-349	Sequence 349, Ap	924	19	19.8	21	7	US-11-234-731-381	Sequence 381, Ap
852	19	19.8	15	7	US-11-295-192A-350	Sequence 350, Ap	925	19	19.8	21	7	US-11-134-871-1429	Sequence 1429, Ap
853	19	19.8	15	7	US-11-295-192A-351	Sequence 351, Ap	926	19	19.8	22	6	US-10-449-902-29113	Sequence 29113, A
854	19	19.8	15	7	US-11-295-192A-595	Sequence 595, Ap	927	19	19.8	22	6	US-10-449-902-30087	Sequence 30087, A
855	19	19.8	15	7	US-11-295-192A-631	Sequence 631, Ap	928	19	19.8	22	7	US-11-213-668-94	Sequence 94, Appl
856	19	19.8	15	7	US-11-295-192A-632	Sequence 632, Ap	929	19	19.8	22	7	US-11-134-871-1760	Sequence 1760, Ap
857	19	19.8	15	7	US-11-295-192A-633	Sequence 633, Ap	930	19	19.8	22	7	US-11-134-871-3002	Sequence 3002, Ap
858	19	19.8	15	7	US-11-295-192A-989	Sequence 989, Ap	931	19	19.8	23	6	US-10-787-734-12	Sequence 12, Appl
859	19	19.8	15	7	US-11-134-871-3469	Sequence 3469, Ap	932	19	19.8	23	6	US-10-787-734-16	Sequence 16, Appl
860	19	19.8	15	7	US-11-346-079-112	Sequence 112, Ap	933	19	19.8	23	6	US-10-787-734-17	Sequence 17, Appl
861	19	19.8	16	6	US-10-526-151-24	Sequence 24, Appl	934	19	19.8	23	6	US-10-787-734-134	Sequence 134, Ap
862	19	19.8	16	6	US-10-531-659-205	Sequence 205, Ap	935	19	19.8	23	6	US-10-787-734-135	Sequence 135, Ap
863	19	19.8	16	6	US-10-526-060-41	Sequence 41, Appl	936	19	19.8	23	6	US-10-787-734-137	Sequence 137, Ap
864	19	19.8	16	7	US-11-122-986-631	Sequence 631, Ap	937	19	19.8	24	6	US-10-787-734-13	Sequence 13, Appl
865	19	19.8	16	7	US-11-134-871-2501	Sequence 2501, Ap	938	19	19.8	24	6	US-10-787-734-23	Sequence 23, Appl
866	19	19.8	16	7	US-11-346-079-7	Sequence 7, Appl	939	19	19.8	24	6	US-10-787-734-25	Sequence 25, Appl
867	19	19.8	16	7	US-10-542-516-36	Sequence 36, Appl	940	19	19.8	24	6	US-10-787-734-106	Sequence 106, Ap
868	19	19.8	17	7	US-11-134-871-2750	Sequence 2750, Ap	941	19	19.8	24	7	US-11-230-593A-4	Sequence 4, Appl
869	19	19.8	17	7	US-11-134-871-2938	Sequence 2938, Ap	942	19	19.8	24	7	US-11-178-538-9	Sequence 9, Appl
870	19	19.8	18	6	US-10-706-435A-18	Sequence 18, Appl	943	19	19.8	24	7	US-11-134-871-1073	Sequence 1073, Ap
871	19	19.8	18	6	US-10-449-902-49314	Sequence 49314, A	944	19	19.8	24	7	US-11-134-871-1846	Sequence 1846, Ap
872	19	19.8	18	6	US-11-253-223-4	Sequence 1, Appl	945	19	19.8	24	7	US-11-134-871-2674	Sequence 2674, Ap
873	19	19.8	18	7	US-11-253-223-4	Sequence 4, Appl	946	19	19.8	24	7	US-11-134-871-2875	Sequence 2875, Ap
874	19	19.8	18	7	US-11-253-223-7	Sequence 7, Appl	947	19	19.8	25	7	US-11-106-014-83	Sequence 83, Appl
875	19	19.8	18	7	US-11-253-223-8	Sequence 8, Appl	948	19	19.8	25	7	US-11-134-871-862	Sequence 862, Ap
876	19	19.8	18	7	US-11-253-223-9	Sequence 9, Appl	949	19	19.8	25	7	US-11-134-871-1506	Sequence 1506, Ap
877	19	19.8	18	7	US-11-253-223-14	Sequence 14, Appl	950	19	19.8	25	7	US-11-134-871-1720	Sequence 1720, Ap
878	19	19.8	18	7	US-11-253-223-15	Sequence 15, Appl	951	19	19.8	25	7	US-11-134-871-1829	Sequence 1829, Ap
879	19	19.8	18	7	US-11-253-223-16	Sequence 16, Appl	952	19	19.8	25	7	US-11-134-871-3093	Sequence 3093, Ap
880	19	19.8	18	7	US-11-253-223-17	Sequence 17, Appl	953	19	19.8	25	7	US-11-134-871-3282	Sequence 3282, Ap
881	19	19.8	18	7	US-11-253-223-20	Sequence 20, Appl	954	19	19.8	26	6	US-10-542-516-37	Sequence 37, Appl
882	19	19.8	18	7	US-11-253-223-21	Sequence 21, Appl	955	19	19.8	26	7	US-11-343-583-30	Sequence 30, Appl
883	19	19.8	18	7	US-11-253-223-22	Sequence 22, Appl	956	19	19.8	26	7	US-11-134-871-372	Sequence 372, Ap
884	19	19.8	18	7	US-11-253-223-23	Sequence 23, Appl	957	19	19.8	26	7	US-11-134-871-935	Sequence 935, Ap
885	19	19.8	18	7	US-11-253-223-24	Sequence 24, Appl	958	19	19.8	26	7	US-11-134-871-942	Sequence 942, Ap
886	19	19.8	18	7	US-11-253-223-25	Sequence 25, Appl	959	19	19.8	26	7	US-11-134-871-1893	Sequence 1893, Ap
887	19	19.8	18	7	US-11-253-223-26	Sequence 26, Appl	960	19	19.8	26	7	US-11-134-871-2365	Sequence 2365, Ap
888	19	19.8	18	7	US-11-253-223-29	Sequence 29, Appl	961	19	19.8	26	7	US-11-296-920-3	Sequence 3, Appl
889	19	19.8	18	7	US-11-253-223-30	Sequence 30, Appl	962	19	19.8	27	7	US-11-170-797-30	Sequence 30, Appl
890	19	19.8	18	7	US-11-253-223-33	Sequence 33, Appl	963	19	19.8	27	7	US-11-134-871-1744	Sequence 1744, Ap
891	19	19.8	18	7	US-11-253-223-34	Sequence 34, Appl	964	19	19.8	27	7	US-11-134-871-1912	Sequence 1912, Ap
892	19	19.8	18	7	US-11-253-223-67	Sequence 67, Appl	965	19	19.8	28	7	US-11-368-225-48	Sequence 48, Appl
893	19	19.8	18	7	US-11-343-583-5	Sequence 5, Appl	966	19	19.8	28	7	US-11-368-225-132	Sequence 132, Ap
894	19	19.8	18	7	US-11-338-681-13	Sequence 13, Appl	967	19	19.8	29	6	US-10-449-902-42220	Sequence 42220, A
895	19	19.8	18	7	US-11-338-681-29	Sequence 29, Appl	968	19	19.8	29	7	US-11-343-583-358	Sequence 358, Ap
896	19	19.8	18	7	US-11-196-917A-104	Sequence 104, Appl	969	19	19.8	29	7	US-11-134-871-2056	Sequence 2056, Ap
897	19	19.8	18	7	US-11-196-917A-107	Sequence 107, Appl	970	19	19.8	29	7	US-11-134-871-2078	Sequence 2078, Ap
898	19	19.8	18	7	US-11-272-521-138	Sequence 138, Appl	971	19	19.8	30	6	US-10-506-630A-27	Sequence 27, Appl
899	19	19.8	18	7	US-11-272-521-184	Sequence 184, Appl	972	19	19.8	30	6	US-10-635-187A-2	Sequence 2, Appl
900	19	19.8	18	7	US-11-134-871-696	Sequence 696, Appl	973	19	19.8	30	7	US-11-343-583-28	Sequence 28, Appl
901	19	19.8	18	7	US-11-134-871-1035	Sequence 1035, Ap	974	19	19.8	30	7	US-11-134-871-2503	Sequence 2503, Ap

975 19 19.8 30 7 US-11-134-871-2772 Sequence 2772, Ap
976 19 19.8 30 7 US-11-254-500-49 Sequence 49, Appl
977 19 19.8 31 6 US-10-506-630A-3 Sequence 3, Appl1
978 19 19.8 31 7 US-11-334-622-28 Sequence 28, Appl
979 19 19.8 31 7 US-11-343-583-279 Sequence 279, App
980 19 19.8 31 7 US-11-134-871-373 Sequence 373, App
981 19 19.8 31 7 US-11-134-871-2476 Sequence 2476, Ap
982 19 19.8 32 7 US-11-134-871-751 Sequence 751, App
983 19 19.8 32 7 US-11-134-871-2062 Sequence 2062, Ap
984 19 19.8 32 7 US-11-200-995-9 Sequence 9, Appl1
985 19 19.8 32 7 US-11-264-074-10 Sequence 10, Appl
986 19 19.8 32 7 US-11-264-074-11 Sequence 11, Appl
987 19 19.8 33 6 US-10-953-349-37416 Sequence 37416, A
988 19 19.8 33 6 US-10-471-571A-1900 Sequence 1900, Ap
989 19 19.8 33 6 US-10-449-502-32590 Sequence 32590, A
990 19 19.8 33 7 US-11-134-871-491 Sequence 491, App
991 19 19.8 33 7 US-11-134-871-708 Sequence 708, App
992 19 19.8 33 7 US-11-274-682-40 Sequence 40, Appl
993 19 19.8 33 7 US-11-274-682-44 Sequence 44, Appl
994 19 19.8 34 6 US-10-953-349-16318 Sequence 16318, A
995 19 19.8 34 6 US-10-471-571A-5204 Sequence 5204, Ap
996 19 19.8 34 6 US-10-523-617-3 Sequence 3, Appl1
997 19 19.8 34 7 US-11-055-098-405 Sequence 405, App
998 19 19.8 34 7 US-11-055-098-409 Sequence 409, App
999 19 19.8 34 7 US-11-055-098-413 Sequence 413, App
1000 19 19.8 34 7 US-11-055-098-417 Sequence 417, App

ALIGNMENTS

RESULT 1
US-11-134-871-3344
; Sequence 3344, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Qualification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3344
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3344

Query Match 34.4%; Score 33; DB 7; Length 31;
Best Local Similarity 42.9%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

Qy 2 EHCNFDVTRLRE 15
:|:|:|:|:|:|
Db 10 DHPTFNKITPNLAE 23

RESULT 2
US-11-178-155-14
; Sequence 14, Application US/11178155
; Publication No. US20060135754A1
; GENERAL INFORMATION:
; APPLICANT: Christensen, Soren
; APPLICANT: Foldager, Lars
; APPLICANT: Valbjorn, Jesper
; APPLICANT: Hallberg Thuesen, Marianne
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Munk, Morten

; TITLE OF INVENTION: NOVEL CARBAMYLATED EPO AND METHOD FOR ITS PRODUCTION
; FILE REFERENCE: 05432/1201616-US2
; CURRENT APPLICATION NUMBER: US/11/178,155
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-178-155-14

Query Match 33.3%; Score 32; DB 7; Length 25;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFDVDTT 11
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Db 10 EHCSLNENIT 19

RESULT 3
US-11-134-871-1716
; Sequence 1716, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Qualification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1716
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-1716

Query Match 33.3%; Score 32; DB 7; Length 33;
Best Local Similarity 54.5%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FNDVTTRLREN 16
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Db 7 FQDPTQOVREN 17

RESULT 4
US-11-178-155-34
; Sequence 34, Application US/11178155
; Publication No. US20060135754A1
; GENERAL INFORMATION:
; APPLICANT: Christensen, Soren
; APPLICANT: Foldager, Lars
; APPLICANT: Valbjorn, Jesper
; APPLICANT: Hallberg Thuesen, Marianne
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Munk, Morten
; TITLE OF INVENTION: NOVEL CARBAMYLATED EPO AND METHOD FOR ITS PRODUCTION
; FILE REFERENCE: 05432/1201616-US2
; CURRENT APPLICATION NUMBER: US/11/178,155
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-178-155-34

Query Match 33.3%; Score 32; DB 7; Length 39;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFNDVTT 11
|||:|:|
DB 16 EHCSLNENIT 25

RESULT 5

US-11-178-155-2
; Sequence 2, Application US/11178155
; Publication No. US20060135754A1
; GENERAL INFORMATION:
; APPLICANT: Christensen, Soren
; APPLICANT: Foldager, Lars
; APPLICANT: Valbjorn, Jesper
; APPLICANT: Hallberg Thuesen, Marianne
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Munk, Morten
; TITLE OF INVENTION: NOVEL CARBAMYLATED EPO AND METHOD FOR ITS PRODUCTION
; FILE REFERENCE: 05432/1201616-US2
; CURRENT APPLICATION NUMBER: US/11/178,155
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-178-155-2

Query Match 32.8%; Score 31.5; DB 7; Length 26;
Best Local Similarity 43.8%; Pred. No. 70;
Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 2 EHCNFNDVTTTLRENE 17
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DB 10 EHCSLN-----ENE 18

RESULT 6

US-11-134-871-7
; Sequence 7, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-7

Query Match 32.3%; Score 31; DB 7; Length 19;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTT 10
:|:|:|:|
DB 2 YEFPCPHNVT 11

RESULT 7

US-11-134-871-3070
; Sequence 3070, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3070
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3070

Query Match 32.3%; Score 31; DB 7; Length 19;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTT 10
:|:|:|:|
DB 2 YEFPCPHNVT 11

RESULT 8

US-10-506-630A-31
; Sequence 31, Application US/10506630A
; Publication No. US20060110789A1
; GENERAL INFORMATION:
; APPLICANT: GOKHALE, Rajesh
; APPLICANT: TSUJI, Stuart
; APPLICANT: KHOSLA, Chaitan
; APPLICANT: WU, Nicholas
; APPLICANT: CANE, David
; TITLE OF INVENTION: METHODS TO MEDIATE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622004601
; CURRENT APPLICATION NUMBER: US/10/506,630A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/06910
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,244
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 60/361,758
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-Terminal Inter-polypeptide linker
US-10-506-630A-31

Query Match 32.3%; Score 31; DB 6; Length 33;
Best Local Similarity 70.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 DVTTRLRENE 17
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DB 20 DARTLREVE 29

RESULT 9

US-10-506-630A-28
; Sequence 28, Application US/10506630A
; Publication No. US20060110789A1
; GENERAL INFORMATION:
; APPLICANT: GORHALE, Rajesh
; APPLICANT: TSUJI, Stuart
; APPLICANT: KHOSLA, Chaitan
; APPLICANT: WU, Nicholas
; APPLICANT: CANE, David
; TITLE OF INVENTION: METHODS TO MEDIATE POLYPEPTIDE SYNTHASE
; TITLE OF INVENTION: MODULE EFFECTIVENESS
; FILE REFERENCE: 300622004601
; CURRENT APPLICATION NUMBER: US/10/506,630A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/06910
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-Terminal Inter-polypeptide linker
US-10-506-630A-28

Query Match 32.3%; Score 31; DB 6; Length 38;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDVTRLRENE 17
: ||| |||||
Db 24 DSVTARLREVE 34

RESULT 10
US-10-449-902-29052
; Sequence 29052, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR FILING DATE: 2002-05-29
; PRIOR FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 29052
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29052

Query Match 31.2%; Score 30; DB 6; Length 38;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HCNFNDVTT 11
: | : | : ||
Db 22 NCHLNSITT 30

RESULT 11
US-11-134-871-3063
; Sequence 3063, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Qualification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3063
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3063

Query Match 30.7%; Score 29.5; DB 7; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 HC-NFNDV 9
||| |||
Db 13 HCPNFSDV 20

RESULT 12
US-10-471-571A-686
; Sequence 686, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: Seqwin99, version 1.03
; SEQ ID NO 686
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-471-571A-686

Query Match 29.7%; Score 28.5; DB 6; Length 36;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 4 CNFNDV-TTFLRENE 17
| | | : : | | |
Db 4 CQFYDIYLLKIRTNE 18

RESULT 13
US-10-560-723-184
; Sequence 184, Application US/10560723
; Publication No. US20060115821A1
; GENERAL INFORMATION:
; APPLICANT: EXONHIT THERAPEUTICALS
; TITLE OF INVENTION: PROSTATE SPECIFIC GENES AND THE USE THEREOF AS TARGETS FOR PROSTATE
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: B0213WO
; CURRENT APPLICATION NUMBER: US/10/560,723
; CURRENT FILING DATE: 2005-12-15
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 184
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-10-560-723-184

Query Match 29.2%; Score 28; DB 6; Length 24;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 CNFNDVTTTL 13
|:|:|:|:|
Db 3 CSFADTQTTL 12

RESULT 14
US-11-243-438-24
Sequence 24, Application US/11243438
Publication No. US20060111292A1
GENERAL INFORMATION:
APPLICANT: Biocrypt B.V.
TITLE OF INVENTION: ORAL ADMINISTRATION OF GENE-REGULATORY PEPTIDES
FILE REFERENCE: 3077-6318pc
CURRENT APPLICATION NUMBER: US/11/243,438
CURRENT FILING DATE: 2005-10-04
PRIOR APPLICATION NUMBER: EP 03076028.4
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076029.2
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076027.6
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076026.8
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076022.7
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076021.9
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076025.0
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076024.3
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076030.0
PRIOR FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: EP 03076023.5
PRIOR FILING DATE: 2003-04-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
LENGTH: 38
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-243-438-24

Query Match 29.2%; Score 28; DB 7; Length 38;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNFNDV 9
|:|:|:|
Db 3 CNYRDV 8

RESULT 15
US-11-134-871-2426
Sequence 2426, Application US/11134871
Publication No. US20060141528A1
GENERAL INFORMATION:
APPLICANT: Aebbersold, Rudolf H.
APPLICANT: Zhang, Hui

TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Quatification of Serum Glycoproteins
FILE REFERENCE: 66661-116
CURRENT APPLICATION NUMBER: US/11/134,871
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: 60/573,593
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 3602
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2426
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-11-134-871-2426

Query Match 28.6%; Score 27.5; DB 7; Length 18;
Best Local Similarity 53.3%; Pred. No. 2.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 6 FNDVT-----TLRE 15
:|:|:|:|:|
Db 4 WNDSTSVQNPTRLRE 18

RESULT 16
US-11-346-079-45
Sequence 45, Application US/11346079
Publication No. US20060149033A1
GENERAL INFORMATION:
APPLICANT: Deshayes, Kurt D.
APPLICANT: Lowman, Henry B.
APPLICANT: Schaffer, Michelle L.
APPLICANT: Sidhu, Sachdev S.
TITLE OF INVENTION: IGF ANTAGONIST PEPTIDES
FILE REFERENCE: P1863R1
CURRENT APPLICATION NUMBER: US/11/346,079
CURRENT FILING DATE: 2006-02-01
PRIOR APPLICATION NUMBER: US/10/098,093
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,904
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 122
SEQ ID NO 45
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-11-346-079-45

Query Match 28.1%; Score 27; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNFND 8
|:|:|:|
Db 3 CFEND 7

RESULT 17
US-11-255-634-4
Sequence 4, Application US/11255634
Publication No. US20060110774A1
GENERAL INFORMATION:
APPLICANT: Fast, Loren
APPLICANT: Lim, Yow-Pin
TITLE OF INVENTION: Methods For Detecting Sepsis
FILE REFERENCE: 21486-070
CURRENT APPLICATION NUMBER: US/11/255,634
CURRENT FILING DATE: 2005-10-20
PRIOR APPLICATION NUMBER: US 60/621,922
PRIOR FILING DATE: 2004-10-21
NUMBER OF SEQ ID NOS: 5

Query Match	28.1%;	Score 27;	DB 7;	Length 16;	
Best Local Similarity	71.4%;	Pred. No. 2.3e+02;			
Matches	5;	Conservative	0;	Mismatches	2; Indels
Qy	3 HCNFNDV 9				
Db	5 HYNFNPV 11				
RESULT 18					
US-11-338-681-28					
Sequence 28, Application US/11338681					
Publication No. US20060127956A1					
GENERAL INFORMATION:					
APPLICANT: Rompuram, Seshi R.					
APPLICANT: Ramanathan, Halasya					
APPLICANT: Bogen, Steven A.					
TITLE OF INVENTION: Quality Control for Cytochemical Assays					
FILE REFERENCE: 1159.1008-001					
CURRENT APPLICATION NUMBER: US/11/338,681					
CURRENT FILING DATE: 2006-01-25					
PRIOR APPLICATION NUMBER: US/09/549,855					
PRIOR FILING DATE: 2000-04-14					
PRIOR APPLICATION NUMBER: US 09/291,351					
PRIOR FILING DATE: 1999-04-14					
NUMBER OF SEQ ID NOS: 42					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 28					
LENGTH: 18					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-11-338-681-28					
Query Match	28.1%;	Score 27;	DB 7;	Length 18;	
Best Local Similarity	37.5%;	Pred. No. 2.6e+02;			
Matches	3;	Conservative	3;	Mismatches	2; Indels
Qy	1 FEHCNFD 8				
Db	4 YQHCPPYD 11				
RESULT 19					
US-11-134-871-2246					
Sequence 2246, Application US/11134871					
Publication No. US20060141528A1					
GENERAL INFORMATION:					
APPLICANT: Aebersold, Rudolf H.					
APPLICANT: Zhang, Hui					
TITLE OF INVENTION: Compositions and Methods for					
TITLE OF INVENTION: Qualification of Serum Glycoproteins					
FILE REFERENCE: 66661-116					
CURRENT APPLICATION NUMBER: US/11/134,871					
CURRENT FILING DATE: 2005-05-20					
PRIOR APPLICATION NUMBER: 60/573,593					
PRIOR FILING DATE: 2004-05-21					
NUMBER OF SEQ ID NOS: 3602					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 2246					
LENGTH: 20					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-11-134-871-2246					
Query Match	28.1%;	Score 27;	DB 7;	Length 18;	
Best Local Similarity	37.5%;	Pred. No. 2.6e+02;			
Matches	3;	Conservative	3;	Mismatches	2; Indels
Qy	1 FEHCNFD 8				
Db	4 YQHCPPYD 11				
RESULT 19					
US-11-134-871-2246					
Sequence 2246, Application US/11134871					
Publication No. US20060141528A1					
GENERAL INFORMATION:					
APPLICANT: Aebersold, Rudolf H.					
APPLICANT: Zhang, Hui					
TITLE OF INVENTION: Compositions and Methods for					
TITLE OF INVENTION: Qualification of Serum Glycoproteins					
FILE REFERENCE: 66661-116					
CURRENT APPLICATION NUMBER: US/11/134,871					
CURRENT FILING DATE: 2005-05-20					
PRIOR APPLICATION NUMBER: 60/573,593					
PRIOR FILING DATE: 2004-05-21					
NUMBER OF SEQ ID NOS: 3602					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 2246					
LENGTH: 20					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-11-134-871-2246					
Query Match	28.1%;	Score 27;	DB 7;	Length 16;	
Best Local Similarity	71.4%;	Pred. No. 2.3e+02;			
Matches	5;	Conservative	0;	Mismatches	2; Indels
Qy	3 HCNFNDV 9				
Db	5 HYNFNPV 11				
RESULT 18					
US-11-338-681-28					
Sequence 28, Application US/11338681					
Publication No. US20060127956A1					
GENERAL INFORMATION:					
APPLICANT: Rompuram, Seshi R.					
APPLICANT: Ramanathan, Halasya					
APPLICANT: Bogen, Steven A.					
TITLE OF INVENTION: Quality Control for Cytochemical Assays					
FILE REFERENCE: 1159.1008-001					
CURRENT APPLICATION NUMBER: US/11/338,681					
CURRENT FILING DATE: 2006-01-25					
PRIOR APPLICATION NUMBER: US/09/549,855					

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RESULT 22
US-11-134-871-2274
; Sequence 2274, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2274
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2274

Query Match      28.1%; Score 27; DB 7; Length 25;
Best Local Similarity 41.7%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      6 FNDVTVTLRENE 17
Db      10 FPDVTNVFTQGE 21

RESULT 23
US-11-334-622-37
; Sequence 37, Application US/11334622
; Publication No. US20060112440A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/11/334,622
; PRIOR FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: US/09/554,000
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-334-622-37

Query Match      28.1%; Score 27; DB 7; Length 28;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 FNDVTVTLRE 15
Db      6 FPDNYTVLRK 15

RESULT 24
US-11-134-871-2816
; Sequence 2816, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; TITLE OF INVENTION: COMBINATION IMMUNOTHERAPIES FOR MODULATION OF PATHOGENIC
; FILE REFERENCE: UCSD1450-2
; TITLE OF INVENTION: IMMUNE RESPONSES IN IMMUNE MEDIATED DISEASES
; APPLICANT: Zhang, Hui

; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2816
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2816

Query Match      28.1%; Score 27; DB 7; Length 29;
Best Local Similarity 38.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      2 EHCNFDVTVTLRL 14
Db      14 DHQQLNDTALRL 26

RESULT 25
US-11-055-093-283
; Sequence 283, Application US/11055093
; Publication No. US20060094652A1
; GENERAL INFORMATION:
; APPLICANT: LEVI, ODILE ESTHER
; APPLICANT: HANLEY, MICHAEL R.
; APPLICANT: JODKA, CAROLYN M.
; APPLICANT: LEWIS, DIANA Y.
; APPLICANT: SOARES, CHRISTOPHER J.
; APPLICANT: GHOSH, SOUMITRA S.
; APPLICANT: D'SOUZA, LAWRENCE
; APPLICANT: PARKES, DAVID
; APPLICANT: MACK, CHRISTINE M.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH SELECTABLE PROPERTIES
; FILE REFERENCE: 18528.740
; CURRENT APPLICATION NUMBER: US/11/055,093
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 60/543,407
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 283
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-11-055-093-283

Query Match      28.1%; Score 27; DB 7; Length 30;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 NDVTVTLRE 15
Db      2 NDVTVTLRE 10

RESULT 26
US-10-490-949-38
; Sequence 38, Application US/10490949
; Publication No. US20060093574A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: METHODS FOR EPITOPE-SPECIFIC AND CYTOKINE/ANTICYTOKINE
; TITLE OF INVENTION: COMBINATION IMMUNOTHERAPIES FOR MODULATION OF PATHOGENIC
; TITLE OF INVENTION: IMMUNE RESPONSES IN IMMUNE MEDIATED DISEASES
; FILE REFERENCE: UCSD1450-2
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; CURRENT APPLICATION NUMBER: US/10/490,949
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/US02/30578
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/339,284
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/325,499
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-490-949-38

Query Match 28.1%; Score 27; DB 6; Length 33;
Best Local Similarity 31.2%; Pred. No. 5e+02;
Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 2 EHCNFNDVTRLRENE 17
: ||| :
Db 2 QKCFQDAYVLLSEKK 17
: ||| :
: ||| :
: ||| :

RESULT 27
US-11-055-093-60
; Sequence 60, Application US/11055093
; Publication No. US20060094652A1
; GENERAL INFORMATION:
; APPLICANT: LEVY, ODILE ESTHER
; APPLICANT: HANLEY, MICHAEL R.
; APPLICANT: JODKA, CAROLYN M.
; APPLICANT: LEWIS, DIANA Y.
; APPLICANT: SOARES, CHRISTOPHER J.
; APPLICANT: GHOSH, SOMITRA S.
; APPLICANT: D'SOUZA, LAWRENCE
; APPLICANT: PARKES, DAVID
; APPLICANT: MACK, CHRISTINE M.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH SELECTABLE PROPERTIES
; FILE REFERENCE: 18528.740
; CURRENT APPLICATION NUMBER: US/11/055,093
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 60/543,407
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 60
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (37)
; OTHER INFORMATION: Ser-OH
; US-11-055-093-60

Query Match 28.1%; Score 27; DB 7; Length 37;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDVTVTRLRE 15
|||||
Db 8 NDVTEYLEE 16
|||||

RESULT 28
US-11-122-986-811
; Sequence 811, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL

; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patent in Ver. 3.3
; SEQ ID NO 811
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-11-122-986-811

Query Match 27.6%; Score 26.5; DB 7; Length 17;
Best Local Similarity 53.8%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 5 NFNDVTRLRENE 17
||:||||:
Db 1 NFDD-TTDTVEE 12
||:||||:
||:||||:

RESULT 29
US-11-343-583-90
; Sequence 90, Application US/11343583
; Publication No. US20060122370A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN DANIEL
; APPLICANT: MIN, HOSUNG
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801A
; CURRENT APPLICATION NUMBER: US/11/343,583
; CURRENT FILING DATE: 2006-01-30
; PRIOR APPLICATION NUMBER: US/10/269,695
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/414,155
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328,624
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 90
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide capable of binding to Ang-2
; US-11-343-583-90

Query Match 27.6%; Score 26.5; DB 7; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 2 EHCNFNDVT-TLRLRE 15
|||:::|::|
Db 5 EHCNDWDPWTCHEHRE 19

RESULT 30

US-11-234-731-118
; Sequence 118, Application US/11234731
; Publication No. US20060140934A1
; GENERAL INFORMATION:
; APPLICANT: GREGG, COLIN V.
; APPLICANT: XIONG, FEI
; APPLICANT: SITNEY, KAREN C.
; TITLE OF INVENTION: MODIFIED Fc MOLECULES
; FILE REFERENCE: A-914
; CURRENT APPLICATION NUMBER: US/11/234,731
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: 60/612,680
; PRIOR FILING DATE: 2004-09-24
; NUMBER OF SEQ ID NOS: 659
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide capable of binding to Ang-2
US-11-234-731-118

Query Match 27.6%; Score 26.5; DB 7; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 2 EHCNFNDVT-TLRLRE 15
|||:::|::|
Db 5 EHCNDWDPWTCHEHRE 19

RESULT 31

US-11-343-583-273
; Sequence 273, Application US/11343583
; Publication No. US20060122370A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN DANIEL
; APPLICANT: MIN, HOSUNG
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801A
; CURRENT APPLICATION NUMBER: US/11/343,583
; CURRENT FILING DATE: 2006-01-30
; PRIOR APPLICATION NUMBER: US/10/269,695
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/414,155
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328,624
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 273
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptibodies capable of binding to Ang-2
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa = Fc
US-11-343-583-273

Query Match 27.6%; Score 26.5; DB 7; Length 31;
Best Local Similarity 40.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 2 EHCNFNDVT-TLRLRE 15
|||:::|::|
Db 14 EHCNDWDPWTCHEHRE 28

RESULT 32

US-10-490-949-39
; Sequence 39, Application US/10490949
; Publication No. US20060093574A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: METHODS FOR EPITOPE-SPECIFIC AND CYTOKINE/ANTICYTOKINE
; TITLE OF INVENTION: COMBINATION IMMUNOTHERAPIES FOR MODULATION OF PATHOGENIC
; TITLE OF INVENTION: IMMUNE RESPONSES IN IMMUNE MEDIATED DISEASES
; FILE REFERENCE: UCSD1450-2
; CURRENT APPLICATION NUMBER: US/10/490,949
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/US02/30578
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/339,284
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/325,499
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-490-949-39

Query Match 27.1%; Score 26; DB 6; Length 15;
Best Local Similarity 35.7%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 CNFNDVTVTLRLRENE 17
|||:::|::|
Db 2 CEFQDAYVLLSEKK 15

RESULT 33

US-11-264-509A-68
; Sequence 68, Application US/11264509A
; Publication No. US20060100148A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Rong
; APPLICANT: Zhang, Rong
; APPLICANT: Kong, Rong
; TITLE OF INVENTION: PEPTIDE VIRAL ENTRY PEPTIDES
; FILE REFERENCE: JB06227US01
; CURRENT APPLICATION NUMBER: US/11/264,509A
; CURRENT FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/624,204
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV peptide
US-11-264-509A-68

Query Match 27.1%; Score 26; DB 7; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFND 8
|||:::|::|

```
Db          4 ERCNLED 10

RESULT 34
US-11-338-681-27
; Sequence 27, Application US/11338681
; Publication No. US20060127956A1
; GENERAL INFORMATION:
; APPLICANT: Rompuram, Seshi R.
; APPLICANT: Ramanathan, Halasya
; APPLICANT: Bogen, Steven A.
; TITLE OF INVENTION: Quality Control for Cytochemical Assays
; FILE REFERENCE: 1159.1008-001
; CURRENT APPLICATION NUMBER: US/11/338,681
; CURRENT FILING DATE: 2006-01-25
; PRIOR APPLICATION NUMBER: US/09/549,855
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/291,351
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-338-681-27

Query Match      27.1%; Score 26; DB 7; Length 18;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FEHCNFND 8
      ||| |||
Db      4 FELCKEND 11

RESULT 35
US-11-134-871-2753
; Sequence 2753, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2753
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2753

Query Match      27.1%; Score 26; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      8 DVTTRLRE 15
      ||| |||
Db     11 DITVEIRE 18

RESULT 36
US-11-262-044-6
; Sequence 6, Application US/11262044
; Publication No. US20060110759A1
; GENERAL INFORMATION:
; APPLICANT: ZHENG, BOJIAN
; APPLICANT: GUAN, YI
; APPLICANT: HUANG, JIANDONG
; APPLICANT: HE, MING-LIANG
; TITLE OF INVENTION: SYNTHETIC PEPTIDE TARGETING CRITICAL SITES ON THE
; TITLE OF INVENTION: SARS-ASSOCIATED CORONAVIRUS SPIKE PROTEIN RESPONSIBLE
; TITLE OF INVENTION: FOR VIRAL INFECTION AND METHOD OF USE THEREOF
; FILE REFERENCE: V0690.0056
; CURRENT APPLICATION NUMBER: US/11/262,044
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/630,334
; PRIOR FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-262-044-6

Query Match      27.1%; Score 26; DB 7; Length 20;
Best Local Similarity 23.5%; Pred. No. 4.3e+02;
Matches 4; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy      1 FEHCNFNDVTVTRLRENE 17
      :: ||| ||| ::
Db      1 YQDVNCTDVSATIHADQ 17

RESULT 37
US-11-134-871-3277
; Sequence 3277, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3277
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3277

Query Match      27.1%; Score 26; DB 7; Length 21;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 HCNFND 8
      ||| |||
Db      4 HCRFDE 9

RESULT 38
US-11-134-871-2818
; Sequence 2818, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
```


; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2818
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2818

Query Match 27.1%; Score 26; DB 7; Length 22;
Best Local Similarity 46.2%; Pred. No. 4.8e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 NFNDVTRLRENE 17
||||| :||| :|
DB 4 NFNDHSPLTNDE 16

RESULT 39
US-11-134-871-688
; Sequence 688, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-688

Query Match 27.1%; Score 26; DB 7; Length 25;
Best Local Similarity 50.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
||| | :|
DB 10 FEMCSLSD 17

RESULT 40
US-09-949-925-228
; Sequence 228, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30

; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 228
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-925-228

Query Match 27.1%; Score 26; DB 1; Length 27;
Best Local Similarity 42.9%; Pred. No. 6e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFN 7
::|||
DB 2 YQCCFN 8

RESULT 41
US-11-134-871-772
; Sequence 772, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-772

Query Match 27.1%; Score 26; DB 7; Length 31;
Best Local Similarity 33.3%; Pred. No. 6.9e+02;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FEHCNFDVTR 12
||| :|
DB 7 FPACSFNGTSAQ 18

RESULT 42
US-10-953-349-37372
; Sequence 37372, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37372
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays

US-10-953-349-37372

Query Match 27.1%; Score 26; DB 6; Length 33;
Best Local Similarity 36.4%; Pred. No. 7.4e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 NDTVTRLRENE 17
| : ||| :|||
Db 12 NSIITRWKDS 22

RESULT 43

US-10-449-902-28500
; Sequence 28500, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR FILING DATE: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28500
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-28500

Query Match 27.1%; Score 26; DB 6; Length 35;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTRLRL 14
| : ||| |||
Db 26 FSYVTMLRL 34

RESULT 44

US-11-056-355B-850
; Sequence 850, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 850
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(36)
; OTHER INFORMATION: Ceres Seq. ID no. 12589514
US-11-056-355B-850

Query Match 27.1%; Score 26; DB 7; Length 36;
Best Local Similarity 44.4%; Pred. No. 8.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCNFNDVTT 11
| : ||| |||
Db 7 YCDLKDVRT 15

RESULT 45

US-10-953-349-11980
; Sequence 11980, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11980
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-11980

Query Match 27.1%; Score 26; DB 6; Length 40;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCN 5
| : ||| :
Db 8 YEHCH 12

RESULT 46

US-11-134-871-2342
; Sequence 2342, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2342
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2342

Query Match 26.8%; Score 25.5; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 4 CNF---NDVTRLRL 14
| : ||| :|||
Db 2 CNTTQGNVTSILRL 15

RESULT 47

US-11-122-986-421
; Sequence 421, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD

; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 421
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-11-122-986-421

Query Match 26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 42.9%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTLR 14
||| : : :
Db 2 FEMTFDHDVTMR 15

RESULT 48
US-11-122-986-422
; Sequence 422, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373

; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 422
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-11-122-986-422

Query Match 26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 42.9%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTLR 14
||| : : :
Db 2 FEMTFDHDVTMR 15

RESULT 49
US-11-122-986-423
; Sequence 423, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 423
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-11-122-986-423

Query Match 26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 42.9%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFDVTTLR 14
||| : : :
Db 2 FEMTFDHDVTMR 15

RESULT 50
US-11-295-192A-984
; Sequence 984, Application US/11295192A
; Publication No. US20060110803A1

```
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; APPLICANT: Goudsmit, Jaap
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 984
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-984

Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      7 NDTVTRLRENE 17
      ||: ||| : |
Db      5 NDILSRLDKVE 15

RESULT 51
US-11-295-192A-985
; Sequence 985, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 985
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-985

Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      7 NDTVTRLRENE 17
      ||: ||| : |
Db      4 NDILSRLDKVE 14

RESULT 52
US-11-295-192A-986
; Sequence 986, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 986
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-986

Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      7 NDTVTRLRENE 17
      ||: ||| : |
Db      2 NDILSRLDKVE 12

RESULT 53
US-11-295-192A-987
; Sequence 987, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 987
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-987

Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      7 NDTVTRLRENE 17
      ||: ||| : |
Db      2 NDILSRLDKVE 12

RESULT 54
US-11-295-192A-988
; Sequence 988, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 988
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-988

Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      7 NDTVTRLRENE 17
      ||: ||| : |
Db      4 NDILSRLDKVE 14

RESULT 55
US-11-295-192A-989
; Sequence 989, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 989
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-989

Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      7 NDTVTRLRENE 17
      ||: ||| : |
Db      5 NDILSRLDKVE 15
```

; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof

; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 988

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-11-295-192A-988

Query Match 26.0%; Score 25; DB 7; Length 15;

Best Local Similarity 45.5%; Pred. No. 4.6e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDVTRLRENE 17

Db 1 NDILSLDKVE 11

RESULT 55

US-11-303-372-53

; Sequence 53, Application US/11303372

; Publication No. US20060100149A1

; GENERAL INFORMATION:

; APPLICANT: O'Mahony, Daniel J.

; APPLICANT: Lambkin, Imelda J.

; APPLICANT: Pinilla, Clemencia

; APPLICANT: Houghten, Richard

; TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY

; TITLE OF INVENTION: AGENTS

; FILE REFERENCE: P26,481-A USA

; CURRENT APPLICATION NUMBER: US/11/303,372

; CURRENT FILING DATE: 2005-12-16

; PRIOR APPLICATION NUMBER: US/10/955,656

; PRIOR FILING DATE: 2004-09-30

; PRIOR APPLICATION NUMBER: 10/126,845

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 09/671,089

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: 60/156,246

; PRIOR FILING DATE: 1999-09-27

; NUMBER OF SEQ ID NOS: 119

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 53

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: D form retroinversion peptide

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (1)-(1)

; OTHER INFORMATION: dansylated

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (2)-(16)

; OTHER INFORMATION: D form amino acid

US-11-303-372-53

Query Match 26.0%; Score 25; DB 7; Length 16;

Best Local Similarity 83.3%; Pred. No. 5e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TRLREN 16

Db 3 TRLRRN 8

RESULT 56

US-11-176-182-97

; Sequence 97, Application US/11176182

; Publication No. US20060088549A1

; GENERAL INFORMATION:

; APPLICANT: ARNOLD, EDWARD

; APPLICANT: FERSTANDIG ARNOLD, GAIL

; TITLE OF INVENTION: CHIMERIC HIV VACCINE

; FILE REFERENCE: PA04-701-S

; CURRENT APPLICATION NUMBER: US/11/176,182

; CURRENT FILING DATE: 2005-07-07

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 97

; LENGTH: 18

; TYPE: PRT

; ORGANISM: chimeric HIV-HRV

US-11-176-182-97

Query Match 26.0%; Score 25; DB 7; Length 18;

Best Local Similarity 42.9%; Pred. No. 5.6e+02;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CNFNDVT 10

Db 2 CDYEDLT 8

RESULT 57

US-11-338-681-6

; Sequence 6, Application US/11338681

; Publication No. US20060127956A1

; GENERAL INFORMATION:

; APPLICANT: Rompuram, Seshi R.

; APPLICANT: Ramanathan, Halasya

; APPLICANT: Bogen, Steven A.

; TITLE OF INVENTION: Quality Control for Cytochemical Assays

; FILE REFERENCE: 1159.1008-001

; CURRENT APPLICATION NUMBER: US/11/338,681

; PRIOR FILING DATE: 2006-01-25

; PRIOR APPLICATION NUMBER: US/09/549,855

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: US 09/291,351

; PRIOR FILING DATE: 1999-04-14

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-338-681-6

Query Match

Best Local Similarity 26.0%; Score 25; DB 7; Length 18;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EHCNEN 7

Db 12 ENCNSN 17

RESULT 58

US-11-134-871-753

; Sequence 753, Application US/11134871

; Publication No. US20060141528A1

; GENERAL INFORMATION:

; APPLICANT: Aebersold, Rudolf H.

; APPLICANT: Zhang, Hui

; TITLE OF INVENTION: Compositions and Methods for

; FILE REFERENCE: 66661-116

; CURRENT APPLICATION NUMBER: US/11/134,871

```
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 753
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-753

Query Match          26.0%; Score 25; DB 7; Length 19;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HCNFNDVT 10
   ||| |::|
Db 3 HINHNLT 10

RESULT 59
US-10-505-848-20
; Sequence 20, Application US/10505848
; Publication No. US20060089302A1
; GENERAL INFORMATION:
; APPLICANT: Abulafia-Lapid, Rivka
; APPLICANT: Atlan, Henri
; APPLICANT: Cohen, Irun R.
; TITLE OF INVENTION: Hsp-70-Derived peptides and uses thereof in the diagnosis and
; TITLE OF INVENTION: treatment of autoimmune diseases
; FILE REFERENCE: 14112/US/01
; CURRENT APPLICATION NUMBER: US/10/505,848
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: IL 148401
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: PCT/IL03/00143
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-848-20

Query Match          26.0%; Score 25; DB 6; Length 20;
Best Local Similarity 41.2%; Pred. No. 6.3e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTLRENE 17
   ||| |::|
Db 3 FEGIDFTSITRPFEE 19

RESULT 60
US-11-262-044-21
; Sequence 21, Application US/11262044
; Publication No. US20060110758A1
; GENERAL INFORMATION:
; APPLICANT: ZHENG, BOJIAN
; APPLICANT: GUAN, YI
; APPLICANT: HUANG, JIANDONG
; APPLICANT: HE, MING-LIANG
; TITLE OF INVENTION: SYNTHETIC PEPTIDE TARGETING CRITICAL SITES ON THE
; TITLE OF INVENTION: SARS-ASSOCIATED CORONAVIRUS SPIKE PROTEIN RESPONSIBLE
; TITLE OF INVENTION: FOR VIRAL INFECTION AND METHOD OF USE THEREOF
; FILE REFERENCE: V0690.0056
; CURRENT APPLICATION NUMBER: US/11/262,044
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/630,334
; PRIOR FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: Ser or Pro
US-11-262-044-21

Query Match          26.0%; Score 25; DB 7; Length 20;
Best Local Similarity 23.5%; Pred. No. 6.3e+02;
Matches 4; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTLRENE 17
   ||| |::|
Db 1 YQDVNCTDVXTAIHADQ 17

RESULT 61
US-11-134-871-1332
; Sequence 1332, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1332
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-1332

Query Match          26.0%; Score 25; DB 7; Length 22;
Best Local Similarity 41.7%; Pred. No. 7e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EHCNFNDVTTRL 13
   ||| |::|
Db 7 ENCNNNSPESSL 18

RESULT 62
US-09-731-899-20
; Sequence 20, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; TITLE OF INVENTION: FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
; FILE REFERENCE: 20555/120343-US1
; CURRENT APPLICATION NUMBER: US/09/731,899
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-731-899-20
```

```
Query Match      26.0%; Score 25; DB 1; Length 24;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 TTYLREN 16
DB 17 TTYLKEN 23

RESULT 63
US-11-134-871-2382
; Sequence 2382, Application US/111134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebelsold, Rudolf H.
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2382
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2382

Query Match      26.0%; Score 25; DB 7; Length 26;
Best Local Similarity 36.4%; Pred. No. 8.4e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 NFNDVTRLRE 15
DB 16 NSSDLSQKLKE 26

RESULT 64
US-10-953-613C-697
; Sequence 697, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nespor; Thomas
; TITLE OF INVENTION: HINGE CORE MINETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 697
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-697

Query Match      26.0%; Score 25; DB 6; Length 28;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FNDVTRLRE 15
DB 6 FYDNYTRLRK 15

RESULT 65
US-10-953-613C-698
; Sequence 698, Application US/10953613C
; Publication No. US20060127404A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Chichi;Heavner, George;Knight, David;Ghrayeb, John;Scallan;
; APPLICANT: Bernard;Nespor; Thomas
; TITLE OF INVENTION: HINGE CORE MINETIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5038 NP
; CURRENT APPLICATION NUMBER: US/10/953,613C
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: 60/507,231
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 1021
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 698
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-953-613C-698

Query Match      26.0%; Score 25; DB 6; Length 28;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FNDVTRLRE 15
DB 6 FYDNYTRLRK 15

RESULT 67
US-11-343-583-316
; Sequence 316, Application US/11343583
; Publication No. US20060122370A1
```

GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN DANIEL
; APPLICANT: MIN, HOSUNG
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801A
; CURRENT APPLICATION NUMBER: US/11/343,583
; CURRENT FILING DATE: 2006-01-30
; PRIOR APPLICATION NUMBER: US/10/269,695
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/414,155
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328,624
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 316
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptibodies capable of binding to Ang-2
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa = FC
US-11-343-583-316

Query Match 26.0%; Score 25; DB 7; Length 31;
Best Local Similarity 41.7%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EHCNFDVTVRL 13
| | : : | | |
Db 14 ECEWDPWTCRL 25

RESULT 68
US-11-343-583-317
; Sequence 317, Application US/11343583
; Publication No. US20060122370A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN DANIEL
; APPLICANT: MIN, HOSUNG
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801A
; CURRENT APPLICATION NUMBER: US/11/343,583
; CURRENT FILING DATE: 2006-01-30
; PRIOR APPLICATION NUMBER: US/10/269,695
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/414,155
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328,624
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 317
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptibodies capable of binding to Ang-2
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa = FC
US-11-343-583-317

Query Match 26.0%; Score 25; DB 7; Length 31;
Best Local Similarity 41.7%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EHCNFDVTVRL 13
| | : : | | |
Db 14 ECEWDPWTCRL 25

Db 14 ECEWDPWTCRL 25

RESULT 69
US-11-134-871-2278
; Sequence 2278, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2278
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2278

Query Match 26.0%; Score 25; DB 7; Length 33;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 HCNFNDVTV 11
| | : | |
Db 2 HCSVNGTWT 10

RESULT 70
US-10-471-571A-1330
; Sequence 1330, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1330
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-471-571A-1330

Query Match 26.0%; Score 25; DB 6; Length 34;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTVTR 12
| | : | |
Db 21 FSGVKFNDWTK 32

RESULT 71
US-11-011-026-4
; Sequence 4, Application US/11011026
; Publication No. US20060128628A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, SHOW-LI
; APPLICANT: YANG, CHING-JEN
; APPLICANT: TSAO, YEOU-PING
; TITLE OF INVENTION: HUMAN TISSUE ANTIGEN-BINDING PEPTIDES AND THEIR AMINO
; TITLE OF INVENTION: ACID SEQUENCES

File Reference	Seq ID NOS	Score	DB	Length	Indels	Gaps
FILE REFERENCE: ASI 139						
CURRENT APPLICATION NUMBER: US/11/011,026						
CURRENT FILING DATE: 2004-12-15						
NUMBER OF SEQ ID NOS: 26						
SOFTWARE: PatentIn Ver. 3.3						
SEQ ID NO 4						
LENGTH: 9						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-11-011-026-4						
Query Match	25.0%	Score 24;	DB 7;	Length 9;		
Best Local Similarity	57.1%	Pred. No. 2e+05;				
Matches	4;	Conservative	2;	Mismatches	1;	Indels
QY	7	NDVTTLR 13				
DB	3	NDILSRL 9				
RESULT 72						
US-11-140-487A-1423						
Sequence 1423, Application US/11/140487A						
Publication No. US20060093617A1						
GENERAL INFORMATION:						
APPLICANT: Innogenetics N.V.						
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi						
FILE REFERENCE: 166						
CURRENT APPLICATION NUMBER: US/11/140,487A						
CURRENT FILING DATE: 2005-05-31						
PRIOR APPLICATION NUMBER: EP 04012951.2						
PRIOR FILING DATE: 2004-06-01						
PRIOR APPLICATION NUMBER: EP 04447239.7						
PRIOR FILING DATE: 2004-10-28						
PRIOR APPLICATION NUMBER: EP 05102441.2						
PRIOR FILING DATE: 2005-03-25						
PRIOR APPLICATION NUMBER: US 60/576,310						
PRIOR FILING DATE: 2004-06-03						
PRIOR APPLICATION NUMBER: US 60/622,782						
PRIOR FILING DATE: 2004-10-29						
PRIOR APPLICATION NUMBER: US 60/665,395						
PRIOR FILING DATE: 2005-03-25						
NUMBER OF SEQ ID NOS: 2278						
SOFTWARE: PatentIn version 3.1						
SEQ ID NO 1423						
LENGTH: 10						
TYPE: PRT						
ORGANISM: hepatitis C virus						
US-11-140-487A-1423						
Query Match	25.0%	Score 24;	DB 7;	Length 10;		
Best Local Similarity	50.0%	Pred. No. 4.4e+02;				
Matches	3;	Conservative	3;	Mismatches	0;	Indels
QY	4	CNPNVD 9				
DB	3	CSFSDL 8				
RESULT 73						
US-11-134-871-1093						
Sequence 1093, Application US/11/134871						
Publication No. US20060141528A1						
GENERAL INFORMATION:						
APPLICANT: Abersold, Rudolf H.						
APPLICANT: Zhang, Hui						
TITLE OF INVENTION: Compositions and Methods for						
TITLE OF INVENTION: Quatification of Serum Glycoproteins						
FILE REFERENCE: 66661-116						
CURRENT APPLICATION NUMBER: US/11/134,871						
CURRENT FILING DATE: 2005-05-20						
PRIOR APPLICATION NUMBER: 60/573,593						
PRIOR FILING DATE: 2004-05-21						
FILE REFERENCE: ASI 139						
CURRENT APPLICATION NUMBER: US/11/011,026						
CURRENT FILING DATE: 2004-12-15						
NUMBER OF SEQ ID NOS: 26						
SOFTWARE: PatentIn Ver. 3.3						
SEQ ID NO 4						
LENGTH: 9						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-11-011						

File Reference	Seq ID NOS	Score	DB	Length	Indels	Gaps
FILE REFERENCE: ASI 139	25.0%;	Score 24;	DB 7;	Length 9;		
CURRENT APPLICATION NUMBER: US/11/011,026	57.1%;	Pred. No. 2e+05;				
CURRENT FILING DATE: 2004-12-15						
NUMBER OF SEQ ID NOS: 26						
SOFTWARE: PatentIn Ver. 3.3						
SEQ ID NO 4						
LENGTH: 9						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-11-011-026-4						
Query Match	25.0%;	Score 24;	DB 7;	Length 9;		
Best Local Similarity	57.1%;	Pred. No. 2e+05;				
Matches	4;	Conservative	2;	Mismatches	1;	Indels
QY	7	NDVTTLR 13				
DB	3	NDILSRL 9				
RESULT 72						
US-11-140-487A-1423						
Sequence 1423, Application US/11/140487A						
Publication No. US20060093617A1						
GENERAL INFORMATION:						
APPLICANT: Innogenetics N.V.						
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi						
FILE REFERENCE: 166						
CURRENT APPLICATION NUMBER: US/11/140,487A						
CURRENT FILING DATE: 2005-05-31						
PRIOR APPLICATION NUMBER: EP 04012951.2						
PRIOR FILING DATE: 2004-06-01						
PRIOR APPLICATION NUMBER: EP 04447239.7						
PRIOR FILING DATE: 2004-10-28						
PRIOR APPLICATION NUMBER: EP 05102441.2						
PRIOR FILING DATE: 2005-03-25						
PRIOR APPLICATION NUMBER: US 60/576,310						
PRIOR FILING DATE: 2004-06-03						
PRIOR APPLICATION NUMBER: US 60/622,782						
PRIOR FILING DATE: 2004-10-29						
PRIOR APPLICATION NUMBER: US 60/665,395						
PRIOR FILING DATE: 2005-03-25						
NUMBER OF SEQ ID NOS: 2278						
SOFTWARE: PatentIn version 3.1						
SEQ ID NO 1423						
LENGTH: 10						
TYPE: PRT						
ORGANISM: hepatitis C virus						
US-11-140-487A-1423						
Query Match	25.0%;	Score 24;	DB 7;	Length 10;		
Best Local Similarity	50.0%;	Pred. No. 4.4e+02;				
Matches	3;	Conservative	3;	Mismatches	0;	Indels
QY	4	CNPNV 9				
DB	3	CSFSDL 8				
RESULT 73						
US-11-134-871-1093						
Sequence 1093, Application US/11/134871						
Publication No. US20060141528A1						
GENERAL INFORMATION:						
APPLICANT: Abersold, Rudolf H.						
APPLICANT: Zhang, Hui						
TITLE OF INVENTION: Compositions and Methods for						
FILE REFERENCE: 66661-116						
CURRENT APPLICATION NUMBER: US/11/134,871						
CURRENT FILING DATE: 2005-05-20						
PRIOR APPLICATION NUMBER: 60/573,593						
PRIOR FILING DATE: 2004-05-21						

File Reference	Seq ID NOS	Score	DB	Length	Indels	Gaps
FILE REFERENCE: ASI 139	25.0%;	Score 24;	DB 7;	Length 9;		
CURRENT APPLICATION NUMBER: US/11/011,026	57.1%;	Pred. No. 2e+05;				
CURRENT FILING DATE: 2004-12-15						
NUMBER OF SEQ ID NOS: 26						
SOFTWARE: PatentIn Ver. 3.3						
SEQ ID NO 4						
LENGTH: 9						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-11-011-026-4						
Query Match	25.0%;	Score 24;	DB 7;	Length 9;		
Best Local Similarity	57.1%;	Pred. No. 2e+05;				
Matches	4;	Conservative	2;	Mismatches	1;	Indels
QY	7	NDVTTLR 13				
DB	3	NDILSRL 9				
RESULT 72						
US-11-140-487A-1423						
Sequence 1423, Application US/11/140487A						
Publication No. US20060093617A1						
GENERAL INFORMATION:						
APPLICANT: Innogenetics N.V.						
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi						
FILE REFERENCE: 166						
CURRENT APPLICATION NUMBER: US/11/140,487A						
CURRENT FILING DATE: 2005-05-31						
PRIOR APPLICATION NUMBER: EP 04012951.2						
PRIOR FILING DATE: 2004-06-01						
PRIOR APPLICATION NUMBER: EP 04447239.7						
PRIOR FILING DATE: 2004-10-28						
PRIOR APPLICATION NUMBER: EP 05102441.2						
PRIOR FILING DATE: 2005-03-25						
PRIOR APPLICATION NUMBER: US 60/576,310						
PRIOR FILING DATE: 2004-06-03						
PRIOR APPLICATION NUMBER: US 60/622,782						
PRIOR FILING DATE: 2004-10-29						
PRIOR APPLICATION NUMBER: US 60/665,395						
PRIOR FILING DATE: 2005-03-25						
NUMBER OF SEQ ID NOS: 2278						
SOFTWARE: PatentIn version 3.1						
SEQ ID NO 1423						
LENGTH: 10						
TYPE: PRT						
ORGANISM: hepatitis C virus						
US-11-140-487A-1423						
Query Match	25.0%;	Score 24;	DB 7;	Length 10;		
Best Local Similarity	50.0%;	Pred. No. 4.4e+02;				
Matches	3;	Conservative	3;	Mismatches	0;	Indels
QY	4	CNPNVD 9				
DB	3	CSFSDL 8				
RESULT 73						
US-11-134-871-1093						
Sequence 1093, Application US/11/134871						
Publication No. US20060141528A1						
GENERAL INFORMATION:						
APPLICANT: Abersold, Rudolf H.						
TITLE OF INVENTION: Compositions and Methods for						
FILE REFERENCE: 66661-116						
CURRENT APPLICATION NUMBER: US/11/134,871						
CURRENT FILING DATE: 2005-05-20						
PRIOR APPLICATION NUMBER: 60/573,593						
PRIOR FILING DATE: 2004-05-21						
FILE REFERENCE: ASI 139						
CURRENT APPLICATION NUMBER: US/11/011,026						
CURRENT FILING DATE: 2004-12-15						
NUMBER OF SEQ ID NOS: 26						
SOFTWARE: PatentIn Ver. 3.3						
SEQ ID NO 4						
LENGTH: 9						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-11-011-026-4						
Query Match	25.0%;	Score				

```
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-468-182-1

Query Match      25.0%; Score 24; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 HCNFN 7
Db      5 HCNIS 9

RESULT 76
US-10-468-182-2
; Sequence 2, Application US/10468182
; Publication No. US20060116325A1
; GENERAL INFORMATION:
; APPLICANT: CHERTOV, Oleg
; APPLICANT: OPPENHEIM, Joost J.
; APPLICANT: XIN, Chen
; APPLICANT: MCGRATH, Connor
; APPLICANT: SOWDER II, Raymond C.
; APPLICANT: LUBKOWSKI, Jacek
; APPLICANT: WETZEL, Michele
; APPLICANT: ROGERS, Thomas J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING HIV-CORECEPTOR
; FILE REFERENCE: 15280-426-2
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/10/468,182
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-468-182-2

Query Match      25.0%; Score 24; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 HCNFN 7
Db      5 HCNIS 9

RESULT 77
US-10-468-182-3
; Sequence 3, Application US/10468182
; Publication No. US20060116325A1
; GENERAL INFORMATION:
; APPLICANT: CHERTOV, Oleg
; APPLICANT: OPPENHEIM, Joost J.
; APPLICANT: XIN, Chen
; APPLICANT: MCGRATH, Connor
; APPLICANT: SOWDER II, Raymond C.
; APPLICANT: LUBKOWSKI, Jacek
; APPLICANT: WETZEL, Michele
; APPLICANT: ROGERS, Thomas J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING HIV-CORECEPTOR
; FILE REFERENCE: 15280-426-2
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/10/468,182
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-468-182-3

Query Match      25.0%; Score 24; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 HCNFN 7
Db      5 HCNIS 9

RESULT 78
US-10-468-182-5
; Sequence 5, Application US/10468182
; Publication No. US20060116325A1
; GENERAL INFORMATION:
; APPLICANT: CHERTOV, Oleg
; APPLICANT: OPPENHEIM, Joost J.
; APPLICANT: XIN, Chen
; APPLICANT: MCGRATH, Connor
; APPLICANT: SOWDER II, Raymond C.
; APPLICANT: LUBKOWSKI, Jacek
; APPLICANT: WETZEL, Michele
; APPLICANT: ROGERS, Thomas J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING HIV-CORECEPTOR
; FILE REFERENCE: 15280-426-2
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/10/468,182
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-10-468-182-5

Query Match      25.0%; Score 24; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 HCNFN 7
Db      5 HCNIS 9

RESULT 79
US-10-468-182-8
; Sequence 8, Application US/10468182
; Publication No. US20060116325A1
; GENERAL INFORMATION:
; APPLICANT: CHERTOV, Oleg
; APPLICANT: OPPENHEIM, Joost J.
; APPLICANT: XIN, Chen
; APPLICANT: MCGRATH, Connor
; APPLICANT: SOWDER II, Raymond C.
; APPLICANT: LUBKOWSKI, Jacek
; APPLICANT: WETZEL, Michele
; APPLICANT: ROGERS, Thomas J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING HIV-CORECEPTOR
; FILE REFERENCE: 15280-426-2
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US/10/468,182
; PRIOR FILING DATE: 2002-02-15
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-468-182-8

Query Match      25.0%; Score 24; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 HCNFN 7
Db      5 HCNIS 9
```

```
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING HIV-CORECEPTOR
; FILE REFERENCE: 15280-426-2
; CURRENT APPLICATION NUMBER: US/10/468,182
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: PCT/US02/05063
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269,534
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE KK
US-10-468-182-8

Query Match      25.0%; Score 24; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HCNFN 7
      ||| :
      5 HCNIS 9

RESULT 80
US-10-468-182-9
; Sequence 9, Application US/10468182
; Publication No. US20060116325A1
; GENERAL INFORMATION:
; APPLICANT: CHERTOV, Oleg
; APPLICANT: XIN, Chen
; APPLICANT: OPPENHEIM, Joost J.
; APPLICANT: MCGRATH, Connor
; APPLICANT: SOWDER II, Raymond C.
; APPLICANT: LUBKOWSKI, Jacsek
; APPLICANT: WETZEL, Michele
; APPLICANT: ROGERS, Thomas J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING HIV-CORECEPTOR
; FILE REFERENCE: 15280-426-2
; CURRENT APPLICATION NUMBER: US/10/468,182
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: PCT/US02/05063
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269,534
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE 15D
US-10-468-182-9

Query Match      25.0%; Score 24; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HCNFN 7
      ||| :
      5 HCNIS 9

RESULT 81
US-11-140-487A-2119
; Sequence 2119, Application US/11140487A
; Publication No. US20060093617A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2119
; LENGTH: 15
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-11-140-487A-2119

Query Match      25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 EHCNFDVTT 11
      : | : |||
      6 DECHSTDSTT 15

RESULT 82
US-11-295-192A-624
; Sequence 624, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 624
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-624

Query Match      25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 30.8%; Pred. No. 6.8e+02;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 FEHCNFDVTTTL 13
      : : | ||| :
      3 YQDVNCTDVSTAI 15

RESULT 83
US-11-295-192A-625
; Sequence 625, Application US/11295192A
```

```
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 625
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-625

Query Match      25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 30.8%; Pred. No. 6.8e+02;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTTL 13
   : | | | :
Db 2 YQDVNCTDVSTAI 14

RESULT 84
US-11-295-192A-626
; Sequence 626, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 626
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-626

Query Match      25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 30.8%; Pred. No. 6.8e+02;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTTTL 13
   : | | | :
Db 1 YQDVNCTDVSTAI 13

RESULT 85
US-11-295-192A-980
; Sequence 980, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 980
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-980

Query Match      25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 NDVTTRL 13
   | | : | |
Db 8 NDILSRL 14

RESULT 86
US-11-295-192A-981
; Sequence 981, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 981
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-981

Query Match      25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 NDVTTRL 13
   | | : | |
Db 8 NDILSRL 14

RESULT 87
US-11-295-192A-982
; Sequence 982, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; PRIOR FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 982
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-982

Query Match      25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 NDVTTRL 13
   | | : | |
Db 8 NDILSRL 14
```

; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 982
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-982

Query Match 25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDVTTRL 13
||: |||
Db 7 NDILSRL 13

RESULT 88
US-11-295-192A-983
; Sequence 983, Application US/11295192A
; Publication No. US20060110803A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Ter Meulen, Jan H.
; APPLICANT: Slootstra, Jelle W.
; APPLICANT: Ruijk, Wouter C.
; APPLICANT: Goudsmit, Jaap
; TITLE OF INVENTION: Antigenic peptides of SARS coronavirus and used thereof
; FILE REFERENCE: 0089 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/295,192A
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: PCT/EP2004/051102
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 1264
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 983
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-295-192A-983

Query Match 25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDVTTRL 13
||: |||
Db 6 NDILSRL 12

RESULT 89
US-11-134-871-1623
; Sequence 1623, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20

; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1623
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-1623

Query Match 25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 36.4%; Pred. No. 6.8e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NDVTTRLRENE 17
||: |||
Db 5 NDTSELQNR 15

RESULT 90
US-10-526-062-11
; Sequence 11, Application US/10526062
; Publication No. US20060141563A1
; GENERAL INFORMATION:
; APPLICANT: Biemanns, Ralph
; APPLICANT: Denoel, Philippe
; APPLICANT: Peron, Christiane
; APPLICANT: Goraj, Karine
; APPLICANT: Kortekaas, Jeroen
; APPLICANT: Poolman, Jan
; APPLICANT: Tommassen, Jan
; APPLICANT: Weynants, Vincent
; TITLE OF INVENTION: Mutant Protein and Refolding Method
; FILE REFERENCE: VB60394
; CURRENT APPLICATION NUMBER: US/10/526,062
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: PCT/EP03/009634
; PRIOR FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: GB 0220199.4
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-526-062-11

Query Match 25.0%; Score 24; DB 6; Length 16;
Best Local Similarity 45.5%; Pred. No. 7.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 NDVTTRLRENE 17
||: |||
Db 2 NEEKKNRENE 12

RESULT 91
US-11-219-563-94
; Sequence 94, Application US/11219563
; Publication No. US2006008539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379

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; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-94

Query Match      25.0%; Score 24; DB 7; Length 17;
Best Local Similarity 80.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 FNDVT 10
       :||||
Db      5 YNDVT 9

RESULT 92
US-10-539-402-100
; Sequence 100, Application US/10539402
; Publication No. US20060115477A1
; GENERAL INFORMATION:
; APPLICANT: Xerion Pharmaceuticals AG
; TITLE OF INVENTION: Neuropilin-1 Inhibitor
; FILE REFERENCE: XE12EPC
; CURRENT APPLICATION NUMBER: US/10/539,402
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 60/435,893
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: EP 03000615
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 18
; TYPE: PRT
; ORGANISM: human
US-10-539-402-100

Query Match      25.0%; Score 24; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FEHCN 5
       :|||
Db      4 WRHCN 8

RESULT 93
US-11-061-841-260
; Sequence 260, Application US/11061841
; Publication No. US20060122377A1
; GENERAL INFORMATION:
; APPLICANT: DENNIS, MARK S.
; TITLE OF INVENTION: COR-REPAIRED ANTIBODIES
; FILE REFERENCE: P2070R1
; CURRENT APPLICATION NUMBER: US/11/061,841
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US 60/545,840
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 441
; SEQ ID NO 260
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-061-841-260

Query Match      25.0%; Score 24; DB 7; Length 18;
Best Local Similarity 40.0%; Pred. No. 8.3e+02;

US-11-020-393b-3_copy_42_58.max.rapbn

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      7 NDVTTLREN 16
       :|:|:|:|
Db      6 SDSESLKQN 15

RESULT 94
US-11-253-223-19
; Sequence 19, Application US/11253223
; Publication No. US20060121570A1
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE
; TITLE OF INVENTION: BINDING SITES, MONOCLONAL ANTIBODIES, AND COMPOSITIONS
; FILE REFERENCE: TSRI 334.2
; CURRENT APPLICATION NUMBER: US/11/253,223
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US/08/495,606
; PRIOR FILING DATE: 1995-08-21
; PRIOR APPLICATION NUMBER: PCT/US94/01258
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: US 08/084,542
; PRIOR FILING DATE: 1993-06-28
; PRIOR APPLICATION NUMBER: US 08/012,566
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
; NAME/KEY: VARIANT
; LOCATION: 9
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-253-223-19

Query Match      25.0%; Score 24; DB 7; Length 18;
Best Local Similarity 44.4%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      4 CNFNDVTTR 12
       |:|:|
Db      3 CSFGRTXTTR 11

RESULT 95
US-11-272-521-36
; Sequence 36, Application US/11272521
; Publication No. US20060135431A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: XIONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/11/272,521
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/10/145,206
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Preferred TALL-1 Modulating Domains
US-11-272-521-36

Query Match 25.0%; Score 24; DB 7; Length 18;
Best Local Similarity 66.7%; Pred. No. 8.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 2;

QY 2 EHCNFN 7
| | | |
Db 13 EWCQFN 18

RESULT 96
US-11-134-871-2482
; Sequence 2482, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2482
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-2482

Query Match 25.0%; Score 24; DB 7; Length 18;
Best Local Similarity 30.8%; Pred. No. 8.3e+02; Indels 4; Gaps 0;
Matches 4; Conservative 5; Mismatches 5;

QY 5 NFNDVTRLRENE 17
|:::|:|:|
Db 6 NYSNVSIHLKNPE 18

RESULT 97
US-11-234-731-517
; Sequence 517, Application US/11234731
; Publication No. US20060140934A1
; GENERAL INFORMATION:
; APPLICANT: XIONG, FEI
; APPLICANT: SITNEY, KAREN C.
; TITLE OF INVENTION: MODIFIED PC MOLECULES
; FILE REFERENCE: A-914
; CURRENT APPLICATION NUMBER: US/11/234,731
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: 60/612,680
; PRIOR FILING DATE: 2004-09-24
; NUMBER OF SEQ ID NOS: 659
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 517
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Preferred TALL-1 Modulating Domains
US-11-234-731-517

Query Match 25.0%; Score 24; DB 7; Length 18;
Best Local Similarity 66.7%; Pred. No. 8.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 2;

QY 2 EHCNFN 7

Db 13 EWCQFN 18
| | | |
RESULT 98
US-11-122-986-703
; Sequence 703, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 703
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-11-122-986-703

Query Match 25.0%; Score 24; DB 7; Length 19;
Best Local Similarity 44.4%; Pred. No. 8.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 3;

QY 5 NFNDVTRL 13
| | | |
Db 9 NFTDVKI 17

RESULT 99
US-11-134-871-1495
; Sequence 1495, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Abersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1495
; LENGTH: 19
; TYPE: PRT

; ORGANISM: Homo sapiens
US-11-134-871-1495

Query Match 25.0%; Score 24; DB 7; Length 19;
Best Local Similarity 33.3%; Pred. No. 8.8e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EHCNFNDVTTTL 13
| : : : :
Db 8 ESSNLSEIESRL 19

RESULT 100

US-11-134-871-3447
; Sequence 3447, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
; APPLICANT: Aebersold, Rudolf H.
; APPLICANT: Zhang, Hui
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Quatification of Serum Glycoproteins
; FILE REFERENCE: 66661-116
; CURRENT APPLICATION NUMBER: US/11/134,871
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,593
; PRIOR FILING DATE: 2004-05-21
; NUMBER OF SEQ ID NOS: 3602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3447
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-871-3447

Query Match 25.0%; Score 24; DB 7; Length 21;
Best Local Similarity 50.0%; Pred. No. 9.8e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 NFNDVTTTLR 14
| : : : :
Db 11 NISDPTSPLR 20

Search completed: July 15, 2006, 00:39:55
Job time : 31 secs

249	20	20.8	27	2	A48200	homeotic protein H	322	19	19.8	21	2	I40066	shikimate 5-dehydr
250	20	20.8	28	2	A61281	lysosome homolog A	323	19	19.8	21	2	I51224	sonatotropin - chi
251	20	20.8	28	2	S55729	orotidine-5'-monop	324	19	19.8	21	2	S27039	bibrototoxin - Bibo
252	20	20.8	29	2	S35924	T-cell receptor ga	325	19	19.8	22	2	S00189	motilin - dog (ten
253	20	20.8	30	2	S69125	rRNA N-glycosidase	326	19	19.8	22	2	B32946	serine proteinase
254	20	20.8	30	2	A22977	delta-endotoxin -	327	19	19.8	22	2	B28563	hemoglobin chain I
255	20	20.8	30	2	C43591	51K outer membrane	328	19	19.8	22	2	B44072	hypothetical prote
256	20	20.8	31	2	B82401	hypothetical prote	329	19	19.8	22	2	B44072	mannose-1-phosphat
257	20	20.8	31	2	S78772	ribosomal protein	330	19	19.8	23	2	A47415	hypothetical prote
258	20	20.8	32	2	A03367	lectin - Macrotylo	331	19	19.8	23	2	S07647	hypothetical prote
259	20	20.8	32	2	D86901	hypothetical prote	332	19	19.8	24	2	A05134	neurotoxin V - sco
260	20	20.8	32	2	T17394	vrlN protein - Dic	333	19	19.8	24	2	A20554	hemocyanin subunit
261	20	20.8	32	4	A49016	gag-jund mutant fu	334	19	19.8	25	2	JQ0361	vasoactive intesti
262	20	20.8	33	2	S77568	dipeptidyl-peptida	335	19	19.8	25	2	PH1717	ig heavy chain V r
263	20	20.8	33	2	A60222	myelin basic prote	336	19	19.8	25	2	S78343	hypothetical prote
264	20	20.8	33	2	P95075	hypothetical prote	337	19	19.8	25	2	B85928	hypothetical prote
265	20	20.8	33	2	B70244	hypothetical prote	338	19	19.8	25	2	P20554	hemocyanin subunit
266	20	20.8	33	2	P82472	hypothetical prote	339	19	19.8	26	2	S16336	beta-conglycinin b
267	20	20.8	33	2	S53880	citG protein - Lac	340	19	19.8	27	2	A61071	pituitary adenylat
268	20	20.8	33	2	S48211	phospholipase D -	341	19	19.8	27	2	P39690	neural cell adhesi
269	20	20.8	33	2	C97406	hypothetical prote	342	19	19.8	27	2	S07646	hypothetical prote
270	20	20.8	33	2	PQ0309	glycoprotein B - h	343	19	19.8	27	2	S64717	formin binding pro
271	20	20.8	34	2	A22701	tubulin beta-1 cha	344	19	19.8	27	2	P48200	homeotic protein H
272	20	20.8	36	2	S49315	MSL leader peptide	345	19	19.8	27	2	A44636	homeotic protein H
273	20	20.8	36	2	S45088	probable leader pe	346	19	19.8	27	2	A44629	homeotic protein H
274	20	20.8	36	2	S16943	neuropeptide Y - s	347	19	19.8	27	2	A44641	homeotic protein H
275	20	20.8	36	2	A59064	egg-laying hormone	348	19	19.8	28	2	B60583	glycoprotein hormo
276	20	20.8	36	2	S21594	ig heavy chain V r	349	19	19.8	28	2	A61233	retinol-binding pr
277	20	20.8	36	2	A64540	hypothetical prote	350	19	19.8	28	2	I52627	erythrocyte chemok
278	20	20.8	36	2	G81853	hypothetical prote	351	19	19.8	28	2	G89384	conserved hypothet
279	20	20.8	36	2	C64039	hypothetical prote	352	19	19.8	28	2	S06668	toxin-like protein
280	20	20.8	36	2	B44336	neurotoxin Tx3-5 -	353	19	19.8	28	2	I48178	orphan receptor -
281	20	20.8	37	2	A25028	erythromycin resis	354	19	19.8	28	4	I68614	frame shifted FMRI
282	20	20.8	37	2	S27245	formylmethanofuran	355	19	19.8	29	2	S10061	ig heavy chain (cl
283	20	20.8	37	2	D95008	hypothetical prote	356	19	19.8	29	2	S26229	ribosomal protein
284	20	20.8	38	2	I46861	macrophage migrati	357	19	19.8	29	2	A27688	mammaly-derived gr
285	20	20.8	38	2	I48924	homeobox protein -	358	19	19.8	29	2	S32734	homeotic protein -
286	20	20.8	39	2	B40984	finger protein zfe	359	19	19.8	30	2	B48972	mannose-specific l
287	20	20.8	40	1	XKPO2B	proteinase inhibit	360	19	19.8	30	2	B36277	actin-capping prot
288	20	20.8	40	2	JU0225	sapacin C - flesh	361	19	19.8	30	2	JC1360	hypothetical jK pr
289	20	20.8	40	2	B96843	protein TRLS.1 (i	362	19	19.8	30	2	A44010	kit-ligand (altern
290	20	20.8	40	2	F84316	hypothetical prote	363	19	19.8	30	2	D81532	hypothetical prote
291	20	20.8	40	2	C72398	hypothetical prote	364	19	19.8	30	2	A27634	major fecal allerg
292	20	20.8	40	2	B82382	conserved hypothet	365	19	19.8	31	2	H82818	hypothetical prote
293	20	20.8	40	2	D69279	hypothetical prote	366	19	19.8	32	2	S57233	sex combs reduced
294	20	20.8	40	2	A47753	beta-defensin-10 -	367	19	19.8	32	4	I39971	hypothetical orfx
295	20	20.8	40	4	A58361	protein-tyrosine k	368	19	19.8	33	1	LEPBYB	pyrBI leader pepti
296	19.5	20.3	32	2	S30756	genome polyprotein	369	19	19.8	33	2	PC2249	peptidylprolyl iso
297	19.5	20.3	33	2	C91218	rho operon leader	370	19	19.8	33	2	A03150	retinoic acid-bind
298	19.5	20.3	33	2	D86064	rho operon leader	371	19	19.8	33	2	AE1059	pyrBI operon leade
299	19.5	20.3	33	2	A05111	probable rho leade	372	19	19.8	33	2	D64543	hypothetical prote
300	19.5	20.3	35	2	E95127	hypothetical prote	373	19	19.8	33	2	H82096	hypothetical prote
301	19.5	20.3	36	2	S59093	hypothetical prote	374	19	19.8	34	2	A36626	osteogenic protein
302	19.5	20.3	39	2	A54531	circumsporozoite a	375	19	19.8	34	2	S12554	hydroxymethylgluca
303	19.5	20.3	39	2	AG0838	hypothetical prote	376	19	19.8	34	2	I67424	hERR-2 homolog - r
304	19	19.8	9	2	PT0272	ig heavy chain CRD	377	19	19.8	35	2	S32679	ribosomal protein
305	19	19.8	9	2	A42266	peptidylglycine mo	378	19	19.8	35	2	P84395	hypothetical prote
306	19	19.8	10	2	PH0895	T-cell receptor be	379	19	19.8	35	2	S14364	4-sulfobenzoate 3,
307	19	19.8	11	4	PC2124	aminotransferase c	380	19	19.8	35	2	T42121	hypothetical prote
308	19	19.8	14	2	PH1627	ig H chain V-D-J r	381	19	19.8	35	2	D82607	hypothetical prote
309	19	19.8	15	2	PT0095	H+-transporting tw	382	19	19.8	35	2	B85708	unknown protein en
310	19	19.8	15	2	S36889	ribosomal protein	383	19	19.8	35	2	D97553	hypothetical prote
311	19	19.8	17	2	S20490	phycosystem II chl	384	19	19.8	35	2	P22102	phycocerythrin-545
312	19	19.8	18	2	A56871	retinol-binding pr	385	19	19.8	36	2	B27633	ig lambda-2 chain
313	19	19.8	18	2	PN0175	glutathione transf	386	19	19.8	36	2	I67429	nuclear hormone re
314	19	19.8	18	2	S54272	CYC 75 protein - h	387	19	19.8	36	2	A58864	ceresoylin O - Bac
315	19	19.8	18	2	S51734	T-cell receptor al	388	19	19.8	36	2	T36994	probable transposa
316	19	19.8	19	2	I50153	alpha-actin - chic	389	19	19.8	36	2	S46227	hypothetical prote
317	19	19.8	20	2	C20554	hemocyanin subunit	390	19	19.8	36	2	H70243	hypothetical prote
318	19	19.8	20	2	C60894	gamma crystallin I	391	19	19.8	36	2	T44548	hypothetical prote
319	19	19.8	20	2	A24589	phycosystem II chl	392	19	19.8	36	2	P82827	hypothetical prote
320	19	19.8	20	2	I54283	arylsulfatase A -	393	19	19.8	36	2	G82817	hypothetical prote
321	19	19.8	20	2	S63483	coenzyme F420 hydr	394	19	19.8	37	2	S14892	crystallin (clone

395	19	19.8	37	2	C60580	growth hormone-rel	468	18	18.8	19	2	PH1313	Ig heavy chain DJ
396	19	19.8	37	2	AC2330	50S ribosomal prot	469	18	18.8	20	2	A61526	major milk gland p
397	19	19.8	37	2	AB0592	probable membrane	470	18	18.8	20	2	S28434	major outer membra
398	19	19.8	37	2	F70245	hypothetical prote	471	18	18.8	20	2	FQ0046	citrate (sl)-synth
399	19	19.8	37	2	A45609	calcium-binding pr	472	18	18.8	21	1	A32225	conantokin r - con
400	19	19.8	38	2	B25052	carboxylesterase (473	18	18.8	21	1	D42762	proteasome endopep
401	19	19.8	38	2	A61070	pituitary adenylat	474	18	18.8	21	2	S65611	tubulin beta chain
402	19	19.8	38	2	A49165	pituitary adenylat	475	18	18.8	21	2	D61497	seed protein ws-19
403	19	19.8	38	2	H39690	neural cell adhesi	476	18	18.8	21	2	A59442	Bacillus thuringie
404	19	19.8	38	2	A29790	trichosanthin (ver	477	18	18.8	22	2	S12391	farnE protein - Esc
405	19	19.8	38	2	S05695	photosystem II pro	478	18	18.8	23	2	E54346	pyruvate synthase
406	19	19.8	38	2	S31821	photosystem II pro	479	18	18.8	23	2	S04171	aadA protein - Kle
407	19	19.8	38	2	S03943	hydrogen dehydrog	480	18	18.8	23	2	S24279	hypothetical prote
408	19	19.8	38	2	S63508	protein B betaine-	481	18	18.8	23	2	G69812	hypothetical prote
409	19	19.8	38	2	I70018	kallikrein - mouse	482	18	18.8	23	2	S58859	botulinum neurotox
410	19	19.8	38	2	B49012	orf 5' of megl - m	483	18	18.8	23	4	A58505	interleukin-1 beta
411	19	19.8	38	2	A80747	hypothetical prote	484	18	18.8	24	2	C60525	alpha-lactalbumin
412	19	19.8	38	2	F95019	hypothetical prote	485	18	18.8	24	2	I73584	alpha 1-proteinase
413	19	19.8	38	2	G81904	hypothetical prote	486	18	18.8	24	2	I73582	alpha 1-proteinase
414	19	19.8	38	2	A82450	hypothetical prote	487	18	18.8	24	2	A43503	botulinum toxin ty
415	19	19.8	38	2	A60688	phytochrome - gard	488	18	18.8	24	2	E20554	hemocyanin subunit
416	19	19.8	39	2	A05323	phospholipase A2 (489	18	18.8	24	2	A27262	nicotinic acetylch
417	19	19.8	39	2	A61232	pregnancy-associat	490	18	18.8	24	2	B27262	nicotinic acetylch
418	19	19.8	39	2	A60716	somatotropin intro	491	18	18.8	24	2	I38753	ELAV-like neuronal
419	19	19.8	39	2	F64718	hypothetical prote	492	18	18.8	25	2	I38002	calcium channel be
420	19	19.8	39	2	G83252	hypothetical prote	493	18	18.8	25	2	A49038	Ig lambda chain V
421	19	19.8	39	2	A82359	hypothetical prote	494	18	18.8	25	2	I40061	shikimate 5-dehydr
422	19	19.8	39	2	B82725	hypothetical prote	495	18	18.8	26	1	NTSR3L	neurotoxin III - E
423	19	19.8	39	2	A82707	hypothetical prote	496	18	18.8	26	2	S05222	photosystem I 9K p
424	19	19.8	39	2	F97313	hypothetical prote	497	18	18.8	26	2	PL0027	M protein pepM19 -
425	19	19.8	40	2	A29502	carboxylesterase (498	18	18.8	26	2	A28108	atrial gland pepti
426	19	19.8	40	2	A19940	antithrombin III -	499	18	18.8	26	2	S15879	electron transfer
427	19	19.8	40	2	D81036	hypothetical prote	500	18	18.8	26	2	I49748	homeobox protein -
428	19	19.8	40	2	D81554	hypothetical prote	501	18	18.8	27	2	PH1371	Ig heavy chain DJ
429	19	19.8	40	2	D81554	hypothetical prote	502	18	18.8	27	2	PC2314	X-Pro aminopeptida
430	18.5	19.3	18	2	JS0647	pharmomotropin -	503	18	18.8	27	2	PH1370	Ig heavy chain DJ
431	18.5	19.3	27	2	A58997	kappa-conotoxin pv	504	18	18.8	27	2	B47295	homeodomain protei
432	18.5	19.3	30	2	S30759	genome polyprotein	505	18	18.8	28	2	D38578	protein kinase 4 (
433	18.5	19.3	30	2	S30760	genome polyprotein	506	18	18.8	28	2	I40034	trpE protein - Bac
434	18.5	19.3	32	2	S30755	genome polyprotein	507	18	18.8	28	2	B39191	hypothetical prote
435	18.5	19.3	33	2	G86126	hypothetical prote	508	18	18.8	28	2	C97078	hypothetical prote
436	18.5	19.3	34	2	D44906	Li protein - human	509	18	18.8	29	2	S38749	vimentin homolog -
437	18	18.8	7	2	S08606	hypothetical prote	510	18	18.8	29	2	B81136	hypothetical prote
438	18	18.8	10	2	PT0284	Ig heavy chain CRD	511	18	18.8	29	2	C60743	putrescine carbamo
439	18	18.8	10	2	S27873	hypothetical prote	512	18	18.8	29	2	S78310	hypothetical prote
440	18	18.8	12	2	B61457	seed protein ws-17	513	18	18.8	29	2	S38525	xRNA N-glycosidase
441	18	18.8	13	2	G56046	urinary tract aton	514	18	18.8	29	2	PC4421	multicatalase (EC 3
442	18	18.8	14	2	I64815	carbonic anhydrase	515	18	18.8	29	2	A55891	delta-conotoxin Gm
443	18	18.8	14	2	PH1347	Ig heavy chain DJ	516	18	18.8	30	2	A60517	alpha-1-antitrypsi
444	18	18.8	14	2	PH1625	Ig H chain V-D-J r	517	18	18.8	30	2	C61125	glucagon-like pept
445	18	18.8	14	2	A41589	25K elastin-bindin	518	18	18.8	30	2	B61125	glucagon-like pept
446	18	18.8	14	2	PA0007	lectin B1 - Psopho	519	18	18.8	30	2	A03148	retinol-binding pr
447	18	18.8	15	2	I49407	placental calcium-	520	18	18.8	30	2	S26175	tail tubular prote
448	18	18.8	15	2	PT0222	Ig heavy chain CDR	521	18	18.8	30	2	S68312	glucuronosyltransf
449	18	18.8	15	2	PH1310	Ig heavy chain DJ	522	18	18.8	30	2	S43311	pyrrole-2-carboxyl
450	18	18.8	15	2	PA0005	lectin A1 - Psopho	523	18	18.8	30	2	C32946	serine proteinase
451	18	18.8	15	2	PA0006	lectin A3 - Psopho	524	18	18.8	30	2	D32946	serine proteinase
452	18	18.8	15	2	PA0008	lectin B2 - Psopho	525	18	18.8	30	2	B95020	hypothetical prote
453	18	18.8	16	2	A59046	alpha-conotoxin MI	526	18	18.8	30	2	PC4364	steroid receptor c
454	18	18.8	16	2	PH1778	T cell receptor al	527	18	18.8	31	1	CLHR1A	protamine YI - Atl
455	18	18.8	17	1	A61339	vesiculakinin 1 - e	528	18	18.8	31	1	CLHRV1	protamine YI - Pac
456	18	18.8	17	1	A05168	conantokin G [vali	529	18	18.8	31	2	S44471	glucagon G1 - Nort
457	18	18.8	17	2	S69164	ferredoxin al - Ja	530	18	18.8	31	2	S44472	glucagon G2 - Nort
458	18	18.8	17	2	B61491	seed protein ws-2	531	18	18.8	31	2	S35925	T-cell receptor ga
459	18	18.8	18	2	S02175	acrosin (EC 3.4.21	532	18	18.8	31	2	S27151	gene 30.1 protein
460	18	18.8	18	2	A28060	elastase inhibitor	533	18	18.8	31	2	D70118	hypothetical prote
461	18	18.8	18	2	S29491	GTP-binding protei	534	18	18.8	31	2	A21919	tricarboxylate-bin
462	18	18.8	18	2	H64711	hypothetical prote	535	18	18.8	31	2	D82093	hypothetical prote
463	18	18.8	18	2	B41589	40K elastin-bindin	536	18	18.8	31	2	G82394	hypothetical prote
464	18	18.8	18	2	S58855	botulinum neurotox	537	18	18.8	32	1	Z9BEP1	coat protein C cha
465	18	18.8	18	2	T13132	protein gp45,1 - p	538	18	18.8	32	1	Z9BEPD	coat protein C cha
466	18	18.8	19	2	A38382	15K protein A - ra	539	18	18.8	32	1	Z9BPM3	coat protein C cha
467	18	18.8	19	2	A35301	beta-1,3-glucan-bi	540	18	18.8	32	2	F23454	ovalbumin phosphos

541	18	18.8	32	2	A44906	L1 protein - human	614	17	17.7	10	2	A61289	streptopain (EC 3.
542	18	18.8	32	2	B95081	hypothetical prote	615	17	17.7	12	2	A54315	entactin/nidogen -
543	18	18.8	32	2	A65689	galactose binding	616	17	17.7	12	2	T46656	hypothetical prote
544	18	18.8	33	2	A43312	2',3'-cyclic-nucle	617	17	17.7	13	2	A49637	MHC class II histo
545	18	18.8	33	2	A71297	hypothetical prote	618	17	17.7	13	2	B61620	locustamytotropin I
546	18	18.8	33	2	F85581	unknown protein en	619	17	17.7	13	2	JH0460	coricostatic pept
547	18	18.8	33	2	B58512	bromosleeper pepti	620	17	17.7	14	2	B33098	Ig heavy chain V r
548	18	18.8	34	1	ONGARA	egg-releasing pept	621	17	17.7	14	2	PH1705	214K exoantigen (v
549	18	18.8	34	2	A60686	cytochrome-c oxida	622	17	17.7	14	2	PH1311	Ig heavy chain DJ
550	18	18.8	34	2	S55440	betaA2 crystallin	623	17	17.7	14	2	PH1305	Ig heavy chain DJ
551	18	18.8	34	2	PH1337	Ig heavy chain DJ	624	17	17.7	14	2	PH1306	Ig heavy chain DJ
552	18	18.8	34	2	H81883	hypothetical prote	625	17	17.7	15	1	NRKNAG	alpha-conotoxin GI
553	18	18.8	34	2	G82502	hypothetical prote	626	17	17.7	15	2	PA0110	translation elonga
554	18	18.8	34	2	C44336	neurotoxin Tx3-3 -	627	17	17.7	15	2	T46625	hypothetical prote
555	18	18.8	35	2	I48890	cryptidin-7 - mouse	628	17	17.7	16	2	A24099	crystal protein, 2
556	18	18.8	35	2	I48897	cryptidin-15 - mous	629	17	17.7	17	2	I49048	T-cell receptor be
557	18	18.8	35	2	I48896	cryptidin-13 - mous	630	17	17.7	17	2	PH1340	Ig heavy chain DJ
558	18	18.8	35	2	I48891	cryptidin-8 - mouse	631	17	17.7	17	2	PH1312	Ig heavy chain DJ
559	18	18.8	35	2	I48892	cryptidin-9 - mouse	632	17	17.7	17	1	A58589	alpha-conotoxin EI
560	18	18.8	35	2	AB0612	hypothetical prote	633	17	17.7	18	1	C40433	Nada protein - Cya
561	18	18.8	35	2	E95098	hypothetical prote	634	17	17.7	19	2	A21182	4K prothoracicotro
562	18	18.8	35	2	E70237	hypothetical prote	635	17	17.7	19	2	PA0010	seed storage prote
563	18	18.8	35	2	C69977	hypothetical prote	636	17	17.7	19	2	A41077	protein-diulfide
564	18	18.8	36	1	WISMAA	alpha-amylase inhi	637	17	17.7	19	2	I40063	shikimate 5-dehydr
565	18	18.8	36	2	B31872	retinoic acid-bind	638	17	17.7	20	2	S72501	protein kinase C i
566	18	18.8	36	2	S43284	gallinacin - chick	639	17	17.7	20	2	B53875	creatine kinase (B
567	18	18.8	36	2	A95135	hypothetical prote	640	17	17.7	20	2	A53875	creatine kinase (B
568	18	18.8	36	2	F84791	hypothetical prote	641	17	17.7	20	2	S46205	comosalin (EC 3.4.2
569	18	18.8	36	2	D82466	hypothetical prote	642	17	17.7	20	2	PN0171	peptidylprolyl iso
570	18	18.8	36	2	A63326	hypothetical prote	643	17	17.7	20	2	B38382	15K protein B - ra
571	18	18.8	36	2	B82827	hypothetical prote	644	17	17.7	20	2	S04621	gamma-crystallin I
572	18	18.8	36	2	D82818	hypothetical prote	645	17	17.7	20	2	PC4385	GroEL protein homo
573	18	18.8	36	2	C85910	unknown protein en	646	17	17.7	20	2	PC4386	GroEL protein homo
574	18	18.8	37	2	S39036	lipid transfer pro	647	17	17.7	20	2	S16202	pyrrolidine-5-carbox
575	18	18.8	37	2	C32112	R15 gamma peptide	648	17	17.7	20	2	S66222	defensin AMP2 - Da
576	18	18.8	37	2	E87618	hypothetical prote	649	17	17.7	20	2	S33001	hypothetical prote
577	18	18.8	37	2	H82304	hypothetical prote	650	17	17.7	20	2	B61497	seed protein ws-20
578	18	18.8	37	2	E97596	hypothetical prote	651	17	17.7	20	2	B53283	major cat allergen
579	18	18.8	38	2	A05149	hypothetical prote	652	17	17.7	20	2	S27142	hypothetical prote
580	18	18.8	38	2	F36491	crystallin SIII -	653	17	17.7	20	2	DIRT	dental fluid tra
581	18	18.8	38	2	A60583	phosphoprotein pho	654	17	17.7	21	2	S23361	protein-tyrosine k
582	18	18.8	38	2	S78349	glycoprotein hormo	655	17	17.7	21	2	PH1731	Ig heavy chain V r
583	18	18.8	38	2	S33484	photosystem I prot	656	17	17.7	21	2	PH1730	Ig heavy chain V r
584	18	18.8	38	2	H70165	hypothetical prote	657	17	17.7	21	2	I65270	collagen alpha 1(I
585	18	18.8	38	2	G70236	hypothetical prote	658	17	17.7	21	2	PD0015	actin-binding prot
586	18	18.8	38	2	E81873	hypothetical prote	659	17	17.7	21	2	B59325	probable bacteriop
587	18	18.8	38	2	A56374	glyceraldehyde-3-p	660	17	17.7	22	2	PH1706	Ig heavy chain V r
588	18	18.8	38	2	S50117	activating factor	661	17	17.7	22	2	S07966	T-cell receptor be
589	18	18.8	38	2	A45495	beta-defensin-1 -	662	17	17.7	22	2	PH1714	Ig heavy chain V r
590	18	18.8	39	2	F82329	hypothetical prote	663	17	17.7	22	2	A12846	hypothetical prote
591	18	18.8	39	2	C40984	finger protein 18	664	17	17.7	23	2	PK0011	glutamate-ammonia
592	18	18.8	39	2	A96026	probable transposa	665	17	17.7	23	2	PH1726	Ig heavy chain V r
593	18	18.8	39	2	S01003	fructose 5-dehydro	666	17	17.7	23	2	PH1724	Ig heavy chain V r
594	18	18.8	40	2	T05931	probable 5-methylt	667	17	17.7	23	2	PH1723	Ig heavy chain V r
595	18	18.8	40	2	S77793	transketolase (EC	668	17	17.7	23	2	PH1727	Ig heavy chain V r
596	18	18.8	40	2	B59005	thymosin beta - sc	669	17	17.7	23	2	PH1722	Ig heavy chain V r
597	18	18.8	40	2	S70088	hypothetical prote	670	17	17.7	23	2	PH1725	Ig heavy chain V r
598	18	18.8	40	2	G82271	hypothetical prote	671	17	17.7	23	2	PH1707	Ig heavy chain V r
599	18	18.8	40	2	E82433	hypothetical prote	672	17	17.7	23	2	D25865	gamma-crystallin I
600	18	18.8	40	2	G45495	beta-defensin-9 -	673	17	17.7	23	2	A56661	S-locus specific g
601	18	18.8	40	2	I45495	beta-defensin-7 -	674	17	17.7	23	2	F61491	seed protein ws-6
602	18	18.8	40	2	H71330	hypothetical prote	675	17	17.7	23	2	S74178	4-hydroxyphenylpyr
603	17.5	18.2	23	2	S18837	glycine receptor a	676	17	17.7	23	2	S60570	homeodomain protei
604	17.5	18.2	23	2	S12502	capsid protein - S	677	17	17.7	23	2	S60565	homeodomain protei
605	17.5	18.2	29	2	S00564	enamel protein - r	678	17	17.7	24	2	T42441	protein phosphatas
606	17.5	18.2	32	2	S05754	genome polyprotein	679	17	17.7	24	2	S68391	H+-transporting tw
607	17.5	18.2	32	2	E72307	hypothetical prote	680	17	17.7	24	2	I45851	adenosylmethionine
608	17.5	18.2	35	2	A64108	protein V6, trunca	681	17	17.7	24	2	PH1710	Ig heavy chain V r
609	17	17.7	8	2	PC4131	hypothetical prote	682	17	17.7	24	2	PH1732	Ig heavy chain V r
610	17	17.7	8	2	A25836	L-serine ammonia-1	683	17	17.7	24	2	S53749	histone H4 - rat
611	17	17.7	8	2	T48890	hypothetical prote	684	17	17.7	24	2	A37973	lutropin-choriogon
612	17	17.7	9	2	PC7074	translation elonga	685	17	17.7	24	2	D81853	probable transposa
613	17	17.7	10	2	S63478	dihydrolipoamide d	686	17	17.7	24	2	A53357	neurotoxin Bt-II -

687	17	17.7	24	2	A37825	fibronectin recept	760	17	17.7	30	2	T31444	hypothetical prote
688	17	17.7	25	2	S10850	alpha-amylase inhi	761	17	17.7	30	2	F81360	very hypothetical
689	17	17.7	25	2	PH1734	ig heavy chain v r	762	17	17.7	30	2	PQ444	hypothetical prote
690	17	17.7	25	2	PH1733	ig heavy chain v r	763	17	17.7	31	2	A18671	tissue kallikrein
691	17	17.7	25	2	PH1715	ig heavy chain v r	764	17	17.7	31	2	B61014	defensin R-2 - rat
692	17	17.7	25	2	B25865	gamma-crystallin I	765	17	17.7	31	2	A61014	defensin NP-4 - ra
693	17	17.7	25	2	S21515	finp protein - Esc	766	17	17.7	31	2	A58586	conotoxin MrVIA -
694	17	17.7	25	2	S18400	carboxylic acid re	767	17	17.7	31	2	B58586	conotoxin MrVIB -
695	17	17.7	25	2	A61315	44K lectin - chick	768	17	17.7	31	2	A25210	toxin III homolog
696	17	17.7	25	2	S36378	ig heavy chain v r	769	17	17.7	31	2	S03297	ig alpha chain C r
697	17	17.7	25	2	A39319	fructokinase (EC 2	770	17	17.7	31	2	S03295	ig alpha chain C r
698	17	17.7	25	2	A23605	histone H1.1 - whe	771	17	17.7	31	2	S20223	ig mu chain - mous
699	17	17.7	25	2	PC4445	L-ascorbate peroxi	772	17	17.7	31	2	S00685	hypothetical prote
700	17	17.7	25	2	B89926	hypothetical prote	773	17	17.7	31	2	B82138	hypothetical prote
701	17	17.7	25	2	G41606	homeotic protein S	774	17	17.7	31	2	B4918	lactococin G pept
702	17	17.7	26	2	PH1718	ig heavy chain v r	775	17	17.7	31	2	B23605	histone H1.3 - whe
703	17	17.7	26	2	S55029	CAP3 protein - ant	776	17	17.7	31	2	T01701	hypothetical prote
704	17	17.7	26	2	S20041	hypothetical prote	777	17	17.7	31	2	G81558	hypothetical prote
705	17	17.7	26	2	D82344	IS1004 transposase	778	17	17.7	31	2	G82816	hypothetical prote
706	17	17.7	26	2	I52218	pre-pro-insulin-11	779	17	17.7	31	2	C54195	Na+/K+-exchanging
707	17	17.7	26	2	S68902	xanthine dehydroge	780	17	17.7	32	2	F46376	1-aminocyclopropan
708	17	17.7	26	2	B89834	hypothetical prote	781	17	17.7	32	2	E61014	defensin R-5 - rat
709	17	17.7	26	2	E42694	Hox 4.2 - mouse (f	782	17	17.7	32	2	D61014	defensin NP-1 - ra
710	17	17.7	27	2	JC2507	trypsin inhibitor	783	17	17.7	32	2	E70225	hypothetical prote
711	17	17.7	27	2	C60415	secretin - rabbit	784	17	17.7	32	4	B34962	hypothetical prote
712	17	17.7	27	2	S31605	ig heavy chain v r	785	17	17.7	33	1	WRECP1	protamine-like pro
713	17	17.7	27	2	PH1719	ig heavy chain v r	786	17	17.7	33	1	Z9BPIK	coat protein C cha
714	17	17.7	27	2	PH1720	ig heavy chain v r	787	17	17.7	33	2	B36193	inhibin beta-A cha
715	17	17.7	27	2	TQ0617	cystatin-related p	788	17	17.7	33	2	I54434	thymus leukemia an
716	17	17.7	27	2	PS0442	potassium channel	789	17	17.7	33	2	A60601	keratin, 55K, nucl
717	17	17.7	27	2	JC1280	heat-stable antige	790	17	17.7	33	2	I46601	myosin - pig (frag
718	17	17.7	27	2	PQ0844	DNA-binding protei	791	17	17.7	33	2	F46163	hypothetical prote
719	17	17.7	27	2	A43768	Hu-like protein HB	792	17	17.7	33	2	A82186	hypothetical prote
720	17	17.7	27	2	F70540	hypothetical prote	793	17	17.7	33	2	B82152	hypothetical prote
721	17	17.7	27	2	E44629	homeotic protein H	794	17	17.7	33	2	A58533	CD41 homolog - cha
722	17	17.7	27	2	D44629	homeotic protein H	795	17	17.7	33	2	B81714	hypothetical prote
723	17	17.7	27	2	C48200	homeotic protein H	796	17	17.7	34	2	S57865	N4-(beta-N-acetylgl
724	17	17.7	27	2	D44636	homeotic protein H	797	17	17.7	34	2	C43853	phosphopyruvate hy
725	17	17.7	28	2	A42272	brain-type creatin	798	17	17.7	34	2	PS0335	xylose isomerase (
726	17	17.7	28	2	S20393	trypsin inhibitor	799	17	17.7	34	2	I48887	xylose isomerase (
727	17	17.7	28	2	JK0059	serine proteinase	800	17	17.7	34	2	A19197	class II histocomp
728	17	17.7	28	2	JK0058	trypsin inhibitor	801	17	17.7	34	2	A19197	L1 protein - human
729	17	17.7	28	2	A25802	2S seed storage pr	802	17	17.7	34	2	D4889	major glycoprotein
730	17	17.7	28	2	S72460	ribosomal protein	803	17	17.7	34	2	S68548	hexokinase (EC 2.7
731	17	17.7	28	2	I50169	alpha-1 type-1 col	804	17	17.7	34	2	I49744	phosphofructokinase
732	17	17.7	28	2	A27261	proteinase inhibit	805	17	17.7	34	2	JC4218	phosphofructokinase
733	17	17.7	28	2	T06490	probable ribulose-	806	17	17.7	34	2	H95047	hypothetical prote
734	17	17.7	28	2	A69259	hypothetical prote	807	17	17.7	34	2	D95208	hypothetical prote
735	17	17.7	29	2	PH1328	ig heavy chain DJ	808	17	17.7	34	2	B64017	hypothetical prote
736	17	17.7	29	2	A00774	3-oxoadipate enol-	809	17	17.7	34	2	S35375	brlA protein - Eme
737	17	17.7	29	2	S65747	CDP-paratose synth	810	17	17.7	34	2	A60110	repetitive protein
738	17	17.7	29	2	S03947	hydrogen dehydroge	811	17	17.7	34	2	B97032	transcription regu
739	17	17.7	29	2	A32860	biotin-binding pro	812	17	17.7	34	2	S68084	probable RNA-bindi
740	17	17.7	29	2	A60604	glutathione peroxi	813	17	17.7	34	2	JQ1620	hypothetical 4.3K
741	17	17.7	29	2	AB0717	hypothetical prote	814	17	17.7	35	2	S29725	lignin peroxidase
742	17	17.7	29	2	T52557	translation elonga	815	17	17.7	35	2	S29726	lignin peroxidase
743	17	17.7	29	2	C60110	repetitive protein	816	17	17.7	35	2	S29728	lignin peroxidase
744	17	17.7	30	2	F60691	phycobilisome beta	817	17	17.7	35	2	S68338	trypsin (EC 3.4.21
745	17	17.7	30	2	S08202	peroxidase (EC 1.1	818	17	17.7	35	2	A29663	histone H4 - starf
746	17	17.7	30	2	A05004	pancreatic ribonuc	819	17	17.7	35	2	B44906	L1 protein - human
747	17	17.7	30	2	A61333	trypsin (EC 3.4.21	820	17	17.7	35	2	PC2293	V3 domain peptide
748	17	17.7	30	2	S30333	N-carbamoyl-D-amin	821	17	17.7	35	2	PC2295	V3 domain peptide
749	17	17.7	30	2	S60893	invC protein - Sal	822	17	17.7	35	2	PC2296	V3 domain peptide
750	17	17.7	30	2	S11617	ribosomal protein	823	17	17.7	35	2	T15602	hypothetical prote
751	17	17.7	30	2	S38527	rRNA N-glycosidase	824	17	17.7	35	2	H95100	hypothetical prote
752	17	17.7	30	2	S69124	serine proteinase-	825	17	17.7	35	2	F70205	hypothetical prote
753	17	17.7	30	2	B32946	trypsin-like serin	826	17	17.7	35	2	B82012	hypothetical prote
754	17	17.7	30	2	A32946	hypothetical prote	827	17	17.7	35	2	H82103	hypothetical prote
755	17	17.7	30	2	E72356	hypothetical prote	828	17	17.7	35	2	F82051	hypothetical prote
756	17	17.7	30	2	F70253	hypothetical prote	829	17	17.7	35	2	F85847	unknown protein en
757	17	17.7	30	2	A25497	peptide apy - Amer	830	17	17.7	35	2	H86021	hypothetical prote
758	17	17.7	30	2	B53088	factor IX/factor X	831	17	17.7	35	2	AD2525	hypothetical prote
759	17	17.7	30	2	A53088	factor IX/factor X	832	17	17.7	35	2	PC2297	V3 domain peptide

833	17	17.7	35	2	PC2291	V3 domain peptide	906	17	17.7	40	2	A33921	Balbani ring 1 ch
834	17	17.7	35	2	PC2294	V3 domain peptide	907	16.5	17.2	14	2	S12171	H+-transporting tw
835	17	17.7	36	1	PCAQ	pancreatic hormone	908	16.5	17.2	21	2	S68914	ribosomal protein
836	17	17.7	36	1	A32038	mu-agatoxin I - fu	909	16.5	17.2	24	2	B42272	brain-type creatin
837	17	17.7	36	1	A35030	curtatoxin I - fun	910	16.5	17.2	31	2	A20883	variant surface gl
838	17	17.7	36	2	S38517	mablinin II chain	911	16.5	17.2	36	2	A85682	unknown protein en
839	17	17.7	36	2	A28578	pancreatic hormone	912	16.5	17.2	37	2	S52616	hypothetical prote
840	17	17.7	36	2	S33401	ig heavy chain V r	913	16.5	17.2	38	1	GCR1K	glucagon-like pept
841	17	17.7	36	2	S08552	ribosomal protein	914	16.5	17.2	40	2	I39426	alpha-albumin - hu
842	17	17.7	36	2	A60146	65K heat shock pro	915	16	16.7	8	2	A32523	peptidyl-dipeptida
843	17	17.7	36	2	A60706	vascular endotheli	916	16	16.7	10	2	JC1367	thyloliberin poten
844	17	17.7	36	2	A69827	hypothetical prote	917	16	16.7	10	2	S62208	polyferredoxin - M
845	17	17.7	36	2	E82854	hypothetical prote	918	16	16.7	10	2	E44644	neurotoxin-associa
846	17	17.7	36	2	A82598	hypothetical prote	919	16	16.7	11	2	PH0922	T-cell receptor be
847	17	17.7	36	2	S17507	cytokine - rabbit	920	16	16.7	11	2	S35490	type II site-speci
848	17	17.7	37	1	A42040	kaliotoxin I (vali	921	16	16.7	12	2	C30503	IG gamma-2b chain
849	17	17.7	37	1	S32038	mu-agatoxin IV - f	922	16	16.7	12	2	A42324	cytochrome P450c27
850	17	17.7	37	1	E32038	mu-agatoxin V - fu	923	16	16.7	12	2	JQ2308	hypothetical 1.4K
851	17	17.7	37	1	F32038	mu-agatoxin VI - f	924	16	16.7	12	2	JQ2318	hypothetical 1.4K
852	17	17.7	37	1	A43933	antigen 5 epitope	925	16	16.7	13	2	AB0764	his operon leader
853	17	17.7	37	2	S03837	hcr protein - wood	926	16	16.7	13	2	A61210	antibiotic G82270
854	17	17.7	37	2	AH0637	conserved hypothet	927	16	16.7	14	2	A43847	IG mu chain V regi
855	17	17.7	37	2	E72269	hypothetical prote	928	16	16.7	14	2	S12904	protein kinase (SC
856	17	17.7	37	2	B31252	metallothionein II	929	16	16.7	15	2	S30608	translational elonga
857	17	17.7	37	2	S14101	apoliophorin III	930	16	16.7	15	2	E49037	TCR delta chain V-
858	17	17.7	37	2	S71912	hemoglobin, extrac	931	16	16.7	15	2	B26501	lipoprotein lipase
859	17	17.7	38	2	S70800	Ivi protein III -	932	16	16.7	15	2	A61522	7.5k surfactant-as
860	17	17.7	38	2	A54471	agitoxin 1 - scorp	933	16	16.7	15	2	D54226	light-harvesting p
861	17	17.7	38	2	C54471	agitoxin 3 - scorp	934	16	16.7	15	2	S60341	protein kinase (SC
862	17	17.7	38	2	B54471	agitoxin 2 - scorp	935	16	16.7	15	2	I78533	gene agouti protei
863	17	17.7	38	2	B60117	neurotoxin type D	936	16	16.7	16	2	PH0766	T-cell receptor be
864	17	17.7	38	2	A32112	R15 alpha 1 osmore	937	16	16.7	16	2	PH1476	T-cell receptor be
865	17	17.7	38	2	S68260	hypothetical prote	938	16	16.7	16	2	S35627	uvax protein - pha
866	17	17.7	38	2	S02600	hypothetical prote	939	16	16.7	16	2	S29631	beta-glucosidase (
867	17	17.7	38	2	I70022	kallikrein - mouse	940	16	16.7	16	2	A31963	pyruvate dehydroge
868	17	17.7	38	2	S07972	regulatory protein	941	16	16.7	16	2	I79565	hypothetical TCIs/
869	17	17.7	38	2	I39963	ribosomal protein	942	16	16.7	17	2	E40442	integrase homolog
870	17	17.7	38	2	T34678	hypothetical prote	943	16	16.7	17	2	S61451	hypothetical 2.1K
871	17	17.7	38	2	JN0613	defensin 4K - scor	944	16	16.7	17	2	JQ2310	hypothetical 2.1K
872	17	17.7	38	2	S27242	defensin - blue da	945	16	16.7	17	2	JQ2320	hypothetical 2.1K
873	17	17.7	38	2	S74088	defensin - Mediter	946	16	16.7	17	2	A32595	bombolitin I - Ame
874	17	17.7	39	2	S54330	trypsin inhibitor	947	16	16.7	18	2	B44995	alkanal monooxygen
875	17	17.7	39	2	I49418	insulin I precursor	948	16	16.7	18	2	D59137	protein P16 - gold
876	17	17.7	39	2	C55995	prostaglandin B2 r	949	16	16.7	19	2	S57558	T cell receptor V-
877	17	17.7	39	2	S48644	oxidase - Malayan	950	16	16.7	19	2	I49039	T-cell receptor be
878	17	17.7	39	2	H95146	hypothetical prote	951	16	16.7	19	2	A49780	promoter P8 hypoch
879	17	17.7	39	2	C70210	hypothetical prote	952	16	16.7	19	2	T37096	small hypothetical
880	17	17.7	39	2	B82419	hypothetical prote	953	16	16.7	20	2	S13274	ferredoxin [2Fe-2S
881	17	17.7	39	2	S70808	Ivi protein VI - V	954	16	16.7	20	2	PN0115	insulin-like growt
882	17	17.7	39	2	S34264	hypothetical prote	955	16	16.7	20	2	S29495	enhancing factor -
883	17	17.7	39	2	T15158	hypothetical prote	956	16	16.7	20	2	D60894	gamma crystallin V
884	17	17.7	39	2	A48544	neuropeptide F - b	957	16	16.7	20	2	A36045	thrombospondin hom
885	17	17.7	39	2	B45193	zinc finger protei	958	16	16.7	20	2	A44921	hydroxypyruvate re
886	17	17.7	39	2	C83904	hypothetical prote	959	16	16.7	20	2	S18582	hypothetical prote
887	17	17.7	40	2	S00264	creatine kinase (S	960	16	16.7	20	2	A25335	myosin-light-chain
888	17	17.7	40	2	T12209	14-3-3 like protei	961	16	16.7	20	2	S03508	T-cell receptor al
889	17	17.7	40	2	S50021	trypsin-like prote	962	16	16.7	20	2	P00300	large protein - bo
890	17	17.7	40	2	B41440	protein disulfide-	963	16	16.7	20	2	C44920	2-halobenzoate 1,2
891	17	17.7	40	2	A37458	ribulose-bisphosph	964	16	16.7	20	2	S50743	proteinase inhibit
892	17	17.7	40	2	C39560	myotoxin a 5 - pra	965	16	16.7	21	2	S65605	oligomeric protein (B
893	17	17.7	40	2	A44336	neurotoxin Tx3-1 -	966	16	16.7	21	2	A60420	lens intrinsic mem
894	17	17.7	40	2	S26797	IG heavy chain V r	967	16	16.7	21	2	A36902	orfB2 - Escherich
895	17	17.7	40	2	S72464	ribosomal protein	968	16	16.7	21	2	D48518	PEBI 5'-region hyp
896	17	17.7	40	2	S61539	ribosomal protein	969	16	16.7	21	2	S47198	T-cell receptor J-
897	17	17.7	40	2	JX0070	metagrin - turkey	970	16	16.7	21	2	S47212	T-cell receptor J-
898	17	17.7	40	2	I49405	beta-galactoside-b	971	16	16.7	21	2	T12935	hypothetical prote
899	17	17.7	40	2	A05301	hemoglobin alpha-2	972	16	16.7	22	2	B40256	interleukin-7 rece
900	17	17.7	40	2	E45495	beta-defensin-5 -	973	16	16.7	22	2	C35865	gamma-crystallin I
901	17	17.7	40	2	D96733	hypothetical prote	974	16	16.7	22	2	T15870	hypothetical prote
902	17	17.7	40	2	S27709	hypothetical prote	975	16	16.7	22	2	S35624	uvax protein - pha
903	17	17.7	40	2	S16331	rRNA N-glycosidase	976	16	16.7	23	2	I61239	heparin-binding ep
904	17	17.7	40	2	G81568	hypothetical prote	977	16	16.7	23	2	S31210	collagen alpha 2(I
905	17	17.7	40	2	G82685	hypothetical prote	978	16	16.7	23	2	S13268	heat shock protein

979 16 16.7 23 2 S35694
 980 16 16.7 23 2 S48186
 981 16 16.7 24 2 T42259
 982 16 16.7 24 2 B60422
 983 16 16.7 24 2 A05298
 984 16 16.7 24 2 S29749
 985 16 16.7 24 2 I67553
 986 16 16.7 24 2 S43011
 987 16 16.7 24 2 T42846
 988 16 16.7 24 2 T08160
 989 16 16.7 24 2 G20554
 990 16 16.7 24 2 S07645
 991 16 16.7 24 2 S38766
 992 16 16.7 24 2 G85602
 993 16 16.7 24 2 S01808
 994 16 16.7 25 2 A60621
 995 16 16.7 25 2 S03500
 996 16 16.7 25 2 T06233
 997 16 16.7 25 2 A25865
 998 16 16.7 25 2 PH1907
 999 16 16.7 25 2 B53415
 1000 16 16.7 25 2 T09001

ALIGNMENTS

RESULT 1
 S01810
 hemoglobin AIV - tube worm (Lamellibrachia sp.) (fragment)
 C;Species: Lamellibrachia sp.
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: S01810
 R;Suzuki, T.; Takagi, T.; Ohta, S.
 Biochem. J. 255, 541-545, 1988
 A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
 A;Reference number: S01807; MUID:85076216; PMID:3202832
 A;Accession: S01810
 A;Molecule type: protein
 A;Residues: 1-32 <SUZ>
 A;Cross-references: UNIPROT:P20413; UNIPARC:UPI000012B515

Query Match 35.4%; Score 34; DB 2; Length 32;
 Best Local Similarity 38.5%; Pred. No. 66;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 HCNFNDVTTLRLRE 15
 ||:|:|:|:|:|:
 DB 12 HCSYEDADIVWRE 24

RESULT 2
 PN0458
 basic eosinophil protein B3 - horse (fragment)
 C;Species: Equus caballus (domestic horse)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Accession: PN0458; C44528
 R;Piller, K.; Portmann, P.
 Biochem. Biophys. Res. Commun. 192, 373-380, 1993
 A;Title: Isolation and characterization of four basic proteins from horse eosinophilic g
 A;Reference number: PN0456; MUID:93249399; PMID:8484750
 A;Accession: PN0458
 A;Molecule type: protein
 A;Residues: 1-35 <PIL>
 A;Cross-references: UNIPROT:Q7M2P7; UNIPARC:UPI000017C443
 A;Experimental source: blood

Query Match 32.3%; Score 31; DB 2; Length 35;
 Best Local Similarity 42.9%; Pred. No. 2.2e+02;
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 CNFNDVTTLRLRE 17
 ||:|:|:|:|:|:
 DB 12 HCSYEDADIVWRE 24

Db 3 CREIVVSTAMKYNE 16
 RESULT 3
 A61612
 allatostatin - tobacco hornworm
 C;Species: Manduca sexta (tobacco hornworm)
 C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C;Accession: A61612
 R;Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, I.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
 A;Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.
 A;Reference number: A61612; MUID:92052112; PMID:1946359
 A;Accession: A61612
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <KRA>
 A;Cross-references: UNIPROT:P42559; UNIPARC:UPI00001258A8
 C;Keywords: neuropeptide; pyroglutamic acid
 F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.2%; Score 28; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNNDVT 10
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 DB 4 FRCYFNPIS 13

RESULT 4
 B90996
 probable transcription regulator [imported] - Escherichia coli (strain O157:H7, substrain
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: B90996
 R;Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: B90996
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-22 <HAY>
 A;Cross-references: UNIPROT:Q8X365; UNIPARC:UPI000000D29ED; GB:BA0000007; PIDN:BA036361.1;
 A;Experimental source: strain O157:H7, substrain RMD 0509952
 C;Genetics:
 A;Gene: ECe2938

Query Match 29.2%; Score 28; DB 2; Length 22;
 Best Local Similarity 55.6%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 CNFNDVTTR 12
 ||:|:|:|:
 DB 13 CDINPVTLR 21

RESULT 5
 S01811
 hemoglobin AIV - tube worm (Lamellibrachia sp.) (fragment)
 C;Species: Lamellibrachia sp.
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
 C;Accession: S01811
 R;Suzuki, T.; Takagi, T.; Ohta, S.
 Biochem. J. 255, 541-545, 1988
 A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably
 A;Reference number: S01807; MUID:89076216; PMID:3202832
 A;Accession: S01811
 A;Molecule type: protein
 A;Residues: 1-30 <SUZ>
 A;Cross-references: UNIPARC:UPI000017BD8A

Query Match 29.2%; Score 28; DB 2; Length 30;
Best Local Similarity 30.8%; Pred. No. 5.8e+02;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 HCNFNDVTRLRE 15
||:| :|
Db 10 HCSYDAEIVMSE 22

RESULT 6
C95169
hypothetical protein SP1454 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95169
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-40 <KUR>
A:Cross-references: UNIPROT:Q97PV5; UNIPARC:UPI000005185F; GB:AE005672; PIDN:AAK75548.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1454

Query Match 29.2%; Score 28; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 HCNFNDVTRLRE 17
||| :| :|
Db 26 HENFEYVTPWLQGD 40

RESULT 7
F82854
hypothetical protein XP0058 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: F82854
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82854
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-40 <SIM>
A:Cross-references: UNIPROT:Q9PH86; UNIPARC:UPI00000C22AF; GB:AE003859; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima J.P.; Krieger, J.E.; Kuranae, E.E.; Laigz
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:

A:Gene: XP0058

Query Match 29.2%; Score 28; DB 2; Length 40;
Best Local Similarity 38.5%; Pred. No. 7.8e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 NFNDVTRLRE 17
| :| :| :|
Db 23 NVDTLTTRTNND 35

RESULT 8
S17166
62K protein - marbled electric ray
C:Species: Torpedo marmorata (marbled electric ray)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S17166
R:Vogel, M.; Kowalewski, H.J.; Zimmermann, H.; Janetzko, A.; Margolis, R.U.; Wollny, H.
Biochem. J. 278, 199-202, 1991
A:Title: Association of the HNK-1 epitope with 5'-nucleotidase from Torpedo marmorata (r
A:Reference number: S17166; MUID:91354203; PMID:1715684
A:Accession: S17166
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <VOG>
A:Cross-references: UNIPARC:UPI000017BF35

Query Match 28.1%; Score 27; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 NDVTRLRE 15
||| :| :|
Db 9 NDVWARVEE 17

RESULT 9
B49200
cystatin-related protein CRP-1 delta, alternate splice form - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B49200; S38814
R:Vercaeren, I.; Winderickx, J.; Devos, A.; Peeters, B.; Heyns, W.
Endocrinology 132, 2496-2502, 1993
A:Title: An effect of androgens on the length of the poly(A)-tail and alternative splic
A:Reference number: A49200; MUID:93178358; PMID:7679983
A:Note: Corrected and republished from Endocrinology 131, 2496-2502, 1992
A:Accession: B49200
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-21 <VER>
A:Cross-references: UNIPROT:P70657; UNIPARC:UPI00000B84CB; GB:S48993; NID:G260884; PIDN
A:Experimental source: Wistar albino
A:Note: sequence extracted from NCBI backbone (NCBIN:119371, NCBI:119372)

Query Match 28.1%; Score 27; DB 2; Length 21;
Best Local Similarity 30.8%; Pred. No. 5.8e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 EHCNFDVTRLR 14
::| :| :| :|
Db 1 DNCPEEQTEQLK 13

RESULT 10
I53263
CRP-1 delta - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I53263
R:Vercaeren, I.; Winderickx, J.; Devos, A.; Peeters, B.; Heyns, W.
Endocrinology 132, 2496-2502, 1993
A:Title: An effect of androgens on the length of the poly(A)-tail and alternative splic

A;Reference number: I53263; MUID:93178358; PMID:7679983
 A;Accession: I53263
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-21 <RES>
 A;Cross-references: UNIPROT:P70657; UNIPARC:UPI00000E84CB; GB:S56135; NID:g266204; PID:g

Query Match 28.1%; Score 27; DB 2; Length 21;
 Best Local Similarity 30.8%; Pred. No. 5.8e+02;
 Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 EHCNFDVTVTLR 14
 :|:|:|:|:|:
 Db 1 DNCFFEQTEQLK 13

RESULT 11
 B60071
 vasoactive intestinal peptide - rhesus macaque
 C;Species: Macaca mulatta (rhesus macaque)
 C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998
 C;Accession: B60071
 R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.
 Regul. Pept. 32, 39-45, 1991
 A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences
 A;Reference number: A60071; MUID:91164506; PMID:2003150
 A;Accession: B60071
 A;Status: protein sequence not shown
 A;Molecule type: protein
 A;Residues: 1-28 <YUA>
 A;Cross-references: UNIPARC:UPI000002D1C0
 A;Note: the sequence is identical with the human sequence
 C;Superfamily: glucagon
 C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 28.1%; Score 27; DB 2; Length 28;
 Best Local Similarity 60.0%; Pred. No. 7.8e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FNDVTVTLRE 15
 :|:|:|:|:|:
 Db 6 FTDNYTVTLRK 15

RESULT 12
 A60304
 vasoactive intestinal peptide - dog
 N;Alternate names: Vip
 C;Species: Canis lupus familiaris (dog)
 C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
 C;Accession: A60304
 R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.
 Regul. Pept. Suppl. 3, S14, 1985
 A;Title: Purification and sequencing of dog and guinea pig VIP's.
 A;Reference number: A60304
 A;Accession: A60304
 A;Molecule type: protein
 A;Residues: 1-28 <ENG>
 A;Cross-references: UNIPROT:P04565; UNIPARC:UPI000002D1C0
 C;Superfamily: glucagon
 C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 28.1%; Score 27; DB 2; Length 28;
 Best Local Similarity 60.0%; Pred. No. 7.8e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 FNDVTVTLRE 15
 :|:|:|:|:|:
 Db 6 FTDNYTVTLRK 15

RESULT 13
 A48968

exo-poly-alpha-galacturonosidase (EC 3.2.1.82) - Clostridium thermosaccharolyticum (frag
 N;Alternate names: exo-poly-alpha-galacturonate hydrolase
 C;Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum
 C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 06-Dec-1996
 C;Accession: A48968
 R;Van Rijssel, M.; Gerwig, G.J.; Hansen, T.A.
 Appl. Environ. Microbiol. 59, 828-836, 1993
 A;Title: Isolation and characterization of an extracellular glycosylated protein complex
 A;Reference number: A48968; MUID:93243739; PMID:8481009
 A;Accession: A48968
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-23 <VAN>
 A;Cross-references: UNIPARC:UPI000017AD0F
 A;Note: Sequence extracted from NCBI backbone (NCBI:P130462)
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.6%; Score 26.5; DB 2; Length 23;
 Best Local Similarity 50.0%; Pred. No. 7.7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 FEH-CNFDVTVT 11
 :|:|:|:|:|:
 Db 6 FEYDXTENDIXT 17

RESULT 14
 H44621
 homeotic protein Hox 1 (clone 1b) - Florida lancelet (fragment)
 C;Species: Branchiostoma floridae (Florida lancelet)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
 C;Accession: H44621
 R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
 A;Title: Expansion of the Hox gene family and the evolution of chordates.
 A;Reference number: A44616; MUID:93317669; PMID:8101001
 A;Accession: H44621
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-27 <PEN>
 A;Cross-references: UNIPROT:Q06866; UNIPARC:UPI000007D50B; GB:L14888; NID:g289483; PIDN:;
 C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 27.1%; Score 26; DB 2; Length 27;
 Best Local Similarity 46.2%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTVTLRENE 17
 :|:|:|:|:|:
 Db 1 HFNKYLTRARRVE 13

RESULT 15
 D48200
 homeotic protein Hox 1 (clone 1d) - sea lamprey (fragment)
 C;Species: Petromyzon marinus (sea lamprey)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
 C;Accession: D48200
 R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
 A;Title: Expansion of the Hox gene family and the evolution of chordates.
 A;Reference number: A44616; MUID:93317669; PMID:8101001
 A;Accession: D48200
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-27 <PEN>
 A;Cross-references: UNIPROT:Q91264; UNIPARC:UPI00000FC9B3; GB:L14904; NID:g290825; PIDN:;
 C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 27.1%; Score 26; DB 2; Length 27;
 Best Local Similarity 46.2%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTTTLRENE 17
: || || || ||
Db 1 HFNKYLTRARRVE 13

RESULT 16

homeotic protein Hox 1 (clone lb) - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: B48200
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: B48200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PEN>
A:Cross-references: UNIPROT:Q07142; UNIPARC:UPI000007D860; GB:U14902; NID:G290847; PIDN:
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 27.1%; Score 26; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 6;

QY 5 NFNDVTTTLRENE 17
: || || || ||
Db 1 HFNKYLTRARRVE 13

RESULT 17

homeotic protein Hox 1 (clone la) - acorn worm (fragment)
C:Species: Saccoglossus kowalevskii
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 31-Dec-2004
C:Accession: B44636
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: B44636
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PEN>
A:Cross-references: UNIPROT:Q26524; UNIPARC:UPI000008310F; GB:L14916; NID:G294802; PIDN:
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 27.1%; Score 26; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 6;

QY 5 NFNDVTTTLRENE 17
: || || || ||
Db 1 HFNKYLTRARRVE 13

RESULT 18

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84161
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laeky, S.
Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504463; PMID:11016950
A:Accession: G84161
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-32 <STO>
A:Cross-references: UNIPROT:Q9HSZ0; UNIPARC:UPI000006350D; GB:AE004437; NID:G10579667; P
C:Genetics:
A:Gene: VNG0019H

Query Match 27.1%; Score 26; DB 2; Length 32;
Best Local Similarity 40.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
Matches 4; Conservative 4; Mismatches 2;

QY 7 NDVTTTLREN 16
||: ||: ||
Db 8 NDLQEKLDQN 17

RESULT 19

H82416
hypothetical protein VCA0796 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82416
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82416
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-32 <HEI>
A:Cross-references: UNIPROT:Q9KLF0; UNIPARC:UPI00000C3657; GB:AE004407; GB:AE003853; NID:
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0796
A:Map position: 2

Query Match 27.1%; Score 26; DB 2; Length 32;
Best Local Similarity 45.5%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 5;

QY 3 HCNFNDVTTTL 13
|| || || || ||
Db 2 HLNFGTKTEKL 12

RESULT 20

toxin GmTx-4 [validated] - Chilean tarantula
C:Species: Grammostola spatulata (Chilean tarantula)
C:Date: 19-Jan-2001 #sequence_revision 19-Jan-2001 #text_change 09-Jul-2004
C:Accession: A59371
R:Suchyna, T.M.; Johnson, J.H.; Hamer, K.; Leykam, J.F.; Gage, D.A.; Clemon, H.F.; Baumga
J. Gen. Physiol. 115, 583-598, 2000
A:Title: Identification of a peptide toxin from Grammostola spatulata spider venom that
A:Reference number: A59371; MUID:20241942; PMID:10779316
A:Accession: A59371
A:Molecule type: protein
A:Residues: 1-34, 'A' <SUC>
A:Cross-references: UNIPROT:Q7YTT39; UNIPARC:UPI0000017A7A0
A:Experimental source: venom
A:Note: the species may be renamed as Phixotricus spatulatus
R:Suchyna, T.M.
submitted to the Protein Sequence Database, January 2001

Query Match 27.1%; Score 26; DB 2; Length 35;
Best Local Similarity 57.1%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 1;

QY 1 FEHCNFN 7

```

Db      27  FKLCNFS 33
      | : ||| :
RESULT 21
A70106
hypothetical protein BB0049 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: A70106
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kertlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Accession: A70106
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-39 <KLB>
A;Cross-references: UNIPROT:O51078; UNIPARC:UPI000005731E; GB:AE001118; GB:AE000783; NID
A;Experimental source: strain B31

Query Match      27.1%; Score 26; DB 2; Length 39;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      5  NFNDVTRLREN 16
      | : ||| :
Db      6  NVNIVSCRQES 17

RESULT 22
PC2215
fibrinogenolytic proteinase A2 (EC 3.4.21.-) - western diamondback rattlesnake (fragment)
N;Alternate names: alpha-fibrinogenase A2
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: PC2215
R;Hung, C.C.; Chiou, S.H.
Biochem. Biophys. Res. Commun. 201, 1414-1423, 1994
A;Title: Isolation of multiple isoforms of alpha-fibrinogenase from the western diamond
viper.
A;Reference number: PC2214; MUID:94296418; PMID:8024586
A;Accession: PC2215
A;Molecule type: protein
A;Residues: 1-15 <HUN>
A;Cross-references: UNIPROT:Q9PRW3; UNIPARC:UPI000000FD6F1
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase

Query Match      26.0%; Score 25; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 8.6e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2  EHCNFPND 8
      | : ||| :
Db      5  DECNIINE 11

RESULT 23
PH0793
T-cell receptor alpha chain (H2 V-alpha-7.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0793
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-h
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0793

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A;Molecule type: mRNA
A;Residues: 1-19 <CAS>
A;Cross-references: UNIPARC:UPI000017C770; EMBL:X60898
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match      26.0%; Score 25; DB 2; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  EHCNFP 6
      | : ||| :
Db      14  ESCNFP 18

RESULT 24
A60489
venombin A (EC 3.4.21.74) - cantil (fragment)
N;Alternate names: Agkistrodon bilineatus serine proteinase; alpha-fibrinogenase; ancrod,
C;Species: Agkistrodon bilineatus (cantil)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60489
R;Nakagaki, T.; Kazim, A.L.; Kiesel, W.
Thromb. Res. 58, 593-602, 1990
A;Title: Isolation and characterization of a protein C activator from tropical moccasin
A;Reference number: A60489; MUID:90350102; PMID:2385829
A;Accession: A60489
A;Molecule type: protein
A;Residues: 1-20 <NAK>
A;Cross-references: UNIPROT:P33588; UNIPARC:UPI0000138E06
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; venom

Query Match      26.0%; Score 25; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2  EHCNFPND 8
      | : ||| :
Db      5  DECNIINE 11

RESULT 25
A45655
Crotalus atrox serine proteinase (EC 3.4.21.-) - western diamondback rattlesnake (fragment)
N;Alternate names: alpha-fibrinogenase; thrombin-like proteinase
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A45655
R;Chiou, S.H.; Hung, C.C.; Lin, C.W.
Biochem. Int. 26, 105-112, 1992
A;Title: Isolation of a crotalase-like protease with alpha-fibrinogenase activity from th
A;Reference number: A45655; MUID:92313365; PMID:1616487
A;Accession: A45655
A;Molecule type: protein
A;Residues: 1-20 <CHI>
A;Cross-references: UNIPROT:Q9PSS5; UNIPARC:UPI000000FB75C
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:107297)
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; venom

Query Match      26.0%; Score 25; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2  EHCNFPND 8
      | : ||| :
Db      5  DECNIINE 11

RESULT 26
PC2214

```

fibrinogenolytic proteinase A1 (EC 3.4.21.-) - western diamondback rattlesnake (fragment)
 N/Alternate names: alpha-fibrinogenase A1
 C:Species: Crotalus atrox (western diamondback rattlesnake)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: PC2214; PC2216
 R/Hung, C.C.; Chiou, S.H.
 Biochem. Biophys. Res. Commun. 201, 1414-1423, 1994
 A:Title: Isolation of multiple isoforms of alpha-fibrinogenase from the western diamondback viper.
 A:Reference number: PC2214; MUID:94296418; PMID:8024586
 A:Accession: PC2214
 A:Molecule type: protein
 A:Residues: 1-21 <HUN>
 A:Cross-references: UNIPROT:Q9PRW4; UNIPARC:UPI00000FBF50
 A:Note: isoform A1
 A:Accession: PC2216
 A:Molecule type: protein
 A:Residues: 1-15 <HU2>
 A:Cross-references: UNIPARC:UPI00000FDC3C
 A:Note: isoform A3
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase; venom

Query Match 26.0%; Score 25; DB 2; Length 21;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EHCNFND 8
 Db 5 DECNINE 11

RESULT 27
 S60567
 homeodomain protein hrox5 - California red abalone (fragment)
 C:Species: Haliotis rufescens (California red abalone)
 C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 05-Oct-2004
 C:Accession: S60567
 R/Degnan, B.M.; Morse, D.E.
 Mol. Marine Biol. Biotechnol. 2, 1-9, 1993
 A:Title: Identification of eight homeobox-containing transcripts expressed during larval
 A:Reference number: S60564; MUID:93372986; PMID:7689904
 A:Accession: S60567
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-23 <DRG>
 A:Cross-references: UNIPROT:Q25136; UNIPARC:UPI000007C701; EMBL:X79374; NID:9495114; PID
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 23;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 FNDVTRLRENE 17
 Db 1 FNKYLTRARRIE 12

RESULT 28
 B20596
 venom kallikrein (EC 3.4.21.-) EII - western diamondback rattlesnake (fragment)
 C:Species: Crotalus atrox (western diamondback rattlesnake)
 C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C:Accession: B20596
 R/Bjarnason, J.B.; Barish, A.; Drenzo, G.S.; Campbell, R.; Fox, J.W.
 J. Biol. Chem. 258, 12566-12573, 1983
 A:Title: Kallikrein-like enzymes from Crotalus atrox venom.
 A:Reference number: A92397; MUID:84032449; PMID:6355088
 A:Accession: B20596
 A:Molecule type: protein
 A:Residues: 1-25 <BUA>
 A:Cross-references: UNIPROT:Q7L2F6; UNIPARC:UPI0000175C3E
 C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase; venom

Query Match 26.0%; Score 25; DB 2; Length 25;
 Best Local Similarity 42.9%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EHCNFND 8
 Db 5 DECNINE 11

RESULT 29
 A20596
 venom kallikrein (EC 3.4.21.-) EI - western diamondback rattlesnake (fragment)
 C:Species: Crotalus atrox (western diamondback rattlesnake)
 C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C:Accession: A20596
 R/Bjarnason, J.B.; Barish, A.; Drenzo, G.S.; Campbell, R.; Fox, J.W.
 J. Biol. Chem. 258, 12566-12573, 1983
 A:Title: Kallikrein-like enzymes from Crotalus atrox venom.
 A:Reference number: A92397; MUID:84032449; PMID:6355088
 A:Accession: A20596
 A:Molecule type: protein
 A:Residues: 1-25 <BUA>
 A:Cross-references: UNIPROT:Q8QHK2; UNIPARC:UPI0000175C3D
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase; venom

Query Match 26.0%; Score 25; DB 2; Length 25;
 Best Local Similarity 42.9%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EHCNFND 8
 Db 5 DECNINE 11

RESULT 30
 F41606
 homeotic protein Shox1 - hydromedusa (Sarsia sp.) (fragment)
 C:Species: Sarsia sp.
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Oct-2004
 C:Accession: F41606
 R/Murtha, M.T.; Leckman, J.F.; Ruddle, P.H.
 Proc. Natl. Acad. Sci. U.S.A. 88, 10711-10715, 1991
 A:Title: Detection of homeobox genes in development and evolution.
 A:Reference number: A41606; MUID:92073357; PMID:1720547
 A:Accession: F41606
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-25 <MUR>
 A:Cross-references: UNIPROT:Q26666; UNIPARC:UPI00000773F8; GB:M81664; NID:9161297; PID
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:1-25/Domain: homeobox homology (fragment) <HOX>

Query Match 26.0%; Score 25; DB 2; Length 25;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 FNDVTRLRENE 17
 Db 1 FNKYLTRARRVE 12

RESULT 31
 G44629
 homeotic protein Hox 6/7 (clone 6/7) - Florida lancelet (fragment)
 C:Species: Branchiostoma floridae (Florida lancelet)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
 C:Accession: G44629
 R/Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, P.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
 A:Title: Expansion of the Hox gene family and the evolution of chordates.

A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: G44629
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q06863; UNIPARC:UPI0000078E75; GB:L14885; NID:g289479; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRRENE 17
:||| ||| |
Db 1 HFNKYLTRRRRIE 13

RESULT 32
F44629
homeotic protein Hox 6/7 (clone 6/7i) - Florida lancelet (fragment)
C;Species: Branchiostoma floridae (Florida lancelet)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: F44629
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: F44629
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q06871; UNIPARC:UPI000007BCE0; GB:L14880; NID:g289469; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRRENE 17
:||| ||| |
Db 1 HFNKYLTRRRRIE 13

RESULT 33
H44629
homeotic protein Hox 8 (clone 8k) - Florida lancelet (fragment)
C;Species: Branchiostoma floridae (Florida lancelet)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: H44629
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: H44629
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q06873; UNIPARC:UPI00000792C9; GB:L14882; NID:g289467; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRRENE 17
:||| ||| |
Db 1 HFNKYLTRRRRIE 13

RESULT 34
S32732
homeotic protein - planarian (Dugesia tigrina) (fragment)
C;Species: Dugesia tigrina

C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Oct-2004
C;Accession: S32732
R;Lukyanov, S.A.; Tarabykin, V.S.; Lukyanov, K.A.; Bekman, E.P.
submitted to the EMBL Data Library, April 1993
A;Description: Planarian antennapedia-like homeobox genes: cloning and sequence analysis
A;Reference number: S32729
A;Accession: S32732
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-29 <LUK>
A;Cross-references: UNIPROT:Q24686; UNIPARC:UPI000017A321; EMBL:Z22540
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 29;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRRENE 17
:||| ||| |
Db 2 HFNKYLTRRRRIE 14

RESULT 35
S32730
homeotic protein - planarian (Dugesia tigrina) (fragment)
C;Species: Dugesia tigrina
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Oct-2004
C;Accession: S32730
R;Lukyanov, S.A.; Tarabykin, V.S.; Lukyanov, K.A.; Bekman, E.P.
submitted to the EMBL Data Library, April 1993
A;Description: Planarian antennapedia-like homeobox genes: cloning and sequence analysis
A;Reference number: S32729
A;Accession: S32730
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-29 <LUK>
A;Cross-references: UNIPROT:Q24684; UNIPARC:UPI0000076942; EMBL:Z22601; NID:g296583; PIDN:
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 29;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRRENE 17
:||| ||| |
Db 2 HFNKYLTRRRRIE 14

RESULT 36
S32733
homeotic protein - planarian (Dugesia tigrina) (fragment)
C;Species: Dugesia tigrina
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Oct-2004
C;Accession: S32733
R;Lukyanov, S.A.; Tarabykin, V.S.; Lukyanov, K.A.; Bekman, E.P.
submitted to the EMBL Data Library, April 1993
A;Description: Planarian antennapedia-like homeobox genes: cloning and sequence analysis
A;Reference number: S32729
A;Accession: S32733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-29 <LUK>
A;Cross-references: UNIPROT:Q24681; UNIPROT:Q24687; UNIPROT:O76939; UNIPARC:UPI000017A331
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 29;
Best Local Similarity 46.2%; Pred. No. 1.7e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRRENE 17
:||| ||| |
Db 2 HFNKYLTRRRRIE 14

```
RESULT 37
PD0006
cysteine synthase (EC 4.2.99.8) isozyme - spinach (fragment)
N:Alternate names: Csaase 1'; o-acetylserine(thiol)lyase
C:Species: Spinacia oleracea (spinach)
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:Accession: PD0006
R:Yamaguchi, T.; Zhu, X.; Masada, M.
Biosci. Biotechnol. Biochem. 62, 501-507, 1998
A:Title: Purification and characterization of a novel cysteine synthase isozyme from spi
A:Reference number: PD0006; MUID:98233272; PMID:9571779
A:Accession: PD0006
A:Molecule type: mRNA
A:Residues: 1-30 <YAM>
A:Cross-references: UNIPROT:OTMLJ2; UNIPARC:UPI000017AF23
C:Comment: This enzyme localized in chloroplasts.
C:Keywords: carbon-oxygen lyase

Query Match      26.0%; Score 25; DB 2; Length 30;
Best Local Similarity 36.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NDVTRLRENE 17
||: ||: ||
DB 15 NDIEAKLNYNK 25

RESULT 38
S05030
cytochrome b559 component psbE - Synechococcus sp. (strain Copeland) (fragment)
N:Alternate names: photosystem II 8K protein
C:Species: Synechococcus sp.
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 05-Oct-2004
C:Accession: S05030
R:Keuchl, M.; Koike, H.; Inoue, Y.
FEBS Lett. 251, 155-160, 1989
A:Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II
A:Reference number: S05030
A:Accession: S05030
A:Molecule type: protein
A:Residues: 1-33 <IKB>
A:Cross-references: UNIPROT:P12238; UNIPARC:UPI0000132668
A:Note: the source is designated as Synechococcus vulcanus
C:Genetics:
A:Gene: psbE
C:Superfamily: cytochrome b559 alpha subunit
C:Keywords: thylakoid; transmembrane protein

Query Match      26.0%; Score 25; DB 2; Length 33;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTRLR 14
||: ||: ||
DB 9 FSDIITSVR 17

RESULT 39
S69010
mu opioind receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S69010
R:Zimprich, A.; Simon, T.; Hoellt, V.
FEBS Lett. 359, 142-146, 1995
A:Title: Cloning and expression of an isoform of the rat mu opioind receptor (rMOR1B) whi
A:Reference number: S69010; MUID:95172221; PMID:7532594
A:Accession: S69010
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-36 <ZIM>
A:Cross-references: UNIPROT:P33535; UNIPARC:UPI0000170CAD; EMBL:S75669
```

A:Note: the authors translated the codon GTA for residue 34 as Asp
C:Superfamily: vertebrate rhodopsin

Query Match 26.0%; Score 25; DB 2; Length 36;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTRLREN 16
||: ||: ||
DB 8 STRVRQN 14

RESULT 40
I37554
homeobox - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
C:Accession: I37554
R:Moretti, P.; Simmons, P.; Thomas, P.; Haylock, D.; Rathjen, P.; Vadas, M.; D'Andrea, F.
Gene 144, 213-219, 1994
A:Title: Identification of homeobox genes expressed in human haemopoietic progenitor cel
A:Reference number: I37554; MUID:94314219; PMID:7518789
A:Accession: I37554
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-39 <RES>
A:Cross-references: UNIPROT:Q14559; UNIPARC:UPI000006EBFA; EMBL:X74861; NID:g510992; PII
C:Genetics:
A:Gene: HPX-2
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 26.0%; Score 25; DB 2; Length 39;
Best Local Similarity 41.7%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTTR 12
||: ||: ||
DB 12 FEKDRFTGIATR 23

RESULT 41
AD2125
hypothetical protein asl2555 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AD2125
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2125
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-40 <KUR>
A:Cross-references: UNIPROT:Q8YU06; UNIPARC:UPI00000CE497; GB:BA000019; PIDN:BA874254.1
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl2555

Query Match 26.0%; Score 25; DB 2; Length 40;
Best Local Similarity 33.3%; Pred. No. 2.4e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 CNFNDVTRLRE 15
||: ||: ||
DB 17 CNRIGITSKARQ 28

RESULT 42
A23617
conglutin delta-2 small chain - narrow-leaved blue lupine

C;Species: *Lupinus angustifolius* (narrow-leaved blue lupine)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A23617
R;Lilley, G.G.; Inglis, A.S.
FEBS Lett. 195, 235-241, 1986
A;Title: Amino acid sequence of conglutin delta, a sulfur-rich seed protein of *Lupinus albus*
A;Reference number: A91358
A;Accession: A23617
A;Molecule type: protein
A;Residues: 1-37 <LIL>
A;Cross-references: UNIPROT:P09930; UNIPARC:UPI0000127597
C;Superfamily: soybean 2S albumin

Query Match 25.5%; Score 24.5; DB 2; Length 37;
Best Local Similarity 26.7%; Pred. No. 2.7e+03;
Matches 4; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 3 HCNFNDVTTLRRE 17
||| : : : : :
Db 19 HCE-NHIDRIQQQ 32

RESULT 43
H56046
urinary tract stone matrix protein 10, 42K - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: H56046
R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A;Description: Isolation, characterization and sequence of stone proteins.
A;Reference number: A56046
A;Accession: H56046
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <BIN>
A;Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.0%; Score 24; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HCNFNDV 9
||| : : : : :
Db 2 HSYFNDL 8

RESULT 44
A33160
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 31-Dec-2004
C;Accession: A33160
R;Godinot, C.
submitted to the Protein Sequence Database, February 1991
A;Reference number: A33160
A;Accession: A33160
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <GOD>
A;Cross-references: UNIPROT:P35435; UNIPARC:UPI0000175EA7
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; ox

Query Match 25.0%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 DVITRLR 14
| : | : | :
Db 5 DITRLK 11

RESULT 45
S08990
calcimedin, 67K - chicken (fragment)
C;Species: *Gallus gallus* (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C;Accession: S08990
R;Kobayashi, R.; Tashima, Y.
Eur. J. Biochem. 188, 447-453, 1990
A;Title: Purification, biological properties and partial sequence analysis of 67-kDa cal
A;Reference number: S08990; MUID:90201075; PMID:2138541
A;Accession: S08990
A;Molecule type: protein
A;Residues: 1-22 <KOB>
A;Cross-references: UNIPARC:UPI0000177772
C;Superfamily: annexin VI; annexin repeat homology

Query Match 25.0%; Score 24; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NFND 8
||| : : : : :
Db 12 NFND 15

RESULT 46
B38671
peptidylglycine monooxygenase (EC 1.14.17.3) form 4 - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 05-Nov-1999
C;Accession: B38671
R;Stoffers, D.A.; Ouafik, L.; Eipper, B.A.
J. Biol. Chem. 266, 1701-1707, 1991
A;Title: Characterization of novel mRNAs encoding enzymes involved in peptide alpha-amid
A;Reference number: A38671; MUID:91107670; PMID:1988445
A;Accession: B38671
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-23 <STO>
A;Cross-references: UNIPARC:UPI0000170B03; GB:M63662; NID:G206719; PIDN:AAA42068.1; PID:9
C;Keywords: oxidoreductase

Query Match 25.0%; Score 24; DB 2; Length 23;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EHCN 5
||| : : : : :
Db 18 KHCN 21

RESULT 47
A27267
secretin - dog
C;Species: *Canis lupus familiaris* (dog)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A27267
R;Shinomura, Y.; Eng, J.; Yalow, R.S.
Life Sci. 41, 1243-1248, 1987
A;Title: Dog secretin: sequence and biologic activity.
A;Reference number: A27267; MUID:87314204; PMID:3626755
A;Accession: A27267
A;Molecule type: protein
A;Residues: 1-27 <SHI>
A;Cross-references: UNIPROT:P09910; UNIPARC:UPI00000351D3
A;Experimental source: intestine
C;Superfamily: Glucagon
C;Keywords: duplication

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;


```
QY      6 FNDVTTTLREN 16
      |
      | :||||:
Db      6 FTSELSRLRES 16
      |

RESULT 48
I44629
homeotic protein Hox 8 (clone 8l) - Florida lancelet (fragment)
C:Species: Branchiostoma floridae (Florida lancelet)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: I44629
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: I44629
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PEN>
A:Cross-references: UNIPROT:Q06872; UNIPARC:UPI000007E419; GB:IL14881; NID:G289465; PIDN:
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

      Query Match      25.0%; Score 24; DB 2; Length 27;
      Best Local Similarity 46.2%; Pred. No. 2.3e+03;
      Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      5 NFNDVTTTLRENE 17
      :||| ||| |
Db      1 HFNRVLTTRRRRIE 13

RESULT 49
I44616
homeotic protein Hox 8 (clone 8r) - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: I44616
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: I44616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PEN>
A:Cross-references: UNIPROT:Q91263; UNIPARC:UPI00000FD560; GB:IL14903; NID:G290823; PIDN:
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

      Query Match      25.0%; Score 24; DB 2; Length 27;
      Best Local Similarity 50.0%; Pred. No. 2.3e+03;
      Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 FNDVTTTLRENE 17
      || ||| |
Db      2 FNPYLTRKRRIE 13

RESULT 50
H48200
homeotic protein Hox 4 (clone 4h) - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: H48200
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: H48200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PEN>
A:Cross-references: UNIPROT:Q91267; UNIPARC:UPI00000FB987; GB:IL14909; NID:G290835; PIDN:
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
```

```
      Query Match      25.0%; Score 24; DB 2; Length 27;
      Best Local Similarity 46.2%; Pred. No. 2.3e+03;
      Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      5 NFNDVTTTLRENE 17
      :||| ||| |
Db      1 HFNRVLTTRRRRIE 13

RESULT 51
G48200
homeotic protein Hox 4 (clone 4g) - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: G48200
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: G48200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PEN>
A:Cross-references: UNIPROT:Q91270; UNIPARC:UPI0000076F0E; GB:IL14912; NID:G290841; PIDN:
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation
```

```
      Query Match      25.0%; Score 24; DB 2; Length 27;
      Best Local Similarity 46.2%; Pred. No. 2.3e+03;
      Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      5 NFNDVTTTLRENE 17
      :||| ||| |
Db      1 HFNRVLTTRRRRIE 13

RESULT 52
F44616
homeotic protein Hox 6/7 (clones 6/7o and 6/7n) - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C:Accession: F44616; E44616
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: F44616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PEN1>
A:Cross-references: UNIPROT:Q07146; UNIPARC:UPI0000074E10; GB:IL14907; NID:G290831; PIDN:
A:Experimental source: clone 6/7o

      Query Match      25.0%; Score 24; DB 2; Length 27;
      Best Local Similarity 46.2%; Pred. No. 2.3e+03;
      Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      5 NFNDVTTTLRENE 17
      :||| ||| |
Db      1 HFNRVLTTRRRRIE 13
```

```
RESULT 53
G44616
homeotic protein Hox 6/7 (clone 6/7p) - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)

      Query Match      25.0%; Score 24; DB 2; Length 27;
      Best Local Similarity 46.2%; Pred. No. 2.3e+03;
      Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      5 NFNDVTTTLRENE 17
      :||| ||| |
Db      1 HFNRVLTTRRRRIE 13

RESULT 53
G44616
homeotic protein Hox 6/7 (clone 6/7p) - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)
```

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: G44616
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: G44616
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q07148; UNIPARC:UPI000008333B; GB:L14898; NID:g290815; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTTLRRENE 17
: || | | | |
Db 1 HFNYLTRRRRIE 13

RESULT 54
H44616
homeotic protein Hox 8 (clone 8q) - sea lamprey (fragment)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: H44616
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: H44616
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q07151; UNIPARC:UPI00000FC98B; GB:L14901; NID:g290821; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 FNDVTTLRRENE 17
: || | | | |
Db 2 FNPYLTKRRRIE 13

RESULT 55
I48200
homeotic protein Hox 5 (clone 5i) - sea lamprey (fragment)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
C;Accession: I48200
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: I48200
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q07143; UNIPARC:UPI00000FD719; GB:L14891; NID:g290843; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTTLRRENE 17
: || | | | |
Db 1 HFNYLTRRRRIE 13

RESULT 56

G44636
homeotic protein Hox 6/7 (clone 6/7f) - acorn worm (fragment)
C;Species: Saccoglossus kowalevskii
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 05-Oct-2004
C;Accession: G44636
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: G44636
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q26526; UNIPARC:UPI0000078B4B; GB:L14917; NID:g294806; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTTLRRENE 17
: || | | | |
Db 1 HFNYLTRRRRIE 13

RESULT 57

F44636
homeotic protein Hox 5 (clone 5e) - acorn worm (fragment)
C;Species: Saccoglossus kowalevskii
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 05-Oct-2004
C;Accession: F44636
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: F44636
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q26522; UNIPARC:UPI0000075F93; GB:L14914; NID:g294798; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTTLRRENE 17
: || | | | |
Db 1 HFNYLTRRRRIE 13

RESULT 58

A44616
homeotic protein Hox 5 (clone 5j) - sea lamprey (fragment)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 31-Dec-2004
C;Accession: A44616
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: A44616
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 <PEN>
A;Cross-references: UNIPROT:Q91265; UNIPARC:UPI00000PD436; GB:L14906; NID:g290829; PIDN:
C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTRLRRENE 17
: || || || ||
Db 1 HFNRYLTRRRRIE 13

RESULT 59

B44616
homeotic protein Hox 6/7 - sea lamprey (fragment)
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 31-Dec-2004
C:Accession: B44616; D44616
R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A:Title: Expansion of the Hox gene family and the evolution of chordates.
A:Reference number: A44616; MUID:93317669; PMID:8101001
A:Accession: B44616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PE2>
A:Cross-references: UNIPROT:Q07147; UNIPARC:UPI00000FC1EC; GB:L14897; NID:G290827; PIDN:AAA02540.1; PID:
A:Experimental source: clone 6/7k
A:Accession: C44616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PE2>
A:Cross-references: UNIPARC:UPI00000FC1EC; GB:L14905; NID:G290827; PIDN:AAA02540.1; PID:
A:Experimental source: clone 6/7l
A:Accession: D44616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-27 <PE3>
A:Cross-references: UNIPARC:UPI00000FC1EC; GB:L14899; NID:G290817; PIDN:AAA02534.1; PID:
A:Experimental source: clone 6/7m
C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 27;
Best Local Similarity 46.2%; Pred. No. 2.3e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTRLRRENE 17
: || || || || ||
Db 1 HFNRYLTRRRRIE 13

RESULT 60

S21231
calcium-binding protein SCP VI, sarcoplasmic - common lancelet
C:Species: Branchiostoma lanceolatum (common lancelet)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002
C:Accession: S21231
R:Takagi, T.; Valette-Talbi, L.; Cox, J.A.
FEBS Lett. 302, 159-160, 1992
A:Title: Primary structure of three minor isoforms of amphioxus sarcoplasmic calcium-binding protein
A:Reference number: S21153; MUID:92339504; PMID:1633848
A:Accession: S21231
A:Molecule type: protein
A:Residues: 1-28 <TA>
A:Cross-references: UNIPARC:UPI0000177710
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand

Query Match 25.0%; Score 24; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 NFNDVTRLR 14
: || || || ||
Db 19 DPEDMTRYK 28

RESULT 61

S17147

galanin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S17147
R:Norberg, A.; Sillard, R.; Carlquist, M.; Joernvall, H.; Mutt, V.
FEBS Lett. 288, 151-153, 1991
A:Title: Chemical detection of natural peptides by specific structures. Isolation of chicken galanin
A:Reference number: S17147; MUID:91348254; PMID:1715289
A:Accession: S17147
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <NOR>
A:Cross-references: UNIPROT:P30802; UNIPARC:UPI0000012B081
C:Superfamily: galanin

Query Match 25.0%; Score 24; DB 2; Length 29;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HCNFND 8
: || || ||
Db 19 HRSFND 24

RESULT 62

B81006
hypothetical protein NMB2097 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81006
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vitti, P.
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: B81006
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-29 <TET>
A:Cross-references: UNIPROT:Q9JXD6; UNIPARC:UPI00000C486C; GB:AE002559; GB:AE002098; NID:
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB2097

Query Match 25.0%; Score 24; DB 2; Length 29;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HCNFND 7
: || || ||
Db 17 HCRFS 21

RESULT 63

S19943
aadB protein - *Klebsiella pneumoniae* plasmid pLST1000 (fragment)
C:Species: *Klebsiella pneumoniae*
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S19943
R:Zieg, J.; Jiang, H.; McCabe, F.; O'Brien, T.
submitted to the EMBL Data Library, February 1992
A:Description: Molecular characterization and comparison of the regions encoding gentamicin resistance
A:Reference number: S19939
A:Accession: S19943
A:Molecule type: DNA
A:Residues: 1-29 <ZIE>
A:Cross-references: UNIPROT:Q48492; UNIPARC:UPI00000BE952; EMBL:X64367; NID:G43948; PID:
C:Genetics:
A:Gene: aadB
A:Genome: plasmid

Query Match 25.0%; Score 24; DB 2; Length 29;
 Best Local Similarity 62.5%; Pred. No. 2.5e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDVTTTLR 14
 ||||| :
 DB 6 NDVTQQQR 13

RESULT 64

S21153
 calcium-binding protein SCP V, sarcoplasmic - common lancelet
 C;Species: Branchiostoma lanceolatum (common lancelet)
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S21153
 R;Takagi, T.; Valette-Talbi, L.; Cox, J.A.
 FEBS Lett. 302, 159-160, 1992
 A;Title: Primary structure of three minor isoforms of amphioxus sarcoplasmic calcium-binding protein
 A;Reference number: S21153; MUID:92339504; PMID:1633848
 A;Accession: S21153
 A;Molecule type: protein
 A;Residues: 1-30 <TAK>
 A;Cross-references: UNIPROT:P04570; UNIPARC:UPI000017770F
 C;Superfamily: calmodulin; calmodulin repeat homology
 C;Keywords: calcium binding; EF hand

Query Match 25.0%; Score 24; DB 2; Length 30;
 Best Local Similarity 40.0%; Pred. No. 2.6e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 NFNDVTTTLR 14
 :||| :
 DB 21 DFEDMMTRYK 30

RESULT 65

B24987
 regulatory protein xylR - Pseudomonas putida plasmid TOL (fragment)
 C;Species: Pseudomonas putida
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 05-Oct-2004
 C;Accession: B24987
 R;Inouye, S.; Nakazawa, A.; Nakazawa, T.
 Gene 44, 235-242, 1986
 A;Title: Nucleotide sequence of the regulatory gene xylS on the Pseudomonas putida TOL plasmid
 A;Reference number: A91554; MUID:87055240; PMID:3023186
 A;Accession: B24987
 A;Molecule type: DNA
 A;Residues: 1-30 <INO>
 A;Cross-references: UNIPROT:P06519; UNIPARC:UPI00001783BD
 C;Genetics:
 A;Genome: plasmid
 C;Superfamily: response regulator (sigma54-dependent transcriptional activator), FlhA type
 C;Keywords: DNA binding; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 30;
 Best Local Similarity 23.1%; Pred. No. 2.6e+03;
 Matches 3; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFNDVTTTLR 14
 :||| :
 DB 10 QHEDMQDLSSQIR 22

RESULT 66

C95010
 hypothetical protein SP0089 [imported] - Streptococcus pneumoniae (strain TIGR4)
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C;Accession: C95010
 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916
 A;Accession: C95010
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-31 <KUR>
 A;Cross-references: UNIPROT:Q97T66; UNIPARC:UPI0000051BF4; GB:AE005672; PIDN:AAK74276.1;
 A;Experimental source: strain TIGR4
 C;Genetics:
 A;Gene: SP0089

Query Match 25.0%; Score 24; DB 2; Length 31;
 Best Local Similarity 33.3%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 NFNDVTTTLR 16
 :||| :
 DB 19 NLKEVIATKUKAN 30

RESULT 67

S21232
 calcium-binding protein SCP VII, sarcoplasmic - common lancelet
 C;Species: Branchiostoma lanceolatum (common lancelet)
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002
 C;Accession: S21232
 R;Takagi, T.; Valette-Talbi, L.; Cox, J.A.
 FEBS Lett. 302, 159-160, 1992
 A;Title: Primary structure of three minor isoforms of amphioxus sarcoplasmic calcium-binding protein
 A;Reference number: S21153; MUID:92339504; PMID:1633848
 A;Accession: S21232
 A;Molecule type: protein
 A;Residues: 1-32 <TAK>
 A;Cross-references: UNIPARC:UPI0000177711
 C;Superfamily: calmodulin; calmodulin repeat homology
 C;Keywords: calcium binding; EF hand

Query Match 25.0%; Score 24; DB 2; Length 32;
 Best Local Similarity 40.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 NFNDVTTTLR 14
 :||| :
 DB 23 DFEDMMTRYK 32

RESULT 68

I65264
 homeotic protein HOX C6 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Oct-2004
 C;Accession: I65264
 R;Castanonov, V.; Kusaka, M.; Chariot, A.; Gielen, J.; Sobel, M.
 Biochem. Pharmacol. 47, 137-143, 1994
 A;Title: Homeobox genes: potential candidates for the transcriptional control of the trar
 A;Reference number: I52378; MUID:94145486; PMID:7906121
 A;Accession: I65264
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-34 <RES>
 A;Cross-references: UNIPARC:UPI000016841F; GB:S69027; NID:9545301; PIDN:AAD14030.1; PID:
 C;Genetics:
 A;Gene: GDB:HOXC6
 A;Cross-references: GDB:120670; OMIM:142972
 A;Map position: 12q13.3-12q13.3
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 25.0%; Score 24; DB 2; Length 34;
 Best Local Similarity 46.2%; Pred. No. 2.9e+03;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 NFNDVTTTLR 17

A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <STO>
A;Cross-references: UNIPROT:Q9SJ63; UNIPARC:UPI00000A6091; GB:AE002093; NID:g4510382; P:
C;Genetics:
A;Gene: At2g35870
A;Map position: 2

Query Match 25.0%; Score 24; DB 2; Length 36;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EHCNFD 8
|||
DB 9 EHANNE 15

RESULT 72
A85744
unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain O1
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85744
R;Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85744
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-37 <STO>
A;Cross-references: UNIPROT:Q8X323; UNIPARC:UPI00000D0E7C; GB:AE005174; NID:g12515362; P:
C;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2367

Query Match 25.0%; Score 24; DB 2; Length 37;
Best Local Similarity 37.5%; Pred. No. 3.2e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 NFNDVTTR 12
:|::|
DB 15 SFNEITIK 22

RESULT 73
F45186
homeotic protein Ghox 4.7 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: F45186
R;Mackem, S.; Mahon, K.A.
Development 112, 791-806, 1991
A;Title: Ghox 4.7: a chick homeobox gene expressed primarily in limb buds with limb-typ
A;Reference number: A45186; MUID:92037185; PMID:1682126
A;Accession: F45186
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-37 <MAC>
A;Cross-references: UNIPARC:UPI00000FBEEE
A;Note: sequence extracted from NCBI backbone (NCBIP:63341)
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-37/Domain: homeobox homology (fragment) <HOX>

Query Match 25.0%; Score 24; DB 2; Length 37;
Best Local Similarity 46.2%; Pred. No. 3.2e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 NFNDVTTRLENE 17
:|::|

```
Db          7 HFNYLTRRRRIE 19

RESULT 74
G45187
homoeotic protein Ghox 4.7 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: G45187
R;Mackem, S.; Mahon, K.A.
Development 112, 791-806, 1991
A;Title: Ghox 4.7: a chick homeobox gene expressed primarily in limb buds with limb-type
A;Reference number: A45186; MUID:92037185; PMID:1682126
A;Accession: G45187
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-37 <MAC>
A;Cross-references: UNIPARC:UPI00000FCC38
A;Note: sequence extracted from NCBI backbone (NCBIP:63351)
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-37/Domain: homeobox homology (fragment) <HOX>

Query Match      25.0%; Score 24; DB 2; Length 37;
Best Local Similarity 45.5%; Pred. No. 3.2e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy          7 NDVITRLRENE 17
|: ||| |
Db          9 NEFITRQRRRIE 19

RESULT 75
B45187
homoeotic protein Ghox 4.7 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: B45187
R;Mackem, S.; Mahon, K.A.
Development 112, 791-806, 1991
A;Title: Ghox 4.7: a chick homeobox gene expressed primarily in limb buds with limb-type
A;Reference number: A45186; MUID:92037185; PMID:1682126
A;Accession: B45187
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-37 <MAC>
A;Cross-references: UNIPARC:UPI00000FCE37
A;Note: sequence extracted from NCBI backbone (NCBIP:63346)
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-37/Domain: homeobox homology (fragment) <HOX>

Query Match      25.0%; Score 24; DB 2; Length 37;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy          6 FNDVITRLRENE 17
||| ||| |
Db          8 FNPYLTRRRRIE 19

RESULT 76
C90523
hypothetical protein MYPV 0910 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90523
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallissot, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: C90523
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-39 <KUR>

A;Cross-references: UNIPROT:Q98RB8; UNIPARC:UPI00000C7FF4; GB:AL445566; PID:g14089504; P:
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPV_0910
A;Genetic code: SGC3

Query Match      25.0%; Score 24; DB 2; Length 39;
Best Local Similarity 36.4%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy          3 HCNFNDVITRLR 13
|: ||| ::|
Db          10 HINYNCKSSSL 20

RESULT 77
E70241
hypothetical protein BBI14 - Lyme disease spirochete plasmid I/1p28-4
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: E70241
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: E70241
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-37 <KLE>
A;Cross-references: UNIPROT:O50868; UNIPARC:UPI00000568DF; GB:AE000789; NID:g2690079; PII
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid

Query Match      24.5%; Score 23.5; DB 2; Length 37;
Best Local Similarity 35.7%; Pred. No. 3.8e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy          4 CNF-NDVITRLREN 16
||| ||| ::|
Db          18 CNFNDAAEAATKKH 31

RESULT 78
JH0756
sucrose-specific enzyme II - Lactococcus lactis (fragment)
C;Species: Lactococcus lactis
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 09-Jul-2004
C;Accession: JH0756
R;Rauch, P.J.G.; de Vos, W.M.
Gene 121, 55-61, 1992
A;Title: Transcriptional regulation of the Tn5276-located Lactococcus lactis sucrose ope
A;Reference number: JH0754; MUID:93051362; PMID:1330831
A;Accession: JH0756
A;Molecule type: DNA
A;Residues: 1-40 <RAU>
A;Cross-references: UNIPROT:Q04938; UNIPARC:UPI00001329C3; GB:M96669; NID:g149488; PIDN:/
A;Note: the authors translated the codon CGA for residue 23 as Ala
C;Genetics:
A;Gene: sacB
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
C;Keywords: phosphoprotein

Query Match      24.5%; Score 23.5; DB 2; Length 40;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy          3 HCNFNDVITRLR 14
||| |||
Db          24 HC-----ATRLR 30
```

RESULT 79
A11497
transaldolase (EC 2.2.1.2) III - Yeast (*Pichia jadinii*) (fragment)
C:Species: *Pichia jadinii*, *Candida utilis*
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A11497
R:Tsolas, O.; Sun, S.C.
Arch. Biochem. Biophys. 167, 525-533, 1975
A:Title: Isolation of a peptide containing a histidinyI-cysteinyI sequence from the acti
A:Reference number: A11497; MUID:75145197; PMID:1092268
A:Accession: A11497
A:Molecule type: protein
A:Residues: 1-9 <TSO>
A:CROSS-references: UNIPROT:PI7441; UNIPARC:UPI000013688F
C:Keywords: transferase

Query Match 24.0%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCN 5
DB 4 HCN 6

RESULT 80
PS0371
hypothetical protein (psaC region) - *Synechococcus* sp. (fragment)
C:Species: *Synechococcus* sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
R:RhieI, B.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of *Synechococcus* sp. PCC7002 and *Cyanophora paradoxa*: cloning an
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHI>
A:CROSS-references: UNIPARC:UPI00000B1C2C; GB:M86238; NID:gl54574; PID:AAA27351.1; PID:
A:Reference number: JS0694; MUID:92201692; PMID:1551590

Query Match 24.0%; Score 23; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DVTTLRL 14
DB 7 DVTGRLQ 13

RESULT 81
A61117
somatostatin precursor processing enzyme (EC 3.4.21.-) - American goosefish (fragment)
C:Species: *Lophius americanus* (American goosefish)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 13-Sep-1996
R:Mackin, R.B.; Noe, B.D.; Spiess, J.
Endocrinology 129, 2263-2265, 1991
A:Title: Identification of a somatostatin-14-generating propeptide converting enzyme as
A:Reference number: A61117; MUID:92007528; PMID:1680673
A:Accession: A61117
A:Molecule type: protein
A:Residues: 1-17 <MAC>
A:CROSS-references: UNIPARC:UPI0000175CD6
A:Experimental source: pancreatic islets
C:Superfamily: kexin; subtilisin homology
C:Keywords: hydrolase; serine proteinase

Query Match 24.0%; Score 23; DB 2; Length 17;
Best Local Similarity 27.3%; Pred. No. 2.1e+03;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 NPNDVTTLRLRE 15
DB 4 NINDIEVNMXD 14

RESULT 82
S63487
fibrinogenolytic proteinase beta chain - horn viper (fragment)
N:Alternate names: beta-fibrinogenase
C:Species: Cerastes cerastes (horn viper)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
A:Accession: S63487
R:Araraba-Djebbari, F.; Martin-Bauclaire, M.F.; Mauco, G.; Marchot, P.
Eur. J. Biochem. 233, 756-765, 1995
A:Title: Afaacytin, an alpha-beta-fibrinogenase from Cerastes cerastes (horned viper) v.
A:Reference number: S63486; MUID:96085138; PMID:8521839
A:Accession: S63487
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-18 <LAR>
A:CROSS-references: UNIPROT:Q9PRM8; UNIPARC:UPI000000FB392
C:Superfamily: trypsin; trypsin homology

Query Match 24.0%; Score 23; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNMFND 8
DB 7 CNINE 11

RESULT 83
S31613
beta-1,3-glucanase homolog (clone A28) - rape (fragment)
C:Species: *Brassica napus* (rape)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
R:Hird, D.; Worrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.
Submitted to the EMBL Data Library, December 1992
A:Description: The anchor-specific protein encoded by the *Brassica napus* and *Arabidopsi*.
A:Reference number: S31612
A:Accession: S31613
A:Molecule type: mRNA
A:Residues: 1-19 <HIR>
A:CROSS-references: UNIPROT:Q06914; UNIPARC:UPI000009FE3E; EMBL:X69890; NID:gl7735; PID:
A:Experimental source: clone A28
C:Superfamily: beta-1,3-glucanase

Query Match 24.0%; Score 23; DB 2; Length 19;
Best Local Similarity 44.4%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EHCNFNDVT 10
DB 10 DRCKFPFGVT 18

RESULT 84
H49410
t-complex polypeptide 1 homolog (peak 7 fraction) - rabbit (fragments)
N:Alternate names: Chaperonin homolog (peak 7)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 23-Mar-1995
A:Accession: H49410
R:Rommelaeere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; A
Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
A:Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rel
A:Reference number: A49410; MUID:94089752; PMID:7903455
A:Accession: H49410
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-22 <ROM>

A;Cross-references: UNIPARC:UPI000017C5EC
A;Experimental source: reticulocyte

Query Match 24.0%; Score 23; DB 2; Length 22;
Best Local Similarity 62.5%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDVTTLRL 14
||| |||
Db 5 NDAATILR 12

RESULT 85

PH0084
fatty acid-binding protein - common sunflower (fragment)

N;Alternate names: lipid transfer protein
C;Species: Helianthus annuus (common sunflower)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: PH0084

R;Arondel, V.; Vergnolle, C.; Tchang, P.; Kader, J.C.

Mol. Cell. Biochem. 98, 49-56, 1990

A;Title: Bifunctional lipid-transfer fatty acid-binding proteins in plants.

A;Reference number: PH0084; MUID:91094813; PMID:2266969

A;Accession: PH0084

A;Molecule type: protein

A;Residues: 1-24 <ARO>

A;Cross-references: UNIPROT:Q7WLP2; UNIPARC:UPI00001763CF

A;Experimental source: cv. Rodeo

C;Superfamily: phospholipid transfer protein

C;Keywords: lipid binding

Query Match 24.0%; Score 23; DB 2; Length 24;
Best Local Similarity 71.4%; Pred. No. 3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 NDVTTLRL 13
|||||
Db 4 NDVTGNL 10

RESULT 86

S07443

secretin - human

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: S07443

R;Carlquist, M.; Joernvall, H.; Forssmann, W.G.; Thulin, L.; Johansson, C.; Mutt, V.

IRCS Med. Sci. 13, 217-218, 1985

A;Title: Human secretin is not identical to the porcine/bovine hormone.

A;Reference number: S07443

A;Accession: S07443

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-27 <CAR>

A;Cross-references: UNIPARC:UPI000002C75B

C;Genetics:

A;Gene: GDB:SCT

A;Cross-references: GDB:270550

A;Map position: Xp21.1-Xp21.1

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; duplication

F;27/Modified site: amidated carboxyl end (Val) #status predicted

Query Match 24.0%; Score 23; DB 1; Length 27;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 FNDVTTLRL 15
| |||||
Db 6 FTSELSRLR 15

RESULT 87

G44621

homeotic protein Hox 1 (clone 1a) - Florida lancelet (fragment)

C;Species: Branchiostoma floridae (Florida lancelet)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004

C;Accession: G44621

R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.

Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993

A;Title: Expansion of the Hox gene family and the evolution of chordates.

A;Reference number: A44616; MUID:93317669; PMID:8101001

A;Accession: G44621

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-27 <PEN>

A;Cross-references: UNIPROT:Q06867; UNIPARC:UPI000007C0B5; GB:L14876; NID:g289463; PIDN:

C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 24.0%; Score 23; DB 2; Length 27;
Best Local Similarity 38.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRENE 17
: || || ||
Db 1 HYNKYLTRARRVE 13

RESULT 88

E44636

homeotic protein Hox 4 (clone 4d) - acorn worm (fragment)

C;Species: Saccoglossus kowalevskii

C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 05-Oct-2004

C;Accession: E44636

R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.

Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993

A;Title: Expansion of the Hox gene family and the evolution of chordates.

A;Reference number: A44616; MUID:93317669; PMID:8101001

A;Accession: E44636

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-27 <PEN>

A;Cross-references: UNIPROT:Q26523; UNIPARC:UPI0000074B36; GB:L14915; NID:g294800; PIDN:

C;Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 24.0%; Score 23; DB 2; Length 27;
Best Local Similarity 38.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 NFNDVTTLRENE 17
: || || ||
Db 1 HYNKYLTRKRRIE 13

RESULT 89

I55596

lysosomal acid lipase - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C;Accession: I55596

R;Klima, H.; Ullrich, K.; Aslanidis, C.; Fehringer, P.; Lackner, K.J.; Schmitz, G.

J. Clin. Invest. 92, 2713-2718, 1993

A;Title: A splice junction mutation causes deletion of a 72-base exon from the mRNA for

A;Reference number: I55596; MUID:94075617; PMID:8254026

A;Accession: I55596

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: UNIPARC:UPI000011F7AC; GB:S68069; NID:g544574; PIDN:AAB29185.1; PID:

C;Superfamily: triacylglycerol lipase, lingual

Query Match 24.0%; Score 23; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CNFND 8

Db 6 CGFNE 10

RESULT 90

S55442

beta A2 crystallin - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 01-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: S55442

R:Hulsebos, T.J.M.; Cerosaletti, K.M.; Fournier, R.E.K.; Sinke, R.J.; Rocchi, M.; Marzel submitted to the EMBL Data Library, March 1995

A:Description: Identification of the human betaA2 crystallin gene; localization of the g

A:Reference number: S55440

A:Accession: S55442

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-28 <HUL>

A:Cross-references: UNIPROT:P53672; UNIPARC:UPI000016A745; EMBL:X86396; NID:g854106; PID

C:Superfamily: beta-crystallin

C:Keywords: duplication

Query Match 24.0%; Score 23; DB 2; Length 28;

Best Local Similarity 27.3%; Pred. No. 3.5e+03;

Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 EHCNFDVTR 12

Db 16 EFCYGLGTQ 26

RESULT 91

QIBP57

gene 1.5 protein - phase T7

C:Species: phase T7

C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: I43002; I43004; S42294; A04417

R:Dunn, J.J.; Thompson, K.

A:Description: The Nucleic Acid Sequence Database, September 1982

A:Reference number: A94615

A:Accession: I43002

A:Molecule type: DNA

A:Residues: 1-29 <DUN>

A:Cross-references: UNIPROT:P03792; UNIPARC:UPI00001393A1

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 148, 303-330, 1981

A:Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be

A:Reference number: A92866; MUID:82078034; PMID:7310871

A:Accession: I43004

A:Molecule type: DNA

A:Residues: 1-29 <DU2>

A:Cross-references: UNIPARC:UPI00001393A1; GB:V01127; NID:g15498; PIDN:CAA24338.1; PID:9

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 166, 477-535, 1983

A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge

A:Reference number: S42283; MUID:83241725; PMID:6864790

A:Accession: S42294

A:Molecule type: DNA

A:Residues: 1-29 <DUW>

A:Cross-references: UNIPARC:UPI00001393A1; EMBL:V01146; NID:g431187; PIDN:CAA24395.1; PI

C:Genetics:

A:Gene: 1.5

A:Map position: 19.48-19.69

C:Superfamily: phase T7 gene 1.5 protein

Query Match 24.0%; Score 23; DB 1; Length 29;

Best Local Similarity 42.9%; Pred. No. 3.6e+03;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HCNFNDV 9

Db 18 HCSDDDM 24

RESULT 92

C81541

hypothetical protein CP0767 [imported] - Chlamydophila pneumoniae (strain AR39)

C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: C81541

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: C81541

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-30 <REA>

A:Cross-references: UNIPROT:Q9KLZ2; UNIPARC:UPI000000CCCB; GB:AE002236; GB:AE002161; NID

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: CP0767

Query Match 24.0%; Score 23; DB 2; Length 30;

Best Local Similarity 50.0%; Pred. No. 3.7e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FEHCNFD 8

Db 22 FEHDDTD 29

RESULT 93

S31614

beta-1,3-glucanase homolog (clone A11) - rape (fragment)

C:Species: Brassica napus (rape)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S31614

R:Hird, D.; Worrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R. submitted to the EMBL Data Library, December 1992

A:Description: The anther-specific protein encoded by the Brassica napus and Arabidopsis

A:Reference number: S31612

A:Accession: S31614

A:Molecule type: mRNA

A:Residues: 1-32 <HIR>

A:Cross-references: UNIPROT:Q06377; UNIPARC:UPI00000AA72F; EMBL:X69888; NID:g17731; PID:

A:Experimental source: clone A11

C:Superfamily: beta-1,3-glucanase

Query Match 24.0%; Score 23; DB 2; Length 32;

Best Local Similarity 44.4%; Pred. No. 4e+03;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EHCNFDV 10

Db 23 DRCKPFGVT 31

RESULT 94

S22304

hypothetical protein - Streptomyces coelicolor (fragment)

C:Species: Streptomyces coelicolor

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S22304; T42018

R:van Wezel, G.P.; Vijgenboom, E.; Bosch, L. Nucleic Acids Res. 19, 4399-4403, 1991

A:Title: A comparative study of the ribosomal RNA operons of Streptomyces coelicolor A3 (

A:Reference number: S22304; MUID:91360338; PMID:1715981

A:Accession: S22304

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-32 <VAN>

A:Cross-references: UNIPROT:Q00491; UNIPARC:UPI00000AFB2E; EMBL:X60514; NID:g48948; PIDN

A:Note: the authors translated the codon GAT for residue 8 as Asn, AGG for residue 16 as

Query Match 24.0%; Score 23; DB 2; Length 32;
Best Local Similarity 83.3%; Pred. No. 4.e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 DVTRL 13
Db 8 DVLTRL 13

RESULT 95

S22607
ribosomal protein S4, cytosolic - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 05-Oct-2004
C;Accession: S22607
R;Lorenzi, F.; Francesconi, A.; Jappelli, R.; Amaldi, F.
Nucleic Acids Res. 20, 1859-1863, 1992
A;Title: Analysis of mRNAs under translational control during Xenopus embryogenesis: iso
A;Reference number: S22601; MUID:92253404; PMID:1579486
A;Accession: S22607
A;Molecule type: mRNA
A;Residues: 1-33 <LOR>
A;Cross-references: UNIPARC:UPI000017725A
A;Experimental source: clone 5-42
C;Superfamily: ribosomal protein S4
C;Keywords: protein biosynthesis; ribosome

Query Match 24.0%; Score 23; DB 2; Length 33;
Best Local Similarity 55.6%; Pred. No. 4.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 NFNDVTRL 13
Db 10 NGNDFATRL 18

RESULT 96

A30104
cerastobin (EC 3.4.21.-) - Sahara sand viper (fragment)
N;Alternate names: venom serine proteinase
C;Species: Cerastes vipera (Sahara sand viper)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: A30104
R;Farid, T.M.; Tu, A.T.; El-Asmar, M.F.
Biochemistry 28, 371-377, 1989
A;Title: Characterization of cerastobin, a thrombin-like enzyme from the venom of Cerast
A;Reference number: A30104; MUID:89207555; PMID:2539861
A;Accession: A30104
A;Molecule type: protein
A;Residues: 1-35 <FAR>
A;Cross-references: UNIPROT:P18692; UNIPARC:UPI0000138E2B
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; venom

Query Match 24.0%; Score 23; DB 2; Length 35;
Best Local Similarity 60.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CNFND 8
Db 7 CNINE 11

RESULT 97

S18224
filamentous hemagglutinin - Bordetella parapertussis (fragment)
N;Alternate names: fha protein
C;Species: Bordetella parapertussis
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 11-Jan-2000
C;Accession: S18224
R;Scariato, V.; Prugnola, A.; Arico, B.; Rappuoli, R.
Mol. Microbiol. 5, 2493-2498, 1991
A;Title: The bvg-dependent promoters show similar behaviour in different Bordetella spec

A;Reference number: S18223; MUID:92167814; PMID:1791761
A;Accession: S18224
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-35 <SCA>
A;Cross-references: UNIPARC:UPI00001781A7
C;Genetics:
A;Gene: fha
C;Superfamily: Bordetella filamentous hemagglutinin B

Query Match 24.0%; Score 23; DB 2; Length 35;
Best Local Similarity 33.3%; Pred. No. 4.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EHCNFNDVT 10
Db 22 EHCVTGNTS 30

RESULT 98

S11614
ribosomal protein S19.eR [validated] - Halobacterium salinarum (fragment)
N;Alternate names: ribosomal protein HS13
C;Species: Halobacterium salinarum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S11614
R;raguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982
A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaeobac
A;Reference number: S11609
A;Accession: S11614
A;Molecule type: protein
A;Residues: 1-35 <YAG>
A;Cross-references: UNIPROT:Q7M547; UNIPARC:UPI000017CB38
A;Note: the protein is designated as ribosomal protein HS13
A;Note: the source is designated as Halobacterium cutirubrum
C;Keywords: protein biosynthesis; ribosome

Query Match 24.0%; Score 23; DB 2; Length 35;
Best Local Similarity 62.5%; Pred. No. 4.4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 DVTTRLRL 15
Db 18 DLTRLDE 25

RESULT 99

A05135
neurotoxin VIII - scorpion (Buthus occitanus) (fragment)
C;Species: Buthus occitanus tunetanus
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05135
R;Martin, M.F.; Rochat, H.
Toxicol 22, 279-291, 1984
A;Title: Purification of thirteen toxins active on mice from the venom of the North Africa
A;Reference number: A94316; MUID:84224814; PMID:6729843
A;Accession: A05135
A;Molecule type: protein
A;Residues: 1-36 <MAR>
A;Cross-references: UNIPROT:P04098; UNIPARC:UPI00001356EE
C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin

Query Match 24.0%; Score 23; DB 2; Length 36;
Best Local Similarity 36.4%; Pred. No. 4.5e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy 2 EHCNFNDVTTR 12
Db 20 DYC--NDICTK 28

RESULT 100

I51085
 beta-2-microglobulin - Nile tilapia (fragment)
 C:Species: Tilapia nilotica, Oreochromis niloticus (Nile tilapia)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I51085
 R:Dixon, B.; Stet, R.J.M.; van Erp, S.H.M.; Pohajdak, B.
 Immunogenetics 38, 27-34, 1993
 A>Title: Characterization of B2-microglobulin transcripts from two teleost species.
 A:Reference number: I50493; MUID:93216304; PMID:8462991
 A:Accession: I51085
 A>Status: preliminary; translated from GB/EMBL/DBAJ
 A:Molecule type: mRNA
 A:Residues: 1-37 <DIX>
 A:Cross-references: UNIPROT:Q03423; UNIPARC:UPI00001266ED; GB:L05537; NID:g213492; PID:g
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 24.0%; Score 23; DB 2; Length 37;
 Best Local Similarity 42.9%; Pred. No. 4.6e+03;
 Matches 6; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 5 NFN--DVTTRLREN 16
 ||: ||: | : |
 Db 22 NFPPPDITITLLKN 35

Search completed: July 15, 2006, 00:24:54
 Job time : 51 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: July 15, 2006, 00:15:55 ; Search time 293 Seconds
(without alignments)
53.670 Million cell updates/sec

Title: US-09-020-393B-3_COPY_42_58
Perfect score: 96
Sequence: 1 FEHCNFDVTRLRENE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 67510

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.5	38.0	34	2	Q72520_H9HIV1
2	35.5	37.0	39	2	Q9YNX7_human immun
3	34.5	35.9	32	2	Q72524_H9HIV1
4	34.5	35.9	37	2	Q69722_H9HIV1
5	34.5	35.9	39	2	Q9YNY0_H9HIV1
6	34.5	35.9	40	2	Q9PXX8_H9HIV1
7	34	35.4	32	1	GLB4_LAMSP
8	33.5	34.9	32	2	Q9YPG7_9HIV1
9	33.5	34.9	40	2	Q905C1_9HIV1
10	33	34.4	18	2	Q9TWS7_LAMSP
11	33	34.4	31	2	Q70UN7_CHICK
12	33	34.4	32	2	Q7P2F9_FUSNV
13	32.5	33.9	37	2	Q6E1F6_HUMAN
14	32.5	33.9	39	2	Q6W4W4_HUMAN
15	32	33.3	27	2	P94784_ENTFA
16	32	33.3	33	2	Q3BSR7_XANC5
17	32	33.3	38	2	Q7RGG7_PLAYO
18	31.5	32.8	40	2	Q90585_H9HIV1
19	31	32.3	25	2	Q72871_YEAST
20	31	32.3	26	2	Q936D3_STAAU
21	31	32.3	27	2	Q9NBX1_ACRPR
22	31	32.3	28	2	Q9NBX2_ACRCE
23	31	32.3	34	2	Q735G0_BACCL1
24	31	32.3	35	2	Q7M2P7_HORSE
25	31	32.3	36	2	Q4XK38_PLACH
26	31	32.3	37	2	Q2KXF8_MAGGR
27	31	32.3	40	2	Q9NBX3_ACRPL
28	30.5	31.8	36	2	Q9YNX9_human immun
29	30.5	31.8	40	2	Q905C4_9HIV1
30	30	31.2	19	2	Q4XG21_PLACH
31	30	31.2	27	2	Q7YWA3_parazoanthu

32	30	31.2	30	2	Q3KDJ3_PSEPF
33	30	31.2	34	2	Q6W4V8_HUMAN
34	30	31.2	37	2	Q5DV85_9DIPT
35	30	31.2	38	2	Q3AF81_CARHZ
36	30	31.2	40	2	P82561_STRPY
37	29.5	30.7	27	2	Q9YNX4_9HIV1
38	29	30.2	27	2	Q4YFL9_PLABE
39	29	30.2	33	2	Q711X3_BRAEL
40	29	30.2	34	2	Q7VNV8_HABDU
41	29	30.2	34	2	Q6E460_9PERC
42	29	30.2	34	2	Q6E461_9PERC
43	29	30.2	34	2	Q6E462_9PERC
44	29	30.2	34	2	Q6E463_9PERC
45	29	30.2	34	2	Q6E464_9PERC
46	29	30.2	34	2	Q6E465_9PERC
47	29	30.2	34	2	Q6E466_9PERC
48	29	30.2	34	2	Q6E467_9PERC
49	29	30.2	34	2	Q6E468_9PERC
50	29	30.2	34	2	Q6E469_9PERC
51	29	30.2	34	2	Q6E470_9PERC
52	29	30.2	34	2	Q6E471_9PERC
53	29	30.2	34	2	Q6E472_9PERC
54	29	30.2	34	2	Q6E473_9PERC
55	29	30.2	34	2	Q6E474_9PERC
56	29	30.2	34	2	Q6E475_9PERC
57	29	30.2	34	2	Q6E476_9PERC
58	29	30.2	34	2	Q6E477_9PERC
59	29	30.2	35	2	Q2SOL3_9GAMM
60	29	30.2	37	1	TOT1A_ATTRO
61	29	30.2	38	2	Q91XM5_RAT
62	29	30.2	39	2	Q79DP5_BACTU
63	28.5	29.7	36	2	Q5HEU1_STAAC
64	28.5	29.7	39	2	Q40249_9HIV1
65	28	29.2	15	1	ALLS_MANSE
66	28	29.2	16	2	Q7BW21_9ZZZZ
67	28	29.2	19	2	Q7RTM9_HUMAN
68	28	29.2	21	2	Q4X533_PLACH
69	28	29.2	22	2	Q8X365_ECO57
70	28	29.2	24	2	Q4YLA7_PLABE
71	28	29.2	25	2	Q6QV88_PHAVU
72	28	29.2	25	2	Q6QVG1_PHAVU
73	28	29.2	25	2	Q6QVK5_PHAVU
74	28	29.2	25	2	Q6QVK8_PHAVU
75	28	29.2	25	2	Q6QVK9_PHAVU
76	28	29.2	25	2	Q76K95_SERQU
77	28	29.2	28	2	Q9UCG8_HUMAN
78	28	29.2	28	2	Q4YCI4_PLABE
79	28	29.2	28	2	Q9BUB5_9MYRI
80	28	29.2	29	2	Q3EPA2_BACTI
81	28	29.2	31	2	Q5K622_HUMAN
82	28	29.2	33	2	Q4X519_PLACH
83	28	29.2	33	2	Q54AR6_DICDI
84	28	29.2	34	2	Q76K97_SERQU
85	28	29.2	35	2	Q47W92_COLP3
86	28	29.2	35	2	Q73JCO_TREDE
87	28	29.2	35	2	Q8EY54_LRPIN
88	28	29.2	35	2	Q8EY54_LRPIN
89	28	29.2	35	2	Q76K89_SERQU
90	28	29.2	35	2	Q7SLD8_9HIV1
91	28	29.2	35	2	Q9J4E3_9HIV1
92	28	29.2	36	2	Q4X2A2_PLACH
93	28	29.2	36	2	Q6WJCO_9URTH
94	28	29.2	36	2	Q2T8M9_BURTH
95	28	29.2	36	2	Q8EYJ2_LRPIN
96	28	29.2	37	2	Q6LE94_HUMAN
97	28	29.2	37	2	Q5C316_SCHJA
98	28	29.2	37	2	Q5DVA0_9DIPT
99	28	29.2	37	2	Q5DVA1_9DIPT
100	28	29.2	37	2	Q5GN35_9DIPT
101	28	29.2	37	2	Q8P2K5_LRPIN
102	28	29.2	37	2	Q76K92_SERQU
103	28	29.2	39	2	Q4X3R4_PLACH
104	28	29.2	40	2	Q4Y6S6_PLACH

Q3KDJ3	pseudomonas
Q6W4V8	homo sapien
Q5DV85	dilophus sp
Q3AF81	carboxydoth
P82561	streptococ
Q9YNX4	human immun
Q4YFL9	plasmodium
Q711X3	bradyrhizob
Q7VNV8	haemophilus
Q6E460	stellerina
Q6E461	leptocottus
Q6E462	jordanita zo
Q6E463	rhaphocott
Q6E464	chitonotus
Q6E465	artedius co
Q6E466	scorpaenich
Q6E467	zaniolepis
Q6E468	oxylebius p
Q6E469	ophiodon el
Q6E470	hexagrammos
Q6E471	hexagrammos
Q6E472	hexagrammos
Q6E473	hexagrammos
Q6E474	hexagrammos
Q6E475	hexagrammos
Q6E476	hexagrammos
Q6E477	sebastes at
Q2SOL3	habellia che
P83580	atrax robus
Q91XM5	rattus norv
Q79DP5	bacillus th
Q5HEU1	staphylococ
Q40249	human immun
P42559	manduca sex
Q7BW21	incn plasmi
Q7RTM9	homo sapien
Q4X533	plasmodium
Q8X365	escherichia
Q4YLA7	plasmodium
Q6QV88	phaseolus v
Q6QVG1	phaseolus v
Q6QVK5	phaseolus v
Q6QVK8	phaseolus v
Q76K95	seriola qui
Q9UCG8	homo sapien
Q4YCI4	plasmodium
Q5K622	homo sapien
Q4X519	plasmodium
Q54AR6	dictyosteli
Q76K97	seriola qui
Q47W92	colwellia p
Q73JCO	treponema d
Q8EY54	leptospi
Q8EY54	leptospi
Q76K89	seriola qui
Q7SLD8	human immun
Q9J4E3	human immun
Q4X2A2	plasmodium
Q6WJCO	paratombia
Q2T8M9	burkholderi
Q8EYJ2	leptospi
Q6LE94	homo sapien
Q5C316	schistosoma
Q5DVA0	simulium or
Q5DVA1	culex annul
Q5GN35	chironomida
Q8P2K5	leptospi
Q76K92	seriola qui
Q4X3R4	plasmodium
Q4Y6S6	plasmodium

105	28	29.2	40	2	Q8T0Q0	DROSEPHILA	Q8T0Q0	178	26	27.1	25	2	Q8IA07	9ANNE	Q8IA07	perionyx ex
106	28	29.2	40	2	Q9PH86	XYLEFA	Q9PH86	179	26	27.1	25	2	Q8MU00	9ANNE	Q8MU00	eisenia and
107	28	29.2	40	2	Q9PY55	STREPTOCOCC	Q9PY55	180	26	27.1	25	2	Q8T611	ASTRU	Q8T611	plasmodium
108	28	29.2	40	2	Q9S0A5	BORBU	Q9S0A5	181	26	27.1	26	2	Q4Z4P7	PLABE	Q4Z4P7	plasmodium
109	28	29.1	40	2	Q9T5Z8	STELLE	Q9T5Z8	182	26	27.1	26	2	Q571Y6	SEPOF	Q571Y6	sepiia offic
110	28	29.1	13	2	Q8WMM1	PIG	Q8WMM1	183	26	27.1	26	2	Q571Z2	9MOLL	Q571Z2	nautilus po
111	27	28.1	21	2	P70657	RAT	P70657	184	26	27.1	26	2	Q8N066	PLAFA	Q8N066	plasmodium
112	27	28.1	25	2	Q23967	9TURB	Q23967	185	26	27.1	26	2	Q9NJR8	9MOLL	Q9NJR8	euprymna sc
113	27	28.1	25	2	Q25873	9TURB	Q25873	186	26	27.1	27	2	Q02597	BEROV	Q02597	beroe ovata
114	27	28.1	25	2	Q25874	9TURB	Q25874	187	26	27.1	27	2	Q44255	9MTRI	Q44255	ethmoscigma
115	27	28.1	25	2	Q26083	9TURB	Q26083	188	26	27.1	27	2	Q44266	9BILA	Q44266	acanthokara
116	27	28.1	25	2	Q4Y982	PLACH	Q4Y982	189	26	27.1	27	2	Q76528	9ECHN	Q76528	holothuria
117	27	28.1	25	2	Q8T605	ASTRU	Q8T605	190	26	27.1	27	2	Q96316	TRILA	Q96316	trypetesa l
118	27	28.1	26	2	Q4YFH8	PLABE	Q4YFH8	191	26	27.1	27	2	Q96322	ULOAE	Q96322	ulophyaema
119	27	28.1	27	2	Q25485	METISE	Q25485	192	26	27.1	27	2	Q96882	9MAXI	Q96882	elminius mo
120	27	28.1	27	2	Q26207	9TURB	Q26207	193	26	27.1	27	2	Q96889	9MAXI	Q96889	sacculina c
121	27	28.1	27	2	Q4Y9S4	PLABE	Q4Y9S4	194	26	27.1	27	2	P90714	BEROV	P90714	beroe ovata
122	27	28.1	27	2	Q7YWA4	9CNID	Q7YWA4	195	26	27.1	27	2	P90715	BEROV	P90715	beroe ovata
123	27	28.1	27	2	Q8MTL6	9CNID	Q8MTL6	196	26	27.1	27	2	P90717	BEROV	P90717	beroe ovata
124	27	28.1	28	1	VIP CANFA		VIP CANFA	197	26	27.1	27	2	Q06866	BRAPL	Q06866	branchiosto
125	27	28.1	28	1	VIP CAPHI		VIP CAPHI	198	26	27.1	27	2	Q23740	9ANNE	Q23740	stenodrilus
126	27	28.1	28	1	VIP MACMU		VIP MACMU	199	26	27.1	27	2	Q26353	LIMPO	Q26353	limulus pol
127	27	28.1	28	1	VIP SHEEP		VIP SHEEP	200	26	27.1	27	2	Q26354	LIMPO	Q26354	limulus pol
128	27	28.1	30	2	Q2JYH9	9CYAN	Q2JYH9	201	26	27.1	27	2	Q26355	LIMPO	Q26355	limulus pol
129	27	28.1	30	2	Q7VJP8	HELHP	Q7VJP8	202	26	27.1	27	2	Q26356	LIMPO	Q26356	limulus pol
130	27	28.1	31	1	DWTJ3A	BRARE	P83758	203	26	27.1	27	2	Q26389	9ANNE	Q26389	ctenodrilus
131	27	28.1	31	1	DWTJ3B	BRARE	Q9DF10	204	26	27.1	27	2	Q26402	9ANNE	Q26402	stylaria la
132	27	28.1	31	2	Q7YRN9	AILME	Q7YRN9	205	26	27.1	27	2	Q26524	SACKO	Q26524	saccoglossu
133	27	28.1	31	2	Q30CA5	9ROST	Q30CA5	206	26	27.1	27	2	Q6SXT8	EPTST	Q6SXT8	eptatretus
134	27	28.1	31	2	Q734J1	BACCI	Q734J1	207	26	27.1	27	2	Q6SXT9	EPTST	Q6SXT9	eptatretus
135	27	28.1	31	2	Q9DD74	9SALA	Q9DD74	208	26	27.1	27	2	Q94450	CHAVR	Q94450	chaetopteru
136	27	28.1	31	2	Q9DEW0	9SAUR	Q9DEW0	209	26	27.1	27	2	Q9NGI1	9ARAC	Q9NGI1	steatoda tr
137	27	28.1	31	2	Q9DFH6	9SMEG	Q9DFH6	210	26	27.1	27	2	Q9NGJ3	9ARAC	Q9NGJ3	steatoda tr
138	27	28.1	31	2	Q9DFI3	MONAL	Q9DFI3	211	26	27.1	27	2	Q9Y182	9BILA	Q9Y182	priapulid c
139	27	28.1	31	2	Q9DFI4	MONAL	Q9DFI4	212	26	27.1	27	2	Q9Y192	9BILA	Q9Y192	priapulid c
140	27	28.1	31	2	Q9DFI5	MONAL	Q9DFI5	213	26	27.1	27	2	Q61673	MOUSE	Q61673	mus musculu
141	27	28.1	32	2	Q4Y1G3	PLACH	Q4Y1G3	214	26	27.1	27	2	Q07142	PETWA	Q07142	petromyzon
142	27	28.1	32	2	Q4HLR5	CAMLA	Q4HLR5	215	26	27.1	27	2	Q483X3	TETNG	Q483X3	tetraodon n
143	27	28.1	33	2	Q87LM2	VIBPA	Q87LM2	216	26	27.1	27	2	Q90302	CARAU	Q90302	carassius a
144	27	28.1	33	2	Q8SNF0	9CHAR	Q8SNF0	217	26	27.1	27	2	Q91264	PETWA	Q91264	petromyzon
145	27	28.1	33	2	Q8SNF1	9CHAR	Q8SNF1	218	26	27.1	28	2	Q95NM7	LITFO	Q95NM7	lithobius f
146	27	28.1	35	1	TMTX2	MESTA	Q9Bn11	219	26	27.1	28	2	Q9GPK8	9MYRI	Q9GPK8	scutigereil
147	27	28.1	35	1	TMTX3	MESTA	Q9Bn12	220	26	27.1	28	2	Q24218	ORYSA	Q24218	oryza sati
148	27	28.1	35	1	Q4YJH4	PLABE	Q4YJH4	221	26	27.1	29	2	Q59906	PECWA	Q59906	pecten maxi
149	27	28.1	35	2	Q4Z4T3	PLABE	Q4Z4T3	222	26	27.1	29	2	Q967U5	SCHGR	Q967U5	schistocerc
150	27	28.1	35	2	Q5MJ04	MAIZE	Q5MJ04	223	26	27.1	30	2	Q4XK93	PLACH	Q4XK93	plasmodium
151	27	28.1	35	2	Q81S12	BACAN	Q81S12	224	26	27.1	30	2	Q5HRG2	STABQ	Q5HRG2	staphylococ
152	27	28.1	37	2	Q4Z546	PLABE	Q4Z546	225	26	27.1	30	2	Q87K83	VIBPA	Q87K83	vibrio para
153	27	28.1	37	2	Q5DV91	9DIPT	Q5DV91	226	26	27.1	30	2	Q5W971	9FLAV	Q5W971	japanese en
154	27	28.1	37	2	Q5DV93	9DIPT	Q5DV93	227	26	27.1	30	2	Q5W972	9FLAV	Q5W972	japanese en
155	27	28.1	37	2	Q5DV94	9DIPT	Q5DV94	228	26	27.1	30	2	Q5W973	9FLAV	Q5W973	japanese en
156	27	28.1	38	2	Q73LP3	TREDE	Q73LP3	229	26	27.1	30	2	Q5W975	9FLAV	Q5W975	japanese en
157	27	28.1	39	2	Q8VQ37	ECOLI	Q8VQ37	230	26	27.1	30	2	Q5W976	9FLAV	Q5W976	japanese en
158	27	28.1	39	2	Q93MP4	LACSK	Q93MP4	231	26	27.1	30	2	Q5W977	9FLAV	Q5W977	japanese en
159	27	28.1	40	2	Q23759	9DIPT	Q23759	232	26	27.1	30	2	Q5W978	9FLAV	Q5W978	japanese en
160	27	28.1	40	2	Q9TXA3	CAEEL	Q9TXA3	233	26	27.1	30	2	Q5W979	9FLAV	Q5W979	japanese en
161	26.5	27.6	27	2	Q7RB40	PLAYO	Q7RB40	234	26	27.1	30	2	Q5W980	9FLAV	Q5W980	japanese en
162	26.5	27.6	30	2	Q7VLM8	HAEDU	Q7VLM8	235	26	27.1	30	2	Q5W981	9FLAV	Q5W981	japanese en
163	26.5	27.6	32	2	Q4XJL5	FLACH	Q4XJL5	236	26	27.1	30	2	Q5W982	9FLAV	Q5W982	japanese en
164	26.5	27.6	35	2	Q4YB11	COLP3	Q4YB11	237	26	27.1	30	2	Q5W983	9FLAV	Q5W983	japanese en
165	26	27.1	20	2	Q9UCB6	HUMAN	Q9UCB6	238	26	27.1	30	2	Q5W984	9FLAV	Q5W984	japanese en
166	26	27.1	23	2	Q6OV19	PHAVU	Q6OV19	239	26	27.1	30	2	Q5W985	9FLAV	Q5W985	japanese en
167	26	27.1	23	2	Q70ZU8	9BRAD	Q70ZU8	240	26	27.1	30	2	Q5W986	9FLAV	Q5W986	japanese en
168	26	27.1	24	2	Q7RLK1	PLAYO	Q7RLK1	241	26	27.1	30	2	Q5W987	9FLAV	Q5W987	japanese en
169	26	27.1	24	2	Q9XSN6	STRGN	Q9XSN6	242	26	27.1	30	2	Q5W988	9FLAV	Q5W988	japanese en
170	26	27.1	25	2	Q9UD88	HUMAN	Q9UD88	243	26	27.1	30	2	Q5W989	9FLAV	Q5W989	japanese en
171	26	27.1	25	2	Q4LEA6	TUBITU	Q4LEA6	244	26	27.1	30	2	Q5W990	9FLAV	Q5W990	japanese en
172	26	27.1	25	2	Q4LEB6	TUBITU	Q4LEB6	245	26	27.1	31	2	Q9BDF2	OCHPR	Q9BDF2	ochotona pr
173	26	27.1	25	2	Q59HX2	FATYE	Q59HX2	246	26	27.1	31	2	Q35X59	9GAMM	Q35X59	shewanella
174	26	27.1	25	2	Q59HY3	DENOT	Q59HY3	247	26	27.1	31	2	Q99J18	CAVPO	Q99J18	cavia porce
175	26	27.1	25	2	Q59HZ6	LYMST	Q59HZ6	248	26	27.1	32	2	Q9HSZ0	HALSA	Q9HSZ0	halobacteri
176	26	27.1	25	2	Q59I10	9MOLL	Q59I10	249	26	27.1	32	2	Q86LN6	9TURB	Q86LN6	neochillia
177	26	27.1	25	2	Q7JQA6	POLMI	Q7JQA6	250	26	27.1	32	2	Q86LN8	9CAEN	Q86LN8	kellietia ke

251	26	27.1	32	2	08KYL9_BACAN	08ky19 bacillus an	324	25	26.0	27	2	096329_ULOOE	096329 ulophyema
252	26	27.1	32	2	06EZN8_BACAN	06ezn8 bacillus an	325	25	26.0	27	2	006863_BRAFL	006863 branchiosteo
253	26	27.1	32	2	09KLF0_VIBCH	09klf0 vibrio chol	326	25	26.0	27	2	006871_BRAFL	006871 branchiosteo
254	26	27.1	32	2	07TDC3_9FLAV	07tdc3 japanese en	327	25	26.0	27	2	006873_BRAFL	006873 branchiosteo
255	26	27.1	33	2	0724V4_LISMP	0724v4 listeria mo	328	25	26.0	27	2	024930_9TREM	024930 echinoatoma
256	26	27.1	34	2	04Y8D3_PLACH	04y8d3 plasmodium	329	25	26.0	27	2	024931_9TREM	024931 echinoatoma
257	26	27.1	34	2	091143_NOTVI	091143 notophthalm	330	25	26.0	27	2	025482_METSE	025482 metridium s
258	26	27.1	35	2	07QY53_GIALA	07qy53 giardia lam	331	25	26.0	27	2	025576_9CNID	025576 nematostell
259	26	27.1	35	2	095293_PIG	095293 sus scrofa	332	25	26.0	27	2	026202_9TURB	026202 phagocata w
260	26	27.1	36	2	04RDZ9_TETNG	04rdz9 tetraodon n	333	25	26.0	27	2	027342_9ANNE	027342 stylaria la
261	26	27.1	36	2	0991P8_9HIV1	0991p8 human immun	334	25	26.0	27	2	04A1N9_9MOLL	04a1n9 nautilus ma
262	26	27.1	37	2	09TW36_9PEZI	09tw36 ceratocyti	335	25	26.0	27	2	04Y2S2_PLACH	04y2s2 plasmodium
263	26	27.1	37	2	05DV92_9DIPT	05dv92 mycetocysti	336	25	26.0	27	2	09SH27_9TURB	09sh27 symagittif
264	26	27.1	37	2	06WJCI_9TURB	06wjci paratomella	337	25	26.0	27	2	06SX82_EPTST	06sx82 eptatretus
265	26	27.1	37	2	06GUP2_STRGN	06gup2 streptococc	338	25	26.0	27	2	06SXT7_EPTST	06sxt7 eptatretus
266	26	27.1	38	2	07RJ97_PLAYO	07rj97 plasmodium	339	25	26.0	27	2	09MTW2_9CNID	09mtw2 haloclava p
267	26	27.1	38	2	03OYD8_DSDBG	03oyd8 desulfovibr	340	25	26.0	27	2	09N648_ACHTE	09n648 achaeaarana
268	26	27.1	38	2	081PN2_BACAN	081pn2 bacillus an	341	25	26.0	27	2	06JDH7_CANFA	06jdh7 canis famli
269	26	27.1	38	2	042513_PETMA	042513 petromyzon	342	25	26.0	27	2	09YQ86_PCV2	09yq86 porcine cir
270	26	27.1	38	2	042515_PETMA	042515 petromyzon	343	25	26.0	28	2	09BJE2_9MYRI	09bje2 pauropus sp
271	26	27.1	39	1	Y049_BORBU	Y049 borrelia bu	344	25	26.0	28	2	09GPK5_9MYRI	09gpk5 scutigereil
272	26	27.1	39	2	065Q55_MANSN	065qs5 manheimia	345	25	26.0	29	2	02KEG3_MAGGR	02kek3 magnaporthe
273	26	27.1	40	2	04X5D1_PLACH	04x5d1 plasmodium	346	25	26.0	29	2	024684_DUGTI	024684 dugesia tig
274	26	27.1	40	2	04YNL9_PLACH	04ynl9 plasmodium	347	25	26.0	29	2	024686_DUGTI	024686 dugesia tig
275	26	27.1	40	2	03R7M0_XYLFA	03r7m0 xyella fas	348	25	26.0	29	2	024687_DUGTI	024687 dugesia tig
276	26	27.1	40	2	03LFP3_9FLAV	03lfp3 japanese en	349	25	26.0	29	2	05G130_9CIRC	05g130 porcine cir
277	26	27.1	40	2	03YAD5_CHICK	03yad5 gallus gall	350	25	26.0	29	2	077S11_9CIRC	077s11 bovine cir
278	25.5	26.6	26	2	09BP42_CONTE	09bp42 conus texti	351	25	26.0	30	2	04X3U1_PLACH	04x3u1 plasmodium
279	25.5	26.6	31	2	093PE1_YERPS	093pe1 yersinia ps	352	25	26.0	30	2	04XJN4_PLACH	04xjn4 plasmodium
280	25.5	26.6	37	2	05XCG1_STRP6	05xcg1 streptococc	353	25	26.0	30	2	07RS13_PLAYO	07rs13 plasmodium
281	25.5	26.6	39	2	04CKU3_TRYCR	04cku3 trypanosoma	354	25	26.0	30	2	07M1U2_SFIOI	07m1u2 spinacia ol
282	25.5	26.6	40	2	04XMU4_PLACH	04xmu4 plasmodium	355	25	26.0	30	2	04EGH1_LISMO	04egh1 listeria mo
283	25.5	26.6	40	2	08RGY7_FUSNN	08rgy7 fusobacteri	356	25	26.0	30	2	09YR10_PCV2	09yr10 porcine cir
284	25.5	26.6	40	2	09Q584_9HIV1	09q584 human immun	357	25	26.0	30	2	09PRP4_9SAUR	09prp4 lachesis mu
285	25	26.0	15	1	VSP3_AGKBP	P80899 agkistrodon	358	25	26.0	31	2	04X3X3_PLACH	04x3x3 plasmodium
286	25	26.0	15	2	04YPU5_PLACH	04ypu5 plasmodium	359	25	26.0	31	2	09DEV8_9SAUR	09dev8 chrysemys s
287	25	26.0	15	2	09PRW2_CROAT	09prw2 crotalus at	360	25	26.0	32	2	086LN7_9TURB	086ln7 notopiana a
288	25	26.0	15	2	09PRW3_CROAT	09prw3 crotalus at	361	25	26.0	32	2	0736F3_BACCI	0736f3 bacillus ce
289	25	26.0	19	1	TLB1_BOTJA	P81882 bothrops ja	362	25	26.0	33	2	06BJE6_DBBHA	06bje6 debaryomyce
290	25	26.0	19	1	TLB2_BOTJA	P81883 bothrops ja	363	25	26.0	33	2	04YQ82_PLABE	04yq82 plasmodium
291	25	26.0	19	1	TLB3_BOTJA	P81884 bothrops ja	364	25	26.0	33	2	05C0W8_SCHJA	05c0w8 schistosoma
292	25	26.0	20	1	VSP1_AGKBI	P33588 agkistrodon	365	25	26.0	33	2	03DSN8_STRAG	03dsn8 streptococc
293	25	26.0	20	1	VSP1_TRIOK	P20005 trimeresuru	366	25	26.0	33	2	03R4V5_XYLFA	03r4v5 xyella fas
294	25	26.0	20	2	04YB80_PLABE	04yb80 plasmodium	367	25	26.0	33	2	03RC60_XYLFA	03rc60 xyella fas
295	25	26.0	20	2	09PS55_CROAT	09ps55 crotalus at	368	25	26.0	33	2	04EMD8_LISMO	04emd8 listeria mo
296	25	26.0	21	2	08MJP0_CBBPY	08mjp0 cebuella py	369	25	26.0	33	2	04EMD9_LISMO	04emd9 listeria ce
297	25	26.0	21	2	08MJP1_CALJA	08mjp1 callithrix	370	25	26.0	33	2	04MTJ7_BACCE	04mtj7 bacillus ce
298	25	26.0	21	2	08MJP4_SAGFU	08mjp4 saguinus fu	371	25	26.0	33	2	09K123_HSLPY	09k123 helicobacte
299	25	26.0	21	2	09PRW4_CROAT	09prw4 crotalus at	372	25	26.0	33	2	0723R5_LISMF	0723r5 listeria mo
300	25	26.0	22	2	042019_PLABE	042019 plasmodium	373	25	26.0	33	2	0723R6_LISMF	0723r6 listeria mo
301	25	26.0	23	2	096705_9CAEN	096705 ilyanassa o	374	25	26.0	33	2	0731V9_BACCI	0731v9 bacillus ce
302	25	26.0	23	2	025136_HALRU	025136 haliotis ru	375	25	26.0	33	2	081MM6_BACAN	081mm6 bacillus an
303	25	26.0	23	2	026666_9CNID	026666 sarsia sp.	376	25	26.0	34	2	02KHG8_MAGGR	02khg8 magnaporthe
304	25	26.0	25	2	099HW7_PATYE	099hw7 patinopecte	377	25	26.0	35	2	07BQA7_MYCPH	07bqa7 mycobacteri
305	25	26.0	25	2	059115_LIOQJA	059115 liolophura	378	25	26.0	35	2	07VP05_HAEDU	07vp05 haemophilus
306	25	26.0	25	2	059130_9MOLL	059130 aplacophora	379	25	26.0	35	2	04SRP6_TETNG	04srp6 tetraodon n
307	25	26.0	25	2	06SE48_DROSI	06se48 drosofila	380	25	26.0	36	2	07LWA3_TRIMT	07lwa3 tricholoma
308	25	26.0	25	2	081A08_9ANNE	081a08 perionyx ex	381	25	26.0	36	2	04Y3U1_PLACH	04y3u1 plasmodium
309	25	26.0	25	2	08MWT_9ANNE	08mwt4 eisenia and	382	25	26.0	36	2	086GW3_9DIPT	086gw3 zapionus v
310	25	26.0	25	2	09BM60_9BILA	09bm60 sagitta sp.	383	25	26.0	36	2	086GW4_9DIPT	086gw4 scaptodroso
311	25	26.0	25	2	026090_9TURB	026090 polyctelis n	384	25	26.0	36	2	086GW5_HIRPI	086gw5 hirtodroso
312	25	26.0	25	2	06QVD3_PHAVU	06qv3 phaseolus v	385	25	26.0	36	2	086GW6_DROHE	086gw6 drosofila
313	25	26.0	25	2	06QVD3_PHAVU	06qv3 phaseolus v	386	25	26.0	36	2	086GW7_CHYAM	086gw7 chymomyza a
314	25	26.0	25	2	06QVFA_PHAVU	06qv4 phaseolus v	387	25	26.0	36	2	086GW8_DROAD	086gw8 drosofila
315	25	26.0	25	2	06QVGS_PHAVU	06qv5 phaseolus v	388	25	26.0	36	2	086GX4_9DIPT	086gx4 zapionus v
316	25	26.0	25	2	06QVGS_PHAVU	06qv5 phaseolus v	389	25	26.0	36	2	086GX6_CHYAM	086gx6 chymomyza a
317	25	26.0	25	2	06QVH7_PHAVU	06qv7 phaseolus v	390	25	26.0	36	2	05XNQ2_MANES	05xnq2 manihot esc
318	25	26.0	25	2	06QVH8_PHAVU	06qv8 phaseolus v	391	25	26.0	36	2	04L6Z0_STAHJ	04l6z0 staphylococ
319	25	26.0	25	2	06QVJ9_PHAVU	06qv9 phaseolus v	392	25	26.0	37	2	05DV83_HYBFE	05dv83 hybos femor
320	25	26.0	25	2	06Q839_MOUSE	06q839 mus musculus	393	25	26.0	37	2	05DV84_9ASIL	05dv84 empis ap. o
321	25	26.0	25	2	07LZFF_CROAT	07lzf6 crotalus at	394	25	26.0	37	2	08VJLI_MYCTU	08vjli mycobacteri
322	25	26.0	26	2	04XG85_PLACH	04xg85 plasmodium	395	25	26.0	37	2	02MBF6_ECOLI	02mbf6 escherichia
323	25	26.0	26	2	09NJR7_9MOLL	09njr7 euprymna sc	396	25	26.0	37	2	08F1S0_LBPIN	08f1s0 leptospira

397	Q9NYD9_HUMAN	38	2	25	26.0	Q9NYD9 homo sapien	470	24	25.0	25	2	Q8IA11_9ANNE	Q8IA11 perionyx ex
398	Q334H4_TRIMO	38	2	25	26.0	Q334H4 tritium mo	471	24	25.0	25	2	Q8IA14_9ANNE	Q8IA14 perionyx ex
399	Q48AN0_COLF3	38	2	25	26.0	Q48AN0 colwellia p	472	24	25.0	25	2	Q8MWU2_9ANNE	Q8MWU2 eisenia and
400	Q8KYR3_BACAN	38	2	25	26.0	Q8KYR3 bacillus an	473	24	25.0	25	2	Q8MWU5_9ANNE	Q8MWU5 eisenia and
401	Q6EXX5_BACAN	38	2	25	26.0	Q6EXX5 bacillus an	474	24	25.0	25	2	Q8MWU7_9ANNE	Q8MWU7 eisenia and
402	Q14559_HUMAN	39	2	25	26.0	Q14559 homo sapien	475	24	25.0	25	2	Q8T609_ASTRU	Q8T609 asterias ru
403	Q7QVW8_GIALA	39	2	25	26.0	Q7QVW8 giardia lam	476	24	25.0	25	2	Q8T610_ASTRU	Q8T610 asterias ru
404	Q7RSW3_PLAYO	39	2	25	26.0	Q7RSW3 plasmodium	477	24	25.0	25	2	Q8T617_9ECHI	Q8T617 amphura fi
405	Q4ZBE7_9CAUD	39	2	25	26.0	Q4ZBE7 bacterioph	478	24	25.0	25	2	Q8T618_9ECHI	Q8T618 amphura fi
406	Q4ZBE6_9CAUD	39	2	25	26.0	Q4ZBE6 bacterioph	479	24	25.0	25	2	Q9BM56_9BILA	Q9BM56 lineus sp.
407	Q4ZBM3_9VIRU	39	2	25	26.0	Q4ZBM3 bacterioph	480	24	25.0	25	2	Q63988_RAT	Q63988 rattus norv
408	Q4ZDR1_9CAUD	39	2	25	26.0	Q4ZDR1 bacterioph	481	24	25.0	25	2	Q63989_9MURI	Q63989 rattus sp.
409	Q6GUN8_STRGN	39	2	25	26.0	Q6GUN8 streptococ	482	24	25.0	25	2	Q63991_RAT	Q63991 rattus norv
410	Q6G2W5_BORGA	39	2	25	26.0	Q6G2W5 borrelia ga	483	24	25.0	25	2	Q6LD97_9MURI	Q6LD97 rattus sp.
411	Q6S572_MUSCR	39	2	25	26.0	Q6S572 mus caroli	484	24	25.0	26	2	Q62577_9METZ	Q62577 tetracapsul
412	Q4XSX5_PLACH	40	2	25	26.0	Q4XSX5 plasmodium	485	24	25.0	26	2	Q571Y9_9MOLL	Q571Y9 nautilus po
413	Q7R7N1_PLAYO	40	2	25	26.0	Q7R7N1 plasmodium	486	24	25.0	26	2	Q9NJR1_9MOLL	Q9NJR1 eupryma sc
414	Q9NFR2_9MYRI	40	2	25	26.0	Q9NFR2 pachymerium	487	24	25.0	26	2	Q9NJR5_9MOLL	Q9NJR5 eupryma sc
415	Q5IAB1_CERAB	40	2	25	26.0	Q5IAB1 cercoptithe	488	24	25.0	26	2	Q9NJR6_9MOLL	Q9NJR6 eupryma sc
416	Q84932_STRPY	40	2	25	26.0	Q84932 streptococ	489	24	25.0	27	1	SECR_CANFA	P09310 canis fami
417	Q6BCH0_EDNIC	40	2	25	26.0	Q6BCH0 edwardsiell	490	24	25.0	27	2	O02595_BEROV	O02595 beroe ovata
418	Q7VJUV9_HELHP	40	2	25	26.0	Q7VJUV9 helicobacte	491	24	25.0	27	2	O02596_BEROV	O02596 beroe ovata
419	Q8YU06_ANASP	40	2	25	26.0	Q8YU06 anabaena sp	492	24	25.0	27	2	O02598_BEROV	O02598 beroe ovata
420	Q8CQ16_STAES	40	2	25	26.0	Q8CQ16 staphylococ	493	24	25.0	27	2	Q46187_9ECHN	Q46187 holopneuste
421	Q80GP5_9REOV	40	2	25	26.0	Q80GP5 human rotav	494	24	25.0	27	2	Q62578_9MPTZ	Q62578 tetracapsul
422	Q4XBG5_PLACH	24.5	25.5	26	24.5	Q4XBG5 plasmodium	495	24	25.0	27	2	Q96318_TRVLA	Q96318 trypanosoma l
423	Q4XR15_PLACH	24.5	25.5	28	24.5	Q4XR15 plasmodium	496	24	25.0	27	2	Q96324_ULOOE	Q96324 ulophyema
424	Q4XRN5_PLABE	32	2	25	24.5	Q4XRN5 plasmodium	497	24	25.0	27	2	Q96326_ULOOE	Q96326 ulophyema
425	Q4YW79_PLABE	32	2	25	24.5	Q4YW79 plasmodium	498	24	25.0	27	2	Q96327_ULOOE	Q96327 ulophyema
426	Q8CU08_STAES	24.5	25.5	32	24.5	Q8CU08 staphylococ	499	24	25.0	27	2	Q96884_9MAXI	Q96884 elminius mo
427	Q8D25_LUPAN	24.5	25.5	37	1	Q8D25 lupinus ang	500	24	25.0	27	2	Q97464_9MAXI	Q97464 elminius mo
428	QBP2_HVSCR	24.5	25.5	38	1	QBP2 hystric cri	501	24	25.0	27	2	P90722_BEROV	P90722 beroe ovata
429	Q4YKM9_PLABE	24.5	25.5	38	2	Q4YKM9 plasmodium	502	24	25.0	27	2	Q06872_BRAFL	Q06872 branchiosto
430	Q3LXB6_PIG	24.5	25.5	38	2	Q3LXB6 sus scrofa	503	24	25.0	27	2	Q23747_9ANNE	Q23747 ctenodrilus
431	Q8VK45_MYCTU	24.5	25.5	39	2	Q8VK45 mycobacteri	504	24	25.0	27	2	Q24933_9TREM	Q24933 echinostoma
432	Q748F3_GEOSL	24.5	25.5	39	2	Q748F3 geobacter s	505	24	25.0	27	2	Q26203_9TURB	Q26203 phagocata w
433	Q9Q579_9HIV1	24.5	25.5	40	2	Q9Q579 human immun	506	24	25.0	27	2	Q26204_9TURB	Q26204 phagocata w
434	Q9Q589_9HIV1	24.5	25.5	40	2	Q9Q589 human immun	507	24	25.0	27	2	Q26393_9ANNE	Q26393 ctenodrilus
435	Q7M4F7_HUMAN	13	2	24	25.0	Q7M4F7 homo sapien	508	24	25.0	27	2	Q26395_9ANNE	Q26395 ctenodrilus
436	P78482_HUMAN	15	2	24	25.0	P78482 homo sapien	509	24	25.0	27	2	Q26522_SACKO	Q26522 saccoglossu
437	Q9AXV9_BRAOL	16	2	24	25.0	Q9AXV9 brassica ol	510	24	25.0	27	2	Q26526_SACKO	Q26526 saccoglossu
438	Q9AXW2_BRANA	24	25.0	16	2	Q9AXW2 brassica na	511	24	25.0	27	2	Q26527_SACKO	Q26527 saccoglossu
439	Q6J071_HBV	24	25.0	16	2	Q6J071 hepatitis b	512	24	25.0	27	2	Q4A1N8_9MOLL	Q4A1N8 nautilus ma
440	Q79DJ7_BACTU	24	25.0	17	2	Q79DJ7 bacillus th	513	24	25.0	27	2	Q599P9_PECWA	Q599P9 pecten maxi
441	Q34695_HOMAM	18	2	24	25.0	Q34695 homarus ame	514	24	25.0	27	2	Q69H26_9TURB	Q69H26 symaglittif
442	Q4YFB1_PLABE	24	25.0	18	2	Q4YFB1 plasmodium	515	24	25.0	27	2	Q6SXS3_EPTST	Q6SXS3 eptaretus
443	BULB_NARPS	20	1	24	25.0	B0554 narcissus p	516	24	25.0	27	2	Q6SXS5_EPTST	Q6SXS5 eptaretus
444	Q4X7N5_PLACH	20	2	24	25.0	Q4X7N5 plasmodium	517	24	25.0	27	2	Q6SXS7_EPTST	Q6SXS7 eptaretus
445	Q4CKD1_TRYCR	22	2	24	25.0	Q4CKD1 trypanosoma	518	24	25.0	27	2	Q6SXS9_EPTST	Q6SXS9 eptaretus
446	Q4X6H7_PLACH	24	25.0	22	2	Q4X6H7 plasmodium	519	24	25.0	27	2	Q6SXT3_EPTST	Q6SXT3 eptaretus
447	Q7R7L2_PLAYO	22	2	24	25.0	Q7R7L2 plasmodium	520	24	25.0	27	2	Q94453_CHAVR	Q94453 chaetopteru
448	P82580_STRPY	22	2	24	25.0	P82580 streptococ	521	24	25.0	27	2	Q94455_CHAVR	Q94455 chaetopteru
449	Q86MM8_PECWA	23	2	24	25.0	Q86MM8 pecten maxi	522	24	25.0	27	2	Q94457_CHAVR	Q94457 chaetopteru
450	Q7SE62_NEUCR	24	25.0	23	2	Q7SE62 neurospora	523	24	25.0	27	2	Q94459_CHAVR	Q94459 chaetopteru
451	Q4Y383_PLACH	24	25.0	24	2	Q4Y383 plasmodium	524	24	25.0	27	2	Q9NJF3_ACHTE	Q9NJF3 achaeanea
452	Q23965_STURB	24	25.0	25	2	Q23965 dendrocoelu	525	24	25.0	27	2	Q9NJF6_ACHTE	Q9NJF6 achaeanea
453	Q25872_STURB	24	25.0	25	2	Q25872 polycelis f	526	24	25.0	27	2	Q9NJF8_9ARAC	Q9NJF8 steatoda tr
454	Q4LE94_TUBTU	24	25.0	25	2	Q4LE94 tubifex tub	527	24	25.0	27	2	Q9NJG4_9ARAC	Q9NJG4 steatoda tr
455	Q4LEA2_TUBTU	24	25.0	25	2	Q4LEA2 tubifex tub	528	24	25.0	27	2	Q9UA00_PATVU	Q9UA00 patella vul
456	Q4LEB5_TUBTU	24	25.0	25	2	Q4LEB5 tubifex tub	529	24	25.0	27	2	Q9UA01_PATVU	Q9UA01 patella vul
457	Q4LEB8_TUBTU	24	25.0	25	2	Q4LEB8 tubifex tub	530	24	25.0	27	2	Q3DHT8_STRAG	Q3DHT8 streptococ
458	Q59HW4_PATVE	24	25.0	25	2	Q59HW4 patinopecte	531	24	25.0	27	2	Q6JQA3_HBV	Q6JQA3 hepatitis b
459	Q59HW9_PATVE	24	25.0	25	2	Q59HW9 patinopecte	532	24	25.0	27	2	Q07143_PETMA	Q07143 petromyzon
460	Q59HX6_DENOT	24	25.0	25	2	Q59HX6 dentalium o	533	24	25.0	27	2	Q07146_PETMA	Q07146 petromyzon
461	Q59HY0_DENOT	24	25.0	25	2	Q59HY0 dentalium o	534	24	25.0	27	2	Q07147_PETMA	Q07147 petromyzon
462	Q59HY9_LYMST	24	25.0	25	2	Q59HY9 lymnaea sta	535	24	25.0	27	2	Q07148_PETMA	Q07148 petromyzon
463	Q59H21_LYMST	24	25.0	25	2	Q59H21 lymnaea sta	536	24	25.0	27	2	Q07149_PETMA	Q07149 petromyzon
464	Q59I02_9MOLL	24	25.0	25	2	Q59I02 nautilus po	537	24	25.0	27	2	Q07151_PETMA	Q07151 petromyzon
465	Q59I04_9MOLL	24	25.0	25	2	Q59I04 nautilus po	538	24	25.0	27	2	Q789D3_PETMA	Q789D3 petromyzon
466	Q59I05_9MOLL	24	25.0	25	2	Q59I05 nautilus po	539	24	25.0	27	2	Q789D4_PETMA	Q789D4 petromyzon
467	Q59I33_9MOLL	24	25.0	25	2	Q59I33 aplacophora	540	24	25.0	27	2	Q90289_CARAU	Q90289 carassius a
468	Q7JQA7_POLMI	24	25.0	25	2	Q7JQA7 polyandroca	541	24	25.0	27	2	Q90290_CARAU	Q90290 carassius a
469	Q8IA04_9ANNE	24	25.0	25	2	Q8IA04 perionyx ex	542	24	25.0	27	2	Q90291_CARAU	Q90291 carassius a

543	24	25.0	27	2	Q90292_CARAU	Q90292_carassius a	616	24	25.0	36	2	Q867Q7_DROAD	Q867q7 drosophila
544	24	25.0	27	2	Q90293_CARAU	Q90293_carassius a	617	24	25.0	36	2	Q867Q8_CHYAM	Q867q8 chymomyza a
545	24	25.0	27	2	Q91263_PETMA	Q91263 petromyzon	618	24	25.0	36	2	Q86GX5_HIRPI	Q86gx5 hirtodrosop
546	24	25.0	27	2	Q91265_PETMA	Q91265 petromyzon	619	24	25.0	36	2	Q86GV1_9DPT	Q86gv1 zapionus v
547	24	25.0	27	2	Q91267_PETMA	Q91267 petromyzon	620	24	25.0	36	2	Q86GV5_9DPT	Q86gv5 scaptodroso
548	24	25.0	27	2	Q91270_PETMA	Q91270 petromyzon	621	24	25.0	36	2	Q86GV6_CHYAM	Q86gv6 chymomyza a
549	24	25.0	28	2	Q9BUE3_9MYRI	Q9bje1 paupopus sp	622	24	25.0	36	2	Q9TY82_9BILA	Q9ty82 acanthokara
550	24	25.0	28	2	Q9BUE3_9MYRI	Q9bje1 paupopus sp	623	24	25.0	36	2	Q9TY82_9BILA	Q9ty82 acanthokara
551	24	25.0	28	2	Q9GPK6_9MYRI	Q9gpk6 scutigereili	624	24	25.0	36	2	Q9NWU1_AZOSE	Q9nwu1 azoarcus sp
552	24	25.0	29	1	GALA_CHICK	P30802 gallus gall	625	24	25.0	36	2	Q91142_NOTVI	Q91142 notophthalm
553	24	25.0	29	1	GALA_RANRI	P47216 rana ridibu	626	24	25.0	36	2	Q4X5S8_PLACH	Q4x5s8 plasmodium
554	24	25.0	29	2	Q4A3G6_9BASI	Q4a3g6 sporisorium	627	24	25.0	37	2	Q4Z5X2_PLABE	Q4z5x2 plasmodium
555	24	25.0	29	2	Q4XZY1_PLACH	Q4xzy1 plasmodium	628	24	25.0	37	2	Q5DV82_9DPT	Q5dv82 keroplatida
556	24	25.0	29	2	Q7R6T8_PLAYO	Q7r6t8 plasmodium	629	24	25.0	37	2	Q5DV87_9ASIL	Q5dv87 hemipenthes
557	24	25.0	29	2	Q7R7L5_PLAYO	Q7r7l5 plasmodium	630	24	25.0	37	2	Q5DV88_9DPT	Q5dv88 chorisops t
558	24	25.0	29	2	Q48492_KLEBIE	Q48492 klebsiella	631	24	25.0	37	2	Q5DV89_9ASIL	Q5dv89 scenopinus
559	24	25.0	29	2	Q9JXD6_NEIMP	Q9jxd6 neisseria m	632	24	25.0	37	2	Q5DV90_9DPT	Q5dv90 tabanus bro
560	24	25.0	30	2	Q4YLM1_PLABE	Q4ylm1 plasmodium	633	24	25.0	37	2	Q5DV95_9DPT	Q5dv95 culicoides
561	24	25.0	30	2	Q967V3_LITFO	Q967v3 lithobius f	634	24	25.0	37	2	Q5DV96_9DPT	Q5dv96 culicoides
562	24	25.0	30	2	Q967V3_LITFO	Q967v3 lithobius f	635	24	25.0	37	2	Q5DV97_9DPT	Q5dv97 culicoides
563	24	25.0	30	2	Q56273_ARATH	Q56273 arabidopsis f	636	24	25.0	37	2	Q5DV98_9DPT	Q5dv98 culicoides
564	24	25.0	30	2	Q5GOT8_PINTA	Q5got8 pinus taeda	637	24	25.0	37	2	Q5DV99_9DPT	Q5dv99 culicoides
565	24	25.0	30	2	Q41N8_COLP3	Q41n8 colwellia p	638	24	25.0	37	2	Q6SX88_BPTST	Q6sxx8 eptaretus
566	24	25.0	30	2	Q6DQK5_CLOBE	Q6dqk5 clostridium	639	24	25.0	37	2	Q9FSZ3_CICAR	Q9fesz cicier ariet
567	24	25.0	30	2	Q314V3_DSDG	Q314v3 desulfovibr	640	24	25.0	37	2	Q85HT2_9SPER	Q85ht2 gnetum nodi
568	24	25.0	30	2	Q6JQB3_HBV	Q6jqb3 hepatitis b	641	24	25.0	37	2	Q8X3Z3_ECO57	Q8x3z3 escherichia
569	24	25.0	31	2	Q5V4E2_HALMA	Q5v4e2 haloarcula	642	24	25.0	37	2	Q72XM4_BACCI	Q72xm4 bacillus ce
570	24	25.0	31	2	Q4YSB7_PLABE	Q4ysb7 plasmodium	643	24	25.0	37	2	Q8F126_LRPIN	Q8f126 leptospira
571	24	25.0	31	2	Q7R7M1_PLAYO	Q7r7m1 plasmodium	644	24	25.0	37	2	Q9PRK2_9GALL	Q9prk2 gallus sp.
572	24	25.0	31	2	Q7R8M1_PLAYO	Q7r8m1 plasmodium	645	24	25.0	37	2	Q9PRK7_9GALL	Q9prk7 gallus sp.
573	24	25.0	31	2	Q9LEJ3_SOYBN	Q9lej3 glycine max	646	24	25.0	37	2	Q9PRL2_9GALL	Q9prl2 gallus sp.
574	24	25.0	31	2	Q9WVX5_STRUB	Q9wvx5 streptococc	647	24	25.0	37	2	Q41433_9HIV1	Q41433 human immun
575	24	25.0	31	2	Q81H95_BACR	Q81h95 bacillus ce	648	24	25.0	38	2	Q4Z513_PLABE	Q4z513 plasmodium
576	24	25.0	31	2	Q8E9Y0_SHEON	Q8e9y0 shewanella	649	24	25.0	38	2	Q5BX33_SCHJA	Q5bx33 schistosoma
577	24	25.0	31	2	Q8E9Y5_SHEON	Q8e9y5 shewanella	650	24	25.0	38	2	Q3HE85_TRIER	Q3he85 trichodesmi
578	24	25.0	31	2	Q97T66_XTRPN	Q97t66 streptococc	651	24	25.0	38	2	Q3HE85_TRIER	Q3he85 trichodesmi
579	24	25.0	31	2	Q91704_XENLA	Q91704 xenopus lae	652	24	25.0	38	2	Q3HE85_TRIER	Q3he85 trichodesmi
580	24	25.0	31	2	Q9DEVE_9SALA	Q9dev6 cynops orie	653	24	25.0	38	2	Q52K21_STAAC	Q52k21 staphylococ
581	24	25.0	32	2	Q9B031_9VIRU	Q9b031 bacterioph	654	24	25.0	38	2	Q83C59_COXBU	Q83c59 coxiella bu
582	24	25.0	32	2	Q3LBQ0_9MOLU	Q3lbq0 candidatus	655	24	25.0	38	2	Q8QY00_9MURU	Q8qy00 rattus sp.
583	24	25.0	32	2	Q5N115_FRATT	Q5n115 francisella	656	24	25.0	38	2	Q75W93_CVPCA	Q75w93 cyprinus ca
584	24	25.0	32	2	Q5N115_FRATT	Q5n115 francisella	657	24	25.0	38	2	Q10483_9HIV1	Q10483 human immun
585	24	25.0	32	1	DEF1_MESAU	P81465 mesocricetu	658	24	25.0	38	2	Q10488_9HIV1	Q10488 human immun
586	24	25.0	33	1	Q4X417_PLACH	Q4x417 plasmodium	659	24	25.0	38	2	Q10495_9HIV1	Q10495 human immun
587	24	25.0	33	2	Q51BM6_ENTHI	Q51bm6 entamoeba h	660	24	25.0	39	2	Q86PS4_ECHGR	Q86ps4 echinococc
588	24	25.0	33	2	Q6SEW5_9BACT	Q6sew5 uncultured	661	24	25.0	39	2	Q86PS8_9CEST	Q86ps8 mesocetoid
589	24	25.0	33	2	Q89538_9PAPI	Q89538 human papil	662	24	25.0	39	2	Q8MQT1_PHESE	Q8mqt1 pheretima s
590	24	25.0	33	2	Q460H2_9HIV1	Q460h2 human immun	663	24	25.0	39	2	Q8MQT2_PHESE	Q8mqt2 pheretima s
591	24	25.0	34	2	Q16125_HUMAN	Q16125 homo sapien	664	24	25.0	39	2	Q9N016_PIG	Q9n016 sus scrofa
592	24	25.0	34	2	Q8N4M7_HUMAN	Q8n4m7 homo sapien	665	24	25.0	39	2	Q312Q5_DSDG	Q312q5 desulfovibr
593	24	25.0	34	2	Q4YYP5_PLABE	Q4yyp5 plasmodium	666	24	25.0	39	2	Q98R88_MYCPU	Q98rb8 mycoplasma
594	24	25.0	34	2	Q7JNH8_DROME	Q7jnh8 drosophila	667	24	25.0	39	2	Q2LK08_9AMPH	Q2lk08 siren inter
595	24	25.0	34	2	Q86DR0_9BILA	Q86dr0 spadella ce	668	24	25.0	39	2	Q2LK09_9AMPH	Q2lk09 rhinatrema
596	24	25.0	34	2	Q86DR1_9BILA	Q86dr1 spadella ce	669	24	25.0	39	2	Q2LK10_RANTE	Q2lk10 rana tempor
597	24	25.0	34	2	Q6SF03_9BACT	Q6sf03 uncultured	670	24	25.0	39	2	Q2LK11_LEIAR	Q2lk11 leiopelma a
598	24	25.0	34	2	Q579S6_BRUAB	Q579s6 bruceella ab	671	24	25.0	39	2	Q2LK12_ICHBA	Q2lk12 ichtyophis
599	24	25.0	34	2	Q5LFO1_BACFN	Q5lfo1 bacteroides	672	24	25.0	39	2	Q2LK47_9SALA	Q2lk47 triturus he
600	24	25.0	34	2	Q71ZAB_LISMP	Q71zab listeria mo	673	24	25.0	39	2	Q2LK49_RANTE	Q2lk49 rana tempor
601	24	25.0	34	2	Q8VHL4_RAT	Q8vhl4 rattus norv	674	24	25.0	39	2	Q2LK50_LEIAR	Q2lk50 leiopelma a
602	24	25.0	34	2	Q4TH65_TETNG	Q4th65 tetraodon n	675	24	25.0	39	2	Q10485_9HIV1	Q10485 human immun
603	24	25.0	34	2	Q2KKR5_9PERO	Q2kkrs siniperca c	676	24	25.0	39	2	Q10486_9HIV1	Q10486 human immun
604	24	25.0	35	2	Q25284_LOLFO	Q25284 loligo forb	677	24	25.0	40	2	Q7S644_NUCUR	Q7s644 neurospora
605	24	25.0	35	2	Q9MZA7_PIG	Q9mza7 sus scrofa	678	24	25.0	40	2	Q9H3B8_HUMAN	Q9h3b8 homo sapien
606	24	25.0	35	2	Q7VQL1_RHOBA	Q7vql1 rhodopirell	679	24	25.0	40	2	Q7RNU1_PLAYO	Q7rnu1 plasmodium
607	24	25.0	35	2	Q8F6N8_LEPIN	Q8f6n8 leptospira	680	24	25.0	40	2	Q95UB1_9MYRI	Q95ub1 strigamia m
608	24	25.0	35	2	Q6F608_MOUSE	Q6f608 mus musculu	681	24	25.0	40	2	Q95UB2_9MYRI	Q95ub2 necrophioe
609	24	25.0	36	1	LYOX_PIG	P45945 sus scrofa	682	24	25.0	40	2	Q95UB3_9MYRI	Q95ub3 haplophilus
610	24	25.0	36	2	Q9PLE9_HUMAN	Q9ple9 homo sapien	683	24	25.0	40	2	Q95UB4_9MYRI	Q95ub4 geophilus i
611	24	25.0	36	2	Q4XE36_PLACH	Q4xe36 plasmodium	684	24	25.0	40	2	Q95UB5_9MYRI	Q95ub5 geophilus e
612	24	25.0	36	2	Q867Q3_9DPT	Q867q3 zapionus v	685	24	25.0	40	2	Q95UB6_GSOCC	Q95ub6 geophilus c
613	24	25.0	36	2	Q867Q4_9DPT	Q867q4 scaptodroso	686	24	25.0	40	2	Q95UB7_9MYRI	Q95ub7 brachygeoph
614	24	25.0	36	2	Q867Q5_HIRPI	Q867q5 hirtodrosop	687	24	25.0	40	2	Q9NFO9_9MYRI	Q9nfq9 pachymerium
615	24	25.0	36	2	Q867Q6_DROHE	Q867q6 drosophila	688	24	25.0	40	2	Q9NFR1_9MYRI	Q9nfr1 pachymerium

689	24	25.0	40	2	Q9M351_ARATH	Q9M351_arabidopsis	762	23	24.0	25	2	Q8MWT9_9ANNE	Q8MWT9_eisenia and
690	24	25.0	40	2	Q6FD10_ACIAD	Q6fd10_acinetobact	763	23	24.0	25	2	Q8MWU3_9ANNE	Q8mwu3_eisenia and
691	24	25.0	40	2	Q7UTB9_RHOBA	Q7utb9_rhodospirell	764	23	24.0	25	2	Q9BM64_LISNE	Q9bm64_lissomyema
692	24	25.0	40	2	Q8FYU5_BRUSO	Q8fyu5_brucella su	765	23	24.0	26	2	Q7S853_NEUCR	Q7s853_neurospora
693	24	25.0	40	2	Q8F328_LEPIN	Q8f328_leptospiro	766	23	24.0	26	2	Q4Y1M7_PLABE	Q4y1m7_plasmodium
694	24	25.0	40	2	Q2LDK3_SPEPA	Q2ldk3_spermophilu	767	23	24.0	26	2	Q5Y1Y3_SEPOF	Q5y1y3_sepia offic
695	24	25.0	40	2	Q2MDW8_FICHY	Q2mdw8_ficedula hy	768	23	24.0	26	2	Q5Y1Z0_9MOLL	Q5y1z0_nautilus po
696	24	25.0	40	2	Q2MDW9_FICPA	Q2mdw9_ficedula pa	769	23	24.0	26	2	Q9NZJF_9ARAC	Q9njzf_steatoda tr
697	24	25.0	40	2	Q2WDX7_FICAL	Q2wdx7_ficedula al	770	23	24.0	26	2	Q9NJR3_9MOLL	Q9njr3_euprymna sc
698	24	25.0	40	2	Q1O493_9HIVI	Q1o493_human immun	771	23	24.0	26	2	Q8SPZ2_MACMU	Q8spz2_macaca mula
699	24	25.0	40	2	Q41436_9HIVI	Q41436_human immun	772	23	24.0	26	2	Q4RBS4_TETNG	Q4rbs4_tetradon n
700	24	25.0	40	2	Q41437_9HIVI	Q41437_human immun	773	23	24.0	27	2	P90712_BEROV	P90712_beroe ovata
701	23.5	24.5	14	2	Q71GT8_9HYME	Q71gt8_andrena bro	774	23	24.0	27	2	P90721_BEROV	P90721_beroe ovata
702	23.5	24.5	30	2	Q4XDM2_PLACH	Q4xdm2_plasmodium	775	23	24.0	27	2	Q06867_BRAFL	Q06867_branchiosto
703	23.5	24.5	32	2	Q9IWC2_9PAPI	Q9iwc2_phocoena sp	776	23	24.0	27	2	Q2S584_9UROC	Q2s584_oikopleura
704	23.5	24.5	35	2	Q2SP09_9GAMM	Q2sp09_hahellia che	777	23	24.0	27	2	Q26392_9ANNE	Q26392_ctenodrilus
705	23.5	24.5	37	2	Q5O868_BORBU	Q5o868_borrelia bu	778	23	24.0	27	2	Q26523_SACKO	Q26523_saccoglossu
706	23.5	24.5	38	2	Q4YLT0_PLABE	Q4ylt0_plasmodium	779	23	24.0	27	2	Q4A1P1_9MOLL	Q4a1p1_nautilus ma
707	23.5	24.5	38	2	Q5DTB8_OLBEU	Q5dtb8_olea europa	780	23	24.0	27	2	Q4X4G2_PLACH	Q4x4g2_plasmodium
708	23.5	24.5	40	1	PTSB_LACLA	Q04938_lactococcus	781	23	24.0	27	2	Q4XDD6_PLACH	Q4xdd6_plasmodium
709	23	24.0	9	1	TALA3_PICJA	Pl7441_pichia jadi	782	23	24.0	27	2	Q6XSX8_EPTST	Q6sxs8_eptatretus
710	23	24.0	12	2	Q7YNG4_BASHY	Q7yng4_bassia hyss	783	23	24.0	27	2	Q94456_CHAVR	Q94456_chaetopteru
711	23	24.0	12	2	Q9FSA9_9CARY	Q9fsa9_silene aega	784	23	24.0	27	2	Q9BM58_9BTLA	Q9bm58_lineus sp.
712	23	24.0	13	2	P97622_RAT	P97622_rattus norv	785	23	24.0	28	2	Q4XXV0_PLACH	Q4xxv0_plasmodium
713	23	24.0	14	2	Q55326_SYNP2	Q55326_synchococc	786	23	24.0	28	2	Q4YDM0_PLABE	Q4ydm0_plasmodium
714	23	24.0	17	1	JHBP_PLAVG	P56675_platyrepia	787	23	24.0	28	2	Q4Z0N8_PLABE	Q4z0n8_plasmodium
715	23	24.0	18	2	Q4ZSL3_PLABE	Q4zsl3_plasmodium	788	23	24.0	29	1	SCX1_ANDMA	P56215_androctonus
716	23	24.0	18	2	Q9PRM8_CERCE	Q9prm8_cerastes ce	789	23	24.0	29	1	Y15_BPT7	P03792_bacterioph
717	23	24.0	19	2	Q06914_BRANA	Q06914_brassica na	790	23	24.0	29	2	Q5VV22_HUMAN	Q5vv22_homo sapien
718	23	24.0	19	2	Q91329_9HIVI	Q91329_human immun	791	23	24.0	29	2	Q7R7J5_PLAYO	Q7r7j5_plasmodium
719	23	24.0	19	2	Q9WJB1_9HIVI	Q9wjb1_human immun	792	23	24.0	29	2	Q3V7E0_BPT7	Q3v7e0_bacterioph
720	23	24.0	20	1	NLTP1_HELAN	P82007_helianthus	793	23	24.0	29	2	Q6WYR2_BPT7	Q6wyr2_bacterioph
721	23	24.0	20	2	Q16129_HUMAN	Q16129_homo sapien	794	23	24.0	29	2	Q76Z14_9CAUD	Q76z14_yersinia pe
722	23	24.0	20	2	Q4YYZ6_PLABE	Q4yyz6_plasmodium	795	23	24.0	29	2	Q6QVD0_PHAUV	Q6qvd0_phaseolus v
723	23	24.0	20	2	Q94KK4_9ROGA	Q94kk4_ziziphus ma	796	23	24.0	29	2	Q6QVD1_PHAUV	Q6qvd1_phaseolus v
724	23	24.0	21	1	PEDB_HYDAT	P80577_hydra atten	797	23	24.0	29	2	Q6QVD6_PHAUV	Q6qvd6_phaseolus v
725	23	24.0	21	2	Q4YF73_PLABE	Q4yf73_plasmodium	798	23	24.0	29	2	Q6QVF7_PHAUV	Q6qvf7_phaseolus v
726	23	24.0	22	2	Q4XPS5_PLACH	Q4xps5_plasmodium	799	23	24.0	29	2	Q6QVG4_PHAUV	Q6qvg4_phaseolus v
727	23	24.0	22	2	Q4XN91_PLACH	Q4xn91_plasmodium	800	23	24.0	29	2	Q5XYP8_BORGA	Q5xyp8_borrelia ga
728	23	24.0	22	2	Q4Z192_PLABE	Q4z192_plasmodium	801	23	24.0	29	2	Q87NK4_VIBPA	Q87nk4_vibrio para
729	23	24.0	23	2	Q7RMK7_PLAYO	Q7rmk7_plasmodium	802	23	24.0	30	2	Q4XN39_PLACH	Q4xn39_plasmodium
730	23	24.0	23	2	Q86ML8_9BIVA	Q86ml8_yoldia eigh	803	23	24.0	30	2	Q4YZ85_PLABE	Q4yz85_plasmodium
731	23	24.0	23	2	Q86MM4_PECMA	Q86mm4_pecten maxi	804	23	24.0	30	2	Q8RV13_PINPS	Q8rv13_pinus pinas
732	23	24.0	23	2	Q12V98_XENLA	Q712v8_xenopus lae	805	23	24.0	30	2	Q9K1Z2_CHLPN	Q9k1z2_chlamydia p
733	23	24.0	24	2	Q4X3G4_PLACH	Q4x3g4_plasmodium	806	23	24.0	30	2	Q81UD7_BACAN	Q81ud7_bacillus an
734	23	24.0	24	2	Q4XEB7_PLACH	Q4xeb7_plasmodium	807	23	24.0	31	2	Q3INK1_NATPD	Q3ink1_natronomona
735	23	24.0	24	2	Q4XL87_PLACH	Q4xl87_plasmodium	808	23	24.0	31	2	Q4XSG8_PLACH	Q4xsg8_plasmodium
736	23	24.0	24	2	Q4XL87_PLACH	Q4xl87_plasmodium	809	23	24.0	31	2	Q4XHS9_PLACH	Q4xhs9_plasmodium
737	23	24.0	24	2	Q599P8_PECMA	Q599p8_pecten maxi	810	23	24.0	31	2	Q4XW56_PLACH	Q4xw56_plasmodium
738	23	24.0	24	2	Q7RJY9_PLAYO	Q7rjy9_plasmodium	811	23	24.0	31	2	Q4Y7U1_PLACH	Q4y7u1_plasmodium
739	23	24.0	24	2	Q9U922_LINUN	Q9u922_lingula ung	812	23	24.0	31	2	Q9GJY4_MICLA	Q9gjy4_microptamo
740	23	24.0	24	2	Q56Y95_ARATH	Q56y95_arabidopsis	813	23	24.0	31	2	Q9GJZ1_ELEMA	Q9gjz1_elephas max
741	23	24.0	24	2	Q71479_9STRA	Q71479_fragilaria	814	23	24.0	31	2	Q9GJZ2_9EUTH	Q9gjz2_erinaceus e
742	23	24.0	24	2	Q7M1P2_HELAN	Q7m1p2_helianthus	815	23	24.0	31	2	Q9GKZ7_9AMHO	Q9gkz7_amblysomus
743	23	24.0	25	2	Q50027_MYCLE	Q50027_mycobacteri	816	23	24.0	31	2	Q733P7_BACC1	Q733p7_bacillus ce
744	23	24.0	25	2	Q4LE93_TUBTU	Q4le93_tubifex tub	817	23	24.0	32	2	Q4X4S9_PLACH	Q4x4s9_plasmodium
745	23	24.0	25	2	Q4LE95_TUBTU	Q4le95_tubifex tub	818	23	24.0	32	2	Q4X6K3_PLACH	Q4x6k3_plasmodium
746	23	24.0	25	2	Q4LEA0_TUBTU	Q4lea0_tubifex tub	819	23	24.0	32	2	Q4Y388_PLACH	Q4y388_plasmodium
747	23	24.0	25	2	Q4LEA1_TUBTU	Q4lea1_tubifex tub	820	23	24.0	32	2	Q861P4_CRAGI	Q861p4_crassostrea
748	23	24.0	25	2	Q4LEB0_TUBTU	Q4leb0_tubifex tub	821	23	24.0	32	2	Q86LP5_URECA	Q86lp5_urechis cau
749	23	24.0	25	2	Q4LEB1_TUBTU	Q4leb1_tubifex tub	822	23	24.0	32	2	Q8T933_TETHH	Q8t933_tetrahymena
750	23	24.0	25	2	Q4NEB9_THEPA	Q4neb9_thelateria p	823	23	24.0	32	2	Q9NGM5_STRPU	Q9ngm5_strongyloce
751	23	24.0	25	2	Q4YT86_PLABE	Q4yte6_plasmodium	824	23	24.0	32	2	Q06377_BRANA	Q06377_brassica na
752	23	24.0	25	2	Q599Q3_PECMA	Q599q3_pecten maxi	825	23	24.0	32	2	Q2QUT1_ORVSA	Q2qut1_oryza sativ
753	23	24.0	25	2	Q59HW5_PATYE	Q59hw5_patinopecte	826	23	24.0	32	2	P95517_PASHA	P95517_pasteurella
754	23	24.0	25	2	Q59HX7_DENOT	Q59hx7_dentulium o	827	23	24.0	32	2	Q00491_STRCO	Q00491_strptomycella
755	23	24.0	25	2	Q59H20_LYMST	Q59h20_lymaea sta	828	23	24.0	32	2	Q4L6C2_STAHJ	Q4l6c2_staphylococ
756	23	24.0	25	2	Q59I03_9MOLL	Q59i03_nautilus po	829	23	24.0	32	2	Q73GU0_WOLPM	Q73gu0_wolbachia p
757	23	24.0	25	2	Q59I13_LIOJA	Q59i13_liolophura	830	23	24.0	32	2	Q9CVM6_MOUSE	Q9cvm6_mus musculus
758	23	24.0	25	2	Q59I17_LIOJA	Q59i17_liolophura	831	23	24.0	32	2	Q6SKL1_CVHSA	Q6skl1_sars corona
759	23	24.0	25	2	Q59I20_9MOLL	Q59i20_chaetodorma	832	23	24.0	32	2	Q9UIH2_HUMAN	Q9uih2_homo sapien
760	23	24.0	25	2	Q8IA12_9ANNE	Q8ia12_perionyx ex	833	23	24.0	33	2	Q4X863_PLACH	Q4x863_plasmodium
761	23	24.0	25	2	Q8IA13_9ANNE	Q8ia13_perionyx ex	834	23	24.0	33	2	Q9GU25_ENTHI	Q9gu25_entamoeba h

835	23	24.0	33	2	Q50118_MYCLE	Q50118 mycobacteri	908	23	24.0	38	2	Q8DYH6_STRA5	Q8dyh6 streptococ
836	23	24.0	33	2	Q6SRF0_MANSN	Q6srf0 mannheimia	909	23	24.0	38	2	Q8FWY9_BRUSU	Q8fwy9 brucella su
837	23	24.0	33	2	Q6SRF5_HOMO	Q6srf5 piloderma c	910	23	24.0	38	2	Q8CPT7_STAES	Q8cpt7 staphylococ
838	23	24.0	34	2	Q86279_HOMO	Q86279 piloderma b	911	23	24.0	38	2	Q3UXH5_MOUSE	Q3uxh5 mus musculus
839	23	24.0	34	2	Q86213_HUMAN	Q86213 homo sapien	912	23	24.0	38	2	Q6EAW8_9CALI	Q6eaw8 norovirus g
840	23	24.0	34	2	Q4VAX9_PLABE	Q4vax9 plasmodium	913	23	24.0	38	2	Q8PTV6_ORYLA	Q8ptv6 oryzias lat
841	23	24.0	34	2	Q5EG03_RIFPA	Q5eg03 riftia pach	914	23	24.0	38	2	Q8PTV7_ORYLA	Q8ptv7 oryzias lat
842	23	24.0	34	2	Q7RE46_PLAYO	Q7re46 plasmodium	915	23	24.0	38	2	Q4O250_9HIV1	Q4o250 human immun
843	23	24.0	34	2	Q4W2B4_GLOS	Q4w2b4 glossophaga	916	23	24.0	38	2	Q4O252_9HIV1	Q4o252 human immun
844	23	24.0	34	2	Q4B3U0_COLP3	Q4b3u0 colwellia p	917	23	24.0	38	2	Q4O253_9HIV1	Q4o253 human immun
845	23	24.0	34	2	Q2VYR0_STAAB	Q2vyr0 staphylococ	918	23	24.0	38	2	Q4O255_9HIV1	Q4o255 human immun
846	23	24.0	34	2	Q4P552_BRARE	Q4p552 brachydanio	919	23	24.0	39	2	Q2VP71_9ARCB	Q2vp71 uncultured
847	23	24.0	34	2	Q4T9K9_TETNG	Q4t9k9 tetraodon n	920	23	24.0	39	2	Q69H25_9TURB	Q69h25 symagittif
848	23	24.0	35	1	TXI_THEBL	P83745 theraposa	921	23	24.0	39	2	Q5TRJ9_BOVIN	Q5trj9 bos taurus
849	23	24.0	35	1	VSPA_CERVI	P18692 cerastes vi	922	23	24.0	39	2	Q5GQX1_9CAUD	Q5gqx1 bacterioph
850	23	24.0	35	2	Q7M547_HALSA	Q7m547 halobacteri	923	23	24.0	39	2	Q48U46_STRP1	Q48u46 streptococ
851	23	24.0	35	2	Q5BYU0_SCHJA	Q5byu0 schistosoma	924	23	24.0	39	2	Q48ZD4_STRP1	Q48zd4 streptococ
852	23	24.0	35	2	Q5CD06_CRYHO	Q5cd06 cryptospori	925	23	24.0	39	2	Q7P421_FUSNV	Q7p421 fusobacteri
853	23	24.0	35	2	Q2YHR5_9MOLL	Q2yhr5 nautilus po	926	23	24.0	39	2	Q8CKU3_YERPE	Q8cku3 yersinia pe
854	23	24.0	35	2	Q3BUZ2_BACTI	Q3bz2 bacillus th	927	23	24.0	39	2	Q3L5I0_DESDG	Q3l5i0 desulfovibr
855	23	24.0	35	2	Q44I16_CHRSL	Q44i16 chromohalob	928	23	24.0	39	2	Q5XCP3_STRP6	Q5xcp3 streptococ
856	23	24.0	35	2	Q47U76_COLP3	Q47u76 colwellia p	929	23	24.0	39	2	Q87N30_VIBPA	Q87n30 vibrio para
857	23	24.0	35	2	Q3L5W7_DESDG	Q3l5w7 desulfovibr	930	23	24.0	39	2	Q5O897_BORBU	Q5o897 borrelia bu
858	23	24.0	35	2	Q5HHR4_STAAC	Q5hhr4 staphylococ	931	23	24.0	39	2	Q4RSL4_TETNG	Q4rsl4 tetraodon n
859	23	24.0	35	2	Q5NZB3_AZOSE	Q5nzb3 azoarcus sp	932	23	24.0	39	2	Q9OSK7_9HIV1	Q9osk7 human immun
860	23	24.0	35	2	Q87RM4_VIBPA	Q87rm4 vibrio para	933	23	24.0	39	2	Q9OSK8_9HIV1	Q9osk8 human immun
861	23	24.0	35	2	Q7SLI5_9HIV1	Q7sli5 human immun	934	23	24.0	40	2	Q13832_HUMAN	Q13832 homo sapien
862	23	24.0	35	2	Q7ZKY4_9HIV1	Q7zky4 human immun	935	23	24.0	40	2	Q4YPY2_PLABE	Q4ypy2 plasmodium
863	23	24.0	36	1	SCX8_BUTOC	P04098 buthus occi	936	23	24.0	40	2	Q4ZOP9_PLABE	Q4zop9 plasmodium
864	23	24.0	36	2	Q4Y5D6_PLACH	Q4y5d6 plasmodium	937	23	24.0	40	2	Q8V8G2_DROME	Q8v8g2 drosophila
865	23	24.0	36	2	Q4IYY4_PLABE	Q4iyy4 plasmodium	938	23	24.0	40	2	Q6Z687_PIG	Q6z687 sus scrofa
866	23	24.0	36	2	Q4Z9A6_9CAUD	Q4z9a6 staphylococ	939	23	24.0	40	2	Q6X3T8_9VIRU	Q6x3t8 bacillus th
867	23	24.0	36	2	Q6PKV5_9ROSA	Q6pkv5 ericobotrya	940	23	24.0	40	2	Q4MRV4_BACCE	Q4mrv4 bacillus ce
868	23	24.0	36	2	Q6QB12_9GROA	Q6qb12 ericobotrya	941	23	24.0	40	2	Q6G6X8_STAAS	Q6g6x8 staphylococ
869	23	24.0	36	2	Q3NWE5_9GAMM	Q3nwe5 shewanella	942	23	24.0	40	2	Q6GE92_STAAR	Q6ge92 staphylococ
870	23	24.0	36	2	Q3WU10_DESDG	Q3wu10 desulfovibr	943	23	24.0	40	2	Q7MWT3_PORGI	Q7mwt3 porphyromon
871	23	24.0	36	2	Q3KEM3_PSEPF	Q3kem3 pseudomonas	944	23	24.0	40	2	Q8NV58_STAAR	Q8nv58 staphylococ
872	23	24.0	36	2	Q8BE11_SHEON	Q8be11 shewanella	945	23	24.0	40	2	Q730I1_BACCI	Q730i1 bacillus ce
873	23	24.0	36	2	Q6EAW5_9CALI	Q6eaw5 norovirus g	946	23	24.0	40	2	Q81LN2_BACAN	Q81ln2 bacillus an
874	23	24.0	36	2	Q1O497_9HIV1	Q1o497 human immun	947	23	24.0	40	2	Q370I8_MOUSE	Q370i8 mus musculus
875	23	24.0	36	2	Q41428_9HIV1	Q41428 human immun	948	23	24.0	40	2	Q3TYG2_MOUSE	Q3tyg2 mus musculus
876	23	24.0	37	1	B2WG_ORENI	Q03423 oreochromis	949	23	24.0	40	2	Q77B44_9GEMI	Q77b44 maize strea
877	23	24.0	37	1	LCNN_LACLA	P83002 lactococcus	950	23	24.0	40	2	Q9WJ5_9GEMI	Q9wj5 maize strea
878	23	24.0	37	2	Q53S11_HUMAN	Q53s11 homo sapien	951	23	24.0	40	2	Q4RCY7_TETNG	Q4rcy7 tetraodon n
879	23	24.0	37	2	Q4X4T5_PLACH	Q4x4t5 plasmodium	952	22.5	23.4	14	2	Q71GX0_9HYME	Q71gx0 andrena ref
880	23	24.0	37	2	Q4XIL9_PLACH	Q4xil9 plasmodium	953	22.5	23.4	21	2	Q48438_KLBPN	Q48438 klebsiella
881	23	24.0	37	2	Q4VFM9_PLABE	Q4vfm9 plasmodium	954	22.5	23.4	22	2	Q4YAW6_PLABE	Q4yaw6 plasmodium
882	23	24.0	37	2	Q5DV86_9DIPT	Q5dv86 apiloscatop	955	22.5	23.4	24	2	Q8X689_ECO57	Q8x689 escherichia
883	23	24.0	37	2	Q6SXR5_EPTST	Q6sxr5 eptatretus	956	22.5	23.4	24	2	Q8CGM9_MOUSE	Q8cgm9 mus musculus
884	23	24.0	37	2	Q4W2B3_TRACI	Q4w2b3 trachops ci	957	22.5	23.4	31	2	Q4X490_PLACH	Q4x490 plasmodium
885	23	24.0	37	2	Q2PYE6_9BACT	Q2pye6 uncultured	958	22.5	23.4	31	2	Q6NKH5_CORDI	Q6nkh5 corynebacte
886	23	24.0	37	2	Q4KEP8_PSRF5	Q4kep8 pseudomonas	959	22.5	23.4	34	2	Q8EYV1_LEPIN	Q8eyv1 leptospira
887	23	24.0	37	2	Q57DC0_BRUBA	Q57dc0 brucella ab	960	22.5	23.4	34	2	Q8F9C5_LEPIN	Q8f9c5 leptospira
888	23	24.0	37	2	Q7UFV4_RHOBA	Q7ufv4 rhodopirell	961	22.5	23.4	35	2	Q8EZL3_LEPIN	Q8ezl3 leptospira
889	23	24.0	37	2	Q83C23_COXBU	Q83c23 coxiella bu	962	22.5	23.4	39	2	Q8CU20_STAAS	Q8cu20 staphylococ
890	23	24.0	37	2	Q8GOS8_BRUSU	Q8gos8 brucella su	963	22.5	23.4	9	2	Q6LEH2_HUMAN	Q6leh2 homo sapien
891	23	24.0	37	2	Q2YQ62_BRUA2	Q2yq62 brucella ab	964	22	22.9	10	1	UPA9_HUMAN	UPA9 homo sapien
892	23	24.0	37	2	Q8EXM9_LEPIN	Q8exm9 leptospira	965	22	22.9	11	2	Q5DQJ8_9LILI	Q5dqj8 nenga gajah
893	23	24.0	37	2	Q4RYK1_TETNG	Q4ryk1 tetraodon n	966	22	22.9	12	2	Q8IVH0_HUMAN	Q8ivh0 homo sapien
894	23	24.0	37	2	Q1O484_9HIV1	Q1o484 human immun	967	22	22.9	12	2	Q5DQJ9_9LILI	Q5dqj9 nenga gajah
895	23	24.0	37	2	Q1O487_9HIV1	Q1o487 human immun	968	22	22.9	14	2	Q2QHF9_SALET	Q2qhf9 salmonella
896	23	24.0	37	2	Q4O245_9HIV1	Q4o245 human immun	969	22	22.9	16	1	CKX1_CONEP	CKX1 oreochromis
897	23	24.0	38	2	Q8PUM2_METMA	Q8pum2 methanosarc	970	22	22.9	16	2	Q77922_ORENI	Q77922 oreochromis
898	23	24.0	38	2	Q8ZWM3_PYRAE	Q8zwm3 pyrobaculum	971	22	22.9	17	2	Q7RDP8_PLAYO	Q7rdp8 plasmodium
899	23	24.0	38	2	Q7RYE9_NEUCR	Q7rye9 neurospora	972	22	22.9	17	2	Q5J747_COXBU	Q5j747 coxiella bu
900	23	24.0	38	2	Q4XBQ7_PLACH	Q4xbq7 plasmodium	973	22	22.9	17	2	Q6RSJ1_COXBU	Q6rsj1 coxiella bu
901	23	24.0	38	2	Q5BMC6_ONCOV	Q5bmc6 onchoerca	974	22	22.9	17	2	Q9QEX2_HUMAN	Q9qex2 human immun
902	23	24.0	38	2	Q7SW88_9EUCA	Q7sw88 eriocheir j	975	22	22.9	18	2	Q6LD99_HUMAN	Q6ld99 homo sapien
903	23	24.0	38	2	Q6WAS7_HORSE	Q6was7 equus cabal	976	22	22.9	18	2	Q5TM07_9ACAR	Q5tm07 ixodes myrm
904	23	24.0	38	2	Q6EAX3_9BRAS	Q6eax3 draba cf. l	977	22	22.9	18	2	Q7R6U2_PLAYO	Q7r6u2 plasmodium
905	23	24.0	38	2	Q9KLX4_CHLPN	Q9klx4 chlamydia p	978	22	22.9	18	2	Q5O076_MYCLE	Q5o076 mycobacteri
906	23	24.0	38	2	Q2ND75_9SPHN	Q2nd75 erythrobact	979	22	22.9	19	2	Q77923_ORENI	Q77923 oreochromis
907	23	24.0	38	2	Q577B8_BRUBA	Q577b8 brucella ab	980	22	22.9	19	1	DURB_STRGW	P36502 streptococ


```

RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=98019132; PubMed=9358100;
RT      Rencher S.D., Hurwitz J.L.;
RA      "Effect of natural HIV-1 envelope V1-V2 sequence diversity on the
RL      binding of V3-specific and non-V3-specific antibodies.";
RL      J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 16:69-73(1997).
CC      -----
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CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; U76690; AAD00261.1; -: Genomic DNA.
DR      GO; GO:0019031; C:Viral envelope; IEA.
DR      InterPro; IPR000777; GP120.
DR      Pfam; PF00516; GP120; 1.
KW      Envelope protein.
FT      NON_TER 1
FT      NON_TER 39
SQ      SEQUENCE 39 AA; 4460 MW; BCD7525D8A4EA894 CRC64;

Query Match 35.9%; Score 34.5; DB 2; Length 39;
Best Local Similarity 42.9%; Pred. No. 3.9e+02;
Matches 6; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

QY      2 EHCNFNDVTVRLRE 15
DB      ::|||::|:|:|
       21 KNCSEFN-ITTVNRD 33

RESULT 6
ID      Q9PXV8_9HIV1 PRELIMINARY; PRT; 40 AA.
AC      Q9PXV8;
DT      01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT      01-MAY-2000, sequence version 1.
DT      07-FEB-2006, entry version 19.
DE      Envelope glycoprotein GP120 (Fragment).
GN      Name=ENV;
GS      Human immunodeficiency virus 1.
OS      Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC      Lentivirus; Primate lentivirus group.
OX      NCBI_TaxID=11676;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=93276273; PubMed=8502996;
RA      Groenink M., Fouchier R.A., Broersen S., Baker C.H., Koot M.,
RA      van't Wout A.B., Huismans H.G., Miedema F., Tersmette M.,
RA      Schuitemaker H.;
RT      "Relation of phenotype evolution of HIV-1 to envelope V2
RL      configuration.";
RL      Science 260:1513-1516(1993).
CC      -----
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CC      -----
CC      GO; GO:0016021; C:Integral to membrane; IEA.
DR      GO; GO:0019031; C:Viral envelope; IEA.
DR      InterPro; IPR000777; GP120.
DR      Pfam; PF00516; GP120; 1.
KW      AIDS; Transmembrane.
FT      NON_TER 1
FT      NON_TER 40
SQ      SEQUENCE 40 AA; 4706 MW; 0711271C133A9A16 CRC64;

Query Match 35.9%; Score 34.5; DB 2; Length 40;
Best Local Similarity 58.3%; Pred. No. 4e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY      4 CNEFNDVTVRLRE 15
DB      ||::|:|:|:|
       1 CSFN-ITTVSLRD 11

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OX NCBI_TaxID=6424;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93320735; PubMed=7763791;
 RA Suzuki T., Takagi T., Ohta S.,
 RL Zool. Sci. 10:141-146(1993).
 CC -----
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 CC -----
 SQ SEQUENCE 18 AA; 2192 MW; 039D56A0B814670F CRC64;
 Query Match 34.4%; Score 33; DB 2; Length 18;
 Best Local Similarity 28.6%; Pred. No. 2.9e+02;
 Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 2 EHCNFNDVTTTLRE 15
 DB 4 DCHYEDAEIVMKE 17
 RESULT 11
 Q70UN7 CHICK
 ID Q70UN7 CHICK PRELIMINARY; PRT; 31 AA.
 AC Q70UN7;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Soluble vascular endothelial growth factor receptor-1 (Fragment).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pecten Oculi;
 RA Mezquita J., Mezquita B., Pau M., Mezquita C.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 DR EMBL; AJ539548; CAD62460.1; -; mRNA.
 DR EMBL; AJ539547; CAD62459.1; -; mRNA.
 DR GO; GO:0004872; Fireceptor activity; IEA.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 31 AA; 3637 MW; E2672CD91DCA240E CRC64;
 Query Match 34.4%; Score 33; DB 2; Length 31;
 Best Local Similarity 50.0%; Pred. No. 5.4e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 EHCNFNDVTTTL 13
 DB 2 EHCNKAVYSRI 13
 RESULT 12
 Q7P2F9 FUSNV
 ID Q7P2F9 FUSNV PRELIMINARY; PRT; 32 AA.
 AC Q7P2F9;
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Hypothetical cytosolic protein.
 GN Name=FNV0722;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 CC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 CC Fusobacterium.
 OX NCBI_TaxID=209882;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 49256;
 RA Karpatrial V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haselkorn R., Overbeek R., Kyripides N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 DR EMBL; AABF01000106; EAA23611.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 32 AA; 4078 MW; 438C0F962059CE5B CRC64;
 Query Match 34.4%; Score 33; DB 2; Length 32;
 Best Local Similarity 71.4%; Pred. No. 5.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FEHCNPN 7
 DB 26 FOHLNPN 32
 RESULT 13
 Q6EIF6 HUMAN
 ID Q6EIF6 HUMAN PRELIMINARY; PRT; 37 AA.
 AC Q6EIF6;
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
 DT 16-AUG-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE AAA1 variant X.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 CC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Laitinen T., Salmikangas P., Polvi A., Makela S., Laitinen L.A.,
 RA Kere J.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 DR EMBL; AY321515; AAQ87609.1; -; mRNA.
 SQ SEQUENCE 37 AA; 4400 MW; 7DAB9AD5B709DD92 CRC64;
 Query Match 33.9%; Score 32.5; DB 2; Length 37;
 Best Local Similarity 35.0%; Pred. No. 8e+02;
 Matches 7; Conservative 4; Mismatches 6; Indels 3; Gaps 1;
 QY 1 FEHCNPN---VTTTLRENE 17
 DB 17 FSHCNLHAHQFLVRRKQENK 36
 RESULT 14
 Q6W4W4 HUMAN
 ID Q6W4W4 HUMAN PRELIMINARY; PRT; 39 AA.
 AC Q6W4W4;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE AAA1 variant III.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 CC Homo.
 OX NCBI_TaxID=9606;


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RN NUCLEOTIDE SEQUENCE
RX PubMed=15073379; DOI=10.1126/science.1090010;
RA Laitinen T., Polvi A., Rydman P., Vendelin J., Pulkkinen V.,
RA Salminen P., Mäkelä S., Rehn M., Pirskanen A., Rautanen A.,
RA Zucchelli M., Gullsten H., Leino M., Alenius H., Petaeys T.,
RA Hahtela T., Laitinen A., Laprise C., Hudson T.J., Laitinen L.A.,
RA Kere J.,
RT "Characterization of a common susceptibility locus for asthma-related
RT traits.";
RL Science 304:300-304 (2004).
CC
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CC
CC -----
DR EMBL; AY312367; AAQ85135.1; -; mRNA.
DR Ensembl; ENSG0000197085; Homo sapiens.
SQ SEQUENCE 39 AA; 4800 MW; 5EAA5CE8791871EB CRC64;

Query Match 33.9%; Score 32.5; DB 2; Length 39;
Best Local Similarity 35.0%; Pred. No. 8.5e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

Qy 1 FEHCNFND---VTTRLRENE 17
Db 19 FSHCNLHAHQFLVRRKQENK 38

RESULT 15
P94784 ENTFA
ID P94784 ENTFA PRELIMINARY; PRT; 27 AA.
AC P94784;
DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1997, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE ExMB regulator.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;

RN NUCLEOTIDE SEQUENCE.
RA Oh T.-G., Choi E.-C.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC -----
DR EMBL; U86375; AAC71782.1; -; Genomic DNA.
DR GO; GO:0046677; P:response to antibiotic; IEA.
DR InterPro; IPR003391; ERM.
DR Pfam; PF06308; ERM; 1.
SQ SEQUENCE 27 AA; 3109 MW; 3EAA5667114BD2E CRC64;

Query Match 33.3%; Score 32; DB 2; Length 27;
Best Local Similarity 29.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 FEHCNFNDVTTRLRENE 17
Db 4 FQMCNVDKTSVLKQTK 20

RESULT 16
Q3BSR7 XANC5
ID Q3BSR7 XANC5 PRELIMINARY; PRT; 33 AA.
AC Q3BSR7;

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DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Putative filamentous phage phiLf protein.
GN OrderedLocNames=XCV2465;
OS Xanthomonas campestris pv. vesicatoria (strain 85-10).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=316273;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16237009; DOI=10.1128/JB.187.21.7254-7266.2005;
RA Thieme F., Koebnik R., Bekel T., Berger C., Boch J., Buettner D.,
RA Caldana C., Gaigalat L., Goesmann A., Kay S., Kirchner O., Lanz C.,
RA Linke B., McHardy A.C., Meyer F., Mittenhuber G., Nies D.H.,
RA Niesbach-Kloege U., Patschkowski T., Rueckert C., Rupp O.,
RA Schaefer S., Schuster S.C., Vorholter F.J., Weber E., Puhler A.,
RA Bonas U., Bartels D., Kaiser O.;
RT "Insights into genome plasticity and pathogenicity of the plant
RT pathogenic bacterium Xanthomonas campestris pv. vesicatoria revealed
RT by the complete genome sequence.";
RL J. Bacteriol. 187:7254-7266 (2005).
CC
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CC
CC -----
DR EMBL; AM039952; CAJ24142.1; -; Genomic DNA.
KW Complete proteome.
SQ SEQUENCE 33 AA; 3989 MW; 89DBE37213BDA56A CRC64;

Query Match 33.3%; Score 32; DB 2; Length 33;
Best Local Similarity 75.0%; Pred. No. 8.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FNDVTTRL 13
Db 6 FNDFTSRL 13

RESULT 17
Q7RGG7 PLAYO
ID Q7RGG7 PLAYO PRELIMINARY; PRT; 38 AA.
AC Q7RGG7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein (fragment).
GN ORFNames=PY04380;
OS Plasmodium yoelii yoelii.
OX Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=17XNL;
RA MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC EMBL: AABL01001326; EAA16237.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 38 AA; 4196 MW; 91D16D82B3DA856D CRC64;

Query Match 33.3%; Score 32; DB 2; Length 38;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 7; Conservative 3; Mismatches 5; Indels 6; Gaps 1;

QY 3 HCNFN-----DVTTLRLRE 17
DB 12 HDNFNTASISDITNKNDND 32

RESULT 18
Q9Q585_9HIV1 PRELIMINARY; PRT; 40 AA.
AC Q9Q585;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Envelope glycoprotein V2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;

[1]
RN RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=20179240; PubMed=10716496;
RX DOI=10.1097/00002030-200002180-00002;
RA Wang B., Spira T.J., Owen S., Lal R.B., Saksena N.K.;
RT "HIV-1 strains from a cohort of American subjects reveal the presence
RT of a V2 region extension unique to slow progressors and non-
RT progressors.";
RL AIDS 14:213-223(2000).

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CC EMBL: AF203208; AAF24357.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4752 MW; 4F4B09F439C42D2C CRC64;

Query Match 32.8%; Score 31.5; DB 2; Length 40;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 4 CNFNDVTVTLRL 14
DB 1 CSFN-ITTNIR 10

RESULT 19
Q72871_YEAST PRELIMINARY; PRT; 25 AA.
AC Q72871;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE YJL108Cp (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
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RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=s288c;
RX MEDLINE=22728591; PubMed=12844361; DOI=10.1186/gb-2003-4-7-r45;
RA Brachat S., Dietrich F.S., Voegelé S., Zhang Z., Stuart L., Lerch A.,
RA Gates K., Gaffney T.D., Philippsen P.;
RT "Reinvestigation of the Saccharomyces cerevisiae genome annotation by
RT comparison to the genome of a related fungus: Ashbya gossypii.";
RL Genome Biol. 4:RESEARCH45.1-RESEARCH45.13(2003).

[2]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=s288c;
RX MEDLINE=96208490; PubMed=8641269;
RA Galibert F., Alexandraki D., Baur A., Boles E., Chalwatzis N.,
RA Chuat J.-C., Coster F., Cziepluch C., de Haan M., Domdey H.,
RA Durand P., Entian K.-D., Gätius M., Goffeau A., Grivell L.A.,
RA Hennemann A., Herbert C.J., Heumann K., Hilger F., Hollenberg C.P.,
RA Huang M.-E., Jacq C., Jauniaux J.-C., Katsoulou C., Kirchrath L.,
RA Kleine K., Kordes B., Koetter P., Liebi S., Louis E.J., Pohl T.M.,
RA Mewes H.-W., Miosga T., Obermaier B., Perea J., Pohl T.M.,
RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rasmussen S.W.,
RA Rose M., Rossau R., Schaaff-Gerstenschlaeger I., Smits P.H.M.,
RA Scarcez T., Soriano N., To Van D., Tzermia M., Van Broekhoven A.,
RA Vandenbol M., Wedler H., von Wettstein D., Wambutt R., Zagulski M.,
RA Zollner A., Karpfinger-Hartl L.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT X.";
RL EMBL J. 15:2031-2049(1996).

[3]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=s288c;
RX Stuart L.T., Dietrich F.S.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

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CC EMBL: AY227895; AAQ17204.1; -; Genomic DNA.
FT NON_TER 25
FT NON_TER 25
SQ SEQUENCE 25 AA; 2727 MW; 65C3140FF80FAE91 CRC64;

Query Match 32.3%; Score 31; DB 2; Length 25;
Best Local Similarity 54.5%; Pred. No. 9.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 NFNDVTVTLRL 15
DB 4 SFGDATTITSE 14

RESULT 20
Q936D3_STAUA PRELIMINARY; PRT; 26 AA.
ID Q936D3;
AC Q936D3;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Ribonucleotide-diphosphate reductase alpha chain (EC 1.17.4.1)
DE (Fragment).
GN Name=nrds;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;

[1]
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RN4220;
RX MEDLINE=21574164; PubMed=11717286;
RX DOI=10.1128/JB.183.24.7260-7272.2001;
RA Masalha M., Borovok I., Schreiber R., Aharonowitz Y., Cohen G.;
RT "Analysis of transcription of the Staphylococcus aureus aerobic class
RT Ib and anaerobic class III ribonucleotide reductase genes in response
RT to oxygen.";
RL J. Bacteriol. 183:7260-7272(2001).
```

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RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM4220;
RA Borovok I.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ312387; CA43040.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004748; F:ribonucleoside-diphosphate reductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 26
SQ SEQUENCE 26 AA; 3241 MW; D3C2A97CA637EC3A CRC64;

Query Match 32.3%; Score 31; DB 2; Length 26;
Best Local Similarity 31.2%; Pred. No. 9.6e+02;
Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTVTRLEN 16
Db 9 YNHIELNNEVTKRED 24

RESULT 21
ID Q9NBX1_ACRPR PRELIMINARY; PRT; 27 AA.
AC Q9NBX1;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE PaxC homeodomain protein (fragment).
OS Acropora prolifera (Fused staghorn coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Hexacorallia; Scleractinia;
OC Astrocenina; Acroporidae; Acropora.
OX NCBI_TaxID=12781;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20428317; PubMed=10972775;
RA van Oppen M.J.H., Willis B.L., van Vugt H.W.J.A., Miller D.J.;
RT "Examination of species boundaries in the Acropora cervicornis group
(Scleractinia, Chnidaria) using nuclear DNA sequence analyses.";
RL Mol. Ecol. 9:1363-1373(2000).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC -----
DR EMBL; AF238298; AAF97751.1; -; Genomic DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR DNA-binding; Homeobox; Nuclear protein.
KW NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3267 MW; ABB0700308F6E152 CRC64;

Query Match 32.3%; Score 31; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTVTR 12
Db 2 FEKSHYDPVATR 13

RESULT 23
ID Q735G0_BACC1 PRELIMINARY; PRT; 34 AA.
AC Q735G0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
GN ORFNames=BCE 3192;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/ghk258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
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CC -----
DR EMBL; AE017194; AAS42102.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 34 AA; 4199 MW; 98FD856B4CD0C936 CRC64;

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ID Q9NBX2_ACRCE PRELIMINARY; PRT; 28 AA.
AC Q9NBX2;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE PaxC homeodomain protein (fragment).
OS Acropora cervicornis (Staghorn coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Hexacorallia; Scleractinia;
OC Astrocenina; Acroporidae; Acropora.
OX NCBI_TaxID=6130;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20428317; PubMed=10972775;
RA van Oppen M.J.H., Willis B.L., van Vugt H.W.J.A., Miller D.J.;
RT "Examination of species boundaries in the Acropora cervicornis group
(Scleractinia, Chnidaria) using nuclear DNA sequence analyses.";
RL Mol. Ecol. 9:1363-1373(2000).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC -----
DR EMBL; AF238298; AAF97751.1; -; Genomic DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR DNA-binding; Homeobox; Nuclear protein.
KW NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3267 MW; ABB0700308F6E152 CRC64;

Query Match 32.3%; Score 31; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FEHCNFDVTVTR 12
Db 2 FEKSHYDPVATR 13

RESULT 23
ID Q735G0_BACC1 PRELIMINARY; PRT; 34 AA.
AC Q735G0;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
GN ORFNames=BCE 3192;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/ghk258;
RA Raeko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
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CC -----
DR EMBL; AE017194; AAS42102.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 34 AA; 4199 MW; 98FD856B4CD0C936 CRC64;

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Query Match      32.3%; Score 31; DB 2; Length 34;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 NDVTTTLREN 16
DB 9 NDVLRKRVNEN 18

RESULT 24
Q7M2P7_HORSE PRELIMINARY; PRT; 35 AA.
AC Q7M2P7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Basic eosinophil protein B3 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93249399; PubMed=8484750;
RA Piller K., Portmann P.;
RT "Isolation and characterization of four basic proteins from horse
RT eosinophilic granules.";
RL Biochem. Biophys. Res. Commun. 192:373-380(1993).
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CC
DR PIR; P0458; P0458.
DR GO; GO:0008955; P:immune response; IEA.
DR InterPro; IPR002352; E:Major Basic.
DR PANTHER; PTHR10068; E:Major_Basic; 1.
FT NON_TER 1 1
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 4121 MW; 742D424843BBDAB8 CRC64;

Query Match      32.3%; Score 31; DB 2; Length 35;
Best Local Similarity 42.9%; Pred. No. 1.3e+03;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 CNFNDVTTTLREN 17
DB 3 CRFIVVSTAMKYNE 16

RESULT 25
Q4XK38_PLACH PRELIMINARY; PRT; 36 AA.
AC Q4XK38;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
DE ORFNames=PC400348.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriaman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandram M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
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transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC
DR EMBL; CAAJ01005274; CAH82724.1; -; Genomic_DNA.
KW Hypothetical protein..
FT NON_TER 1 1
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 4023 MW; AA2F1701B16F8135 CRC64;

Query Match      32.3%; Score 31; DB 2; Length 36;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 NFNDVTTTLREN 17
DB 17 NSNDITSSLESE 29

RESULT 26
Q2KFJ8_MAGGR PRELIMINARY; PRT; 37 AA.
AC Q2KFJ8;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DT 07-MAR-2006, entry version 1.
DE Hypothetical protein.
DE ORFNames=MG3 ch7g687;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.
OC NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Thon M.R., Pan H., Diener A., Papalas J., Taro A., Mitchell T.,
RA Dean R.A.;
RT "The sequence of Magnaporthe grisea chromosome 7.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; CM000230; EAQ71280.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 37 AA; 4088 MW; DB126P856E7E2306 CRC64;

Query Match      32.3%; Score 31; DB 2; Length 37;
Best Local Similarity 63.6%; Pred. No. 1.4e+03;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 NFNDVTTTLRE 15
DB 9 SFCDATTLRE 19

RESULT 27
Q9NBX3_ACRPL PRELIMINARY; PRT; 40 AA.
AC Q9NBX3;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE PaxC homeodomain protein (Fragment).
OS Acropora palmata (Elkhorn coral).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Scleractinia;
OC Asterozoa; Acroporidae; Acropora.
OC NCBI_TaxID=6131;
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RN NUCLEOTIDE SEQUENCE
RP MEDLINE=20428317; PubMed=10972775;
RA van Oppen M.J.H., Willis B.L., van Vugt H.W.J.A., Miller D.J.;
RT "Examination of species boundaries in the Acropora cervicornis group
RL (Scleractinia, Cnidaria) using nuclear DNA sequence analyses.";
RL Mol. Ecol. 9:1363-1373(2000).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC -----
DR EMBL: AF238297; AAF97750.1; -; Genomic_DNA.
DR HSSP: P05601; 1FEL.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR012287; Homeodomain-rel.
DR Pfam: PF00046; Homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PROSITE: PS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
SQ SEQUENCE 40 AA; 4797 MW; 7F1368FC591FD1AB CRC64;

Query Match 32.3%; Score 31; DB 2; Length 40;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTR 12
   |||::|||
DB 11 FEKSHYFDVATR 22

RESULT 28
Q9YNX9_9HIV1
ID Q9YNX9_9HIV1 PRELIMINARY; PRT; 36 AA.
AC Q9YNX9;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE
RP MEDLINE=98019132; PubMed=9358100;
RA Rencher S.D., Hurwitz J.L.;
RT "Effect of natural HIV-1 envelope V1-V2 sequence diversity on the
RL binding of V3-specific and non-V3-specific antibodies.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 16:69-73(1997).
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CC -----
DR EMBL: U76691; AAD09591.1; -; Genomic DNA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON TER 1
FT NON TER 36
SQ SEQUENCE 36 AA; 4054 MW; 0312C6A9A9889A99 CRC64;

Query Match 31.8%; Score 30.5; DB 2; Length 36;
Best Local Similarity 35.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 2 EHCNFDVTVTLRE 15

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Db 18 QNCSFN-IATSIRD 30
::|||::|||
RESULT 29
Q905C4_9HIV1
ID Q905C4_9HIV1 PRELIMINARY; PRT; 40 AA.
AC Q905C4;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE
RP MEDLINE=21535984; PubMed=11679153; DOI=10.1089/088922201753197079;
RA Jansson M., Backstrom B., Scarlatti G., Bjorndal A., Matsuda S.,
RA Rossi P., Albert J., Wigzell H.;
RT "Length variation of glycoprotein 120 V2 region in relation to
RL biological phenotypes and coreceptor usage of primary HIV type 1
RL isolates.";
RL AIDS Res. Hum. Retroviruses 17:1405-1414(2001).
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CC -----
DR EMBL: AF417523; AAL05063.1; -; Genomic_DNA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW Envelope protein.
FT NON TER 1
FT NON TER 40
SQ SEQUENCE 40 AA; 4760 MW; EBB0940D16AA9F08 CRC64;

Query Match 31.8%; Score 30.5; DB 2; Length 40;
Best Local Similarity 54.5%; Pred. No. 1.9e+03;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 4 CNFNDVTVTLRL 14
   |||::|||
DB 1 CSFK-ITRIR 10

RESULT 30
Q4XG21_PLACH
ID Q4XG21_PLACH PRELIMINARY; PRT; 19 AA.
AC Q4XG21;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC401941.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN NUCLEOTIDE SEQUENCE
RP PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).

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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAJ01006554; CAH84147.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2115 MW; DBC03785868F393C CRC64;

Query Match 31.2%; Score 30; DB 2; Length 19;
Best Local Similarity 46.2%; Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 FEHCNPNVTTRL 13
Db 5 FFHLCINWTTKL 17

RESULT 31
QYWA3 9CNID PRELIMINARY; PRT; 27 AA.
AC QYWA3;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Pox2 (Fragment).
OS Parazoanthus parasiticus.
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Hexacorallia; Zoanthidea;
OC Parazoanthidae; Parazoanthus.
OX NCBI_TaxID=200868;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hill A.L., Wagner A., Hill M.S.;
RT "Hox and paraxox genes from the anthozoan Parazoanthus parasiticus.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -----
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CC -----
DR EMBL; AF525471; AAQ08943.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEOBOX.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 3321 MW; 1E919B3F45CDB7AF CRC64;

Query Match 31.2%; Score 30; DB 2; Length 27;
Best Local Similarity 53.8%; Pred. No. 1.5e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 NFNDVTVTLRENE 17
Db 1 NRRNYLTLRRVE 13

RESULT 32
Q3KD33 PSSEPF PRELIMINARY; PRT; 30 AA.
AC Q3KD33;
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 08-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 4.
DE Probable dehydrogenase.
GN OrderedLocusNames=Pfl_2421;

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OS Pseudomonas fluorescens (strain PFO-1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205922;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Istrati S., Pitluck S., Saunders E.H., Schmutz J.,
RA Larimer F., Land M., Kyrpides N., Anderson I., Richardson P.;
RA "Complete sequence of Pseudomonas fluorescens PFO-1.";
RT Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000094; ABA74162.1; -; Genomic_DNA.
DR InterPro; IPR002453; Beta_tubulin.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 30 AA; 3532 MW; 432B973CA8661915 CRC64;

Query Match 31.2%; Score 30; DB 2; Length 30;
Best Local Similarity 55.6%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 DVTTRLREN 16
Db 7 EITTRIRFN 15

RESULT 33
Q6W4V8 HUMAN PRELIMINARY; PRT; 34 AA.
AC Q6W4V8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE AAA1 variant IX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15073379; DOI=10.1126/science.1090010;
RA Laitinen T., Polvi A., Rydman P., Vendelin J., Pulkkinen V.,
RA Salmikangas P., Mäkelä S., Rehn M., Pirskanen A., Rautanen A.,
RA Zucchelli M., Gullsten H., Leino M., Alenius H., Petäeys T.,
RA Haahela T., Laitinen A., Laprise C., Hudson T.J., Laitinen L.A.,
RA Kere J.;
RT "Characterization of a common susceptibility locus for asthma-related
RT traits.";
RL Science 304:300-304(2004).
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CC -----
DR EMBL; AY312373; AAQ85141.1; -; mRNA.
SQ SEQUENCE 34 AA; 4013 MW; BC6709DD92192A7B CRC64;

Query Match 31.2%; Score 30; DB 2; Length 34;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNPN 7
Db 17 FSHCNLH 23

RESULT 34
QSDV85_9D1PT

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```

ID Q5DV85 9DIPT PRELIMINARY; PRT; 37 AA.
AC Q5DV85;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 23-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Acetylcholinesterase (Fragment).
GN Name=ace-1;
OS Dilophus sp. OR09.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Bibionidae; Bibionidae;
OC Dilophus.
OX NCBI_TaxID=304247;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR09;
RA Huchard E., Martinez M., Douzery E., Alout H., Berthomieu A.,
RA Berticat C., Raymond M., Weill M.;
RA "True flies don't have it. . .";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ865851; CAI29783.1; -; mRNA.
FT NON_TER 1
FT NON_TER 37
FT NON_TER 37
SQ SEQUENCE 37 AA; 4594 MW; 042F8E261A643BCF CRC64;

Query Match 31.2%; Score 30; DB 2; Length 37;
Best Local Similarity 35.7%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 CNFNDVTVRLRENE 17
DB 4 CNVNEFANRYAKEE 17

RESULT 35
ID Q3AFF1_CARHZ PRELIMINARY; PRT; 38 AA.
AC Q3AFF1;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN OrderedlocusNames=CHY_0261;
OS Carboxydothermus hydrogenoformans (strain Z-2901 / DSM 6008).
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae;
OC Carboxydothermus.
OX NCBI_TaxID=246194;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16311624; DOI=10.1371/journal.pgen.0010065;
RA Wu M., Ren Q., Durkin A.S., Daugherty S.C., Brinkac L.M., Dodson R.J.,
RA Madupu R., Sullivan S.A., Kolonay J.F., Nelson W.C., Tallon L.J.,
RA Jones K.M., Ulrich L.E., Gonzalez J.M., Zhulin I.B., Robb F.T.,
RA Eisen J.A.;
RT "Life in hot carbon monoxide: the complete genome sequence of
RT Carboxydothermus hydrogenoformans Z-2901.";
RL PLoS Genet. 1:563-574(2005).
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CC -----
DR EMBL; CP000141; ABB15720.1; -; Genomic_DNA.
DR TIGR; CHY 0261; -
KW Complete Proteome; Hypothetical protein.
SQ SEQUENCE 38 AA; 4585 MW; C4DAAAEE9E7A39D9 CRC64;

Query Match 31.2%; Score 30; DB 2; Length 38;
Best Local Similarity 55.6%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;


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QY 1 FEHCNFNDV 9
DB 17 FYHLNFQDL 25

RESULT 36
ID P82561_STRPY PRELIMINARY; PRT; 40 AA.
AC P82561;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Unknown protein from 2D-page (Fragments).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA VanBogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins.";
RL Submitted (MAY-2000) to Swiss-Prot.
CC -1- MASS SPECTROMETRY: MW=26504.12; METHOD=Electrospray.
CC -----
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CC -----
FT NON_TER 1
FT NON_TER 13
FT NON_TER 14
FT NON_TER 40
SQ SEQUENCE 40 AA; 4677 MW; FD9C6797480D4262 CRC64;

Query Match 31.2%; Score 30; DB 2; Length 40;
Best Local Similarity 45.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 NFNDVTVRLRE 15
DB 20 NFEDLITGIHQ 30

RESULT 37
ID Q9YNX4_9HIV1 PRELIMINARY; PRT; 27 AA.
AC Q9YNX4;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98019132; PubMed=9358100;
RA Rencher S.D., Hurwitz J.L.;
RT "Effect of natural HIV-1 envelope V1-V2 sequence diversity on the
RT binding of V3-specific and non-V3-specific antibodies.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 16:69-73(1997).
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CC -----
DR EMBL; U76696; AAD09596.1; -; Genomic_DNA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Envelope protein.
KW Envelope protein.


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FT  NON TER      1      1
FT  NON TER      27     27
SQ  SEQUENCE    27 AA;  3078 MW;  F4484AGE3CF8829A CRC64;

Query Match      30.7%; Score 29.5; DB 2; Length 27;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      2 EHCNFDVTVRL 13
       :.:||| ||| :
DB      9 KNCSFN-VTTNI 19

RESULT 38
Q4VFL9 PLABE
ID  Q4VFL9 PLABE      PRELIMINARY; PRT; 27 AA.
AC  Q4VFL9
DT  05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2005, sequence version 1.
DT  07-FEB-2006, entry version 4.
DE  Hypothetical protein (Fragment).
GN  ORFNames=PB404363.00.0;
OS  Plasmodium berghei.
OC  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX  NCBI_TaxID=5821;
[1]
NUCLEOTIDE SEQUENCE.
RP  PubMed=15637271; DOI=10.1126/science.1103717;
RX  Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA  Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA  James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA  Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA  Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA  Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA  Sinden R.S.;
RT  "A comprehensive survey of the Plasmodium life cycle by genomic,
RT  transcriptomic, and proteomic analyses.";
RL  Science 307:82-86(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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-----
DR  EMBL; CAAI01005598; CAI03199.1; -; Genomic_DNA.
KW  Hypothetical protein.
FT  NON TER      1
SQ  SEQUENCE    27 AA;  3281 MW;  DC160FDC45AA63D CRC64;

Query Match      30.2%; Score 29; DB 2; Length 27;
Best Local Similarity 71.4%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FEHCNFN 7
       :.:|||
DB      17 FGHLEN 23

RESULT 39
Q711X3 BRAEL
ID  Q711X3 BRAEL      PRELIMINARY; PRT; 33 AA.
AC  Q711X3
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  07-FEB-2006, entry version 5.
DE  NodB protein (Fragment).
GN  Name=nodB;
OS  Bradyrhizobium elkanii.
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC  Bradyrhizobiaceae; Bradyrhizobium.
OX  NCBI_TaxID=29448;
[1]

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RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=USDA61;
RA  Moulain L.;
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
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DR  EMBL; AJ300251; CAC82876.1; -; Genomic DNA.
DR  GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. .; IEA.
DR  GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR  InterPro; IPR002509; Polyac_deacet.
DR  Pfam; PF01522; Polyacac_deac_1; 1.
FT  NON TER      33     33
SQ  SEQUENCE    33 AA;  3588 MW;  9EBC8FDA61A204BC CRC64;

Query Match      30.2%; Score 29; DB 2; Length 33;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 CNFNDVT 10
       :.:|||
DB      12 CNYGDS 18

RESULT 40
Q7VNY8 HAEDU
ID  Q7VNY8 HAEDU      PRELIMINARY; PRT; 34 AA.
AC  Q7VNY8
DT  01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT  01-OCT-2003, sequence version 1.
DT  07-FEB-2006, entry version 9.
DE  Hypothetical protein.
GN  OrderedLocuNames=HD0332; ORFNames=HD_0332;
OS  Haemophilus ducreyi.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Haemophilus.
OX  NCBI_TaxID=730;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC  STRAIN=3500HP / ATCC 700724;
RA  Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA  Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT  "The complete genome sequence of Haemophilus ducreyi.";
RL  Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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-----
DR  EMBL; AE017143; AAP95309.1; -; Genomic DNA.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE    34 AA;  3917 MW;  E2D91C3C778B9F8C CRC64;

Query Match      30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 38.9%; Pred. No. 2.8e+03;
Matches 7; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY      1 FEHC--NFNDVTVRL 16
       :.:||| :.:|||
DB      9 FTHCFISINYCIGRES 26

RESULT 41
Q6E460 9PERC
ID  Q6E460 9PERC      PRELIMINARY; PRT; 34 AA.
AC  Q6E460;
DT  16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT  16-AUG-2004, sequence version 1.
DT  07-FEB-2006, entry version 10.
DE  Creatine kinase (Fragment).
OS  Steellerina xyosterna.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

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OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Agonidae; Brachyopsinae; Stellerina.
OX NCBI_TaxID=283639;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
  approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583148; AAT67127.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTTLRL 14
Db |::|
1 FEEILTLRL 9

RESULT 42
Q6E461_9PERC
ID Q6E461_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E461;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Leptocottus armatus (Pacific staghorn sculpin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Leptocottus.
OX NCBI_TaxID=214925;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
  approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583147; AAT67126.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTTLRL 14
Db |::|
1 FEEILTLRL 9
```

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Db |::|
1 FEEILTLRL 9

RESULT 43
Q6E462_9PERC
ID Q6E462_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E462;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Jordania zonope.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Jordania.
OX NCBI_TaxID=274764;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
  approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583146; AAT67125.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTTLRL 14
Db |::|
1 FEEILTLRL 9

RESULT 44
Q6E463_9PERC
ID Q6E463_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E463;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Rhamphocottus richardsonii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Rhamphocottidae; Rhamphocottus.
OX NCBI_TaxID=283636;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
  approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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DR EMBL; AY583145; AAT67124.1; -; Genomic DNA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
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KW Kinase.
FT NON_TER 1 1
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Query Match 30.2%; Score 29; DB 2; Length 34;
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QY 6 FNDVTRLR 14
| : : ||||
Db 1 FEEILTRLR 9

RESULT 45
Q6E464_9PERC
ID Q6E464_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E464;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Chitonotus pugetensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Chitonotus.
OX NCBI_TaxID=283635;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT approach.
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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DR EMBL; AY583144; AAT67123.1; -; Genomic DNA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
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Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTRLR 14
| : : ||||
Db 1 FEEILTRLR 9

RESULT 46
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ID Q6E465_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E465;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Artedius corallinus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Artedius.
OX NCBI_TaxID=283624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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DR EMBL; AY583143; AAT67122.1; -; Genomic DNA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 34 34
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Query Match 30.2%; Score 29; DB 2; Length 34;
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Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTRLR 14
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Db 1 FEEILTRLR 9

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AC Q6E466;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Scorpaenichthys marmoratus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Scorpaenichthys.
OX NCBI_TaxID=52273;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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DR EMBL; AY583142; AAT67121.1; -; Genomic DNA.
DR GO; GO:0016301; P:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy 6 FNDVTTTLR 14
Db 1 FEEILTLR 9

RESULT 48
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AC Q6E467;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Zaniolepis latipinnis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammoidei; Zaniolepididae; Zaniolepis.
OX NCBI_TaxID=283621;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583141; AAT67120.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrns.
DR PANTHER; PTHR11547; ATP-gua_Ptrns; 1.
DR Pfam; PF00217; ATP-gua_Ptrns; 1.
DR NCBI_TaxID=283621;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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Qy 6 FNDVTTTLR 14
Db 1 FEEILTLR 9

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 49
ID Q6E468_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E468;
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DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Oxyblebium pictus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammoidei; Hexagrammidae; Oxyblebium.
OX NCBI_TaxID=283620;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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Qy 6 FNDVTTTLR 14
Db 1 FEEILTLR 9

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 50
ID Q6E469_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E469;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Ophiodon elongatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammoidei; Hexagrammidae; Ophiodon.
OX NCBI_TaxID=225387;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
Qy 6 FNDVTTTLR 14
Db 1 FEEILTLR 9

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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DR PANTHER; PTHR11547; ATP-gua_Ptrns; 1.
DR Pfam; PF00217; ATP-gua_Ptrns; 1.
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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Qy 6 FNDVTTTLR 14
Db 1 FEEILTLR 9

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 51
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AC Q6E470;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Hexagrammos decagrammus.
OX NCBI_TaxID=283620;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
Qy 6 FNDVTTTLR 14
Db 1 FEEILTLR 9

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammidae; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=274741;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583138; AAT67117.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP_gua_Ptrans.
DR PANTHER; PTHR11547; ATP_gua_Ptrans; 1.
DR Pfam; PF00217; ATP_gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1 1
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Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVITRLR 14
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Db 1 FEEILTRLR 9

RESULT 52
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ID Q6E471 9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E471
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 11.
DE Creatine kinase (Fragment).
OS Hexagrammos stelleri (white-spotted greenling).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammidae; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=192378;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583137; AAT67116.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP_gua_Ptrans.
DR PANTHER; PTHR11547; ATP_gua_Ptrans; 1.
DR Pfam; PF00217; ATP_gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 34 34
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Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVITRLR 14
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Db 1 FEEILTRLR 9

RESULT 53
Q6E472 9PERC
ID Q6E472 9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E472
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Hexagrammos lagocephalus (rock greenling).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammidae; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=192377;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583136; AAT67115.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP_gua_Ptrans.
DR PANTHER; PTHR11547; ATP_gua_Ptrans; 1.
DR Pfam; PF00217; ATP_gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 34 34
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Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVITRLR 14
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Db 1 FEEILTRLR 9

RESULT 54
Q6E473 9PERC
ID Q6E473 9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E473
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Hexagrammos superciliosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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QY 6 FNDVITRLR 14
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Db 1 FEEILTRLR 9

RESULT 53
Q6E472 9PERC
ID Q6E472 9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E472
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Hexagrammos lagocephalus (rock greenling).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammidae; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=192377;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583136; AAT67115.1; -; Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP_gua_Ptrans.
DR PANTHER; PTHR11547; ATP_gua_Ptrans; 1.
DR Pfam; PF00217; ATP_gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVITRLR 14
|::|
Db 1 FEEILTRLR 9

RESULT 54
Q6E473 9PERC
ID Q6E473 9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E473
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Hexagrammos superciliosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammidae; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=283616;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583135; AAT67114.1; -: Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FNDVTTLRL 14
Db 1 FEILTLRL 9

RESULT 55
Q6E474_9PERC
ID Q6E474_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E474;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Hexagrammos octogrammus (masked greenling).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammoidei; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=192375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583134; AAT67113.1; -: Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FNDVTTLRL 14
Db 1 FEILTLRL 9

RESULT 56
Q6E475_9PERC
ID Q6E475_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E475;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).

```

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OS Hexagrammos otakii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammoidei; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=72450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583133; AAT67112.1; -: Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FNDVTTLRL 14
Db 1 FEILTLRL 9

RESULT 57
Q6B476_9PERC
ID Q6E476_9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E476;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Hexagrammos agrammus
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Hexagrammoidei; Hexagrammidae; Hexagrammos.
OX NCBI_TaxID=192376;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
RT approach.";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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CC -----
DR EMBL; AY583132; AAT67111.1; -: Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000749; ATP-gua_Ptrans.
DR PANTHER; PTHR11547; ATP-gua_Ptrans; 1.
DR Pfam; PF00217; ATP-gua_Ptrans; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 3679 MW; DF409F8FE0347540 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;

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Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTRLR 14
| : : ||||
Db 1 FBEILTRLR 9

RESULT 58
Q6E477 9PERC
ID Q6E477 9PERC PRELIMINARY; PRT; 34 AA.
AC Q6E477
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE Creatine kinase (Fragment).
OS Sebastes atrovirens.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Scorpaenidae; Sebastidae; Sebastinae; Sebastes.
OX NCBI_TaxID=72056;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15288071; DOI=10.1016/j.ympev.2004.03.012;
RA Crow K.D., Kanamoto Z., Bernardi G.;
RT "Molecular phylogeny of the hexagrammid fishes using a multi-locus
approach";
RL Mol. Phylogenet. Evol. 32:986-997(2004).
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QY 6 FNDVTRLR 14
| : : ||||
Db 1 FBEILTRLR 9

RESULT 59
Q2SQL3 9GAMM
ID Q2SQL3 9GAMM PRELIMINARY; PRT; 35 AA.
AC Q2SQL3
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=HCH_00142;
OS Haella chejuensis KCTC 2396.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Haellaceae; Haella.
OX NCBI_TaxID=349521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=KCTC 2396;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.-K., Oh T.K., Kim J.F.;
RT "Genomic blueprint of Haella chejuensis, a marine microbe producing
an algicidal agent.";

Query Match 30.2%; Score 29; DB 2; Length 34;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FNDVTRLR 14
| : : ||||
Db 1 FBEILTRLR 9

RESULT 60
TOTIA ATRRO
ID TOTIA ATRRO STANDARD; PRT; 37 AA.
AC P83580;
DT 27-JUN-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-MAR-2006, entry version 19.
DE Omega-atracotoxin-Ar1a (Omega-ACTX-Ar1a).
OS Atrax robustus (Funnel-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Hexathelidae; Atrax.
OX NCBI_TaxID=6903;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
SPECTROMETRY.
RC TISSUE=Venom.
RA Hayes J., Wen S., Yang Q., Hains P.G., Broady K.R., Nicholson G.M.;
RL Submitted (MAY-2003) to Swiss-Prot.
CC -!- FUNCTION: Potent inhibitor of insect, but not mammalian, voltage-
gated calcium channel currents (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=4003; METHOD=Electrospray; RANGE=1-37;
NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the omega-atracotoxin type 1 family.
CC
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QY 6 FNDVTRLR 14
| : : ||||
Db 1 FBEILTRLR 9

RESULT 61
Q2SQL3 9GAMM
ID Q2SQL3 9GAMM PRELIMINARY; PRT; 35 AA.
AC Q2SQL3
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=HCH_00142;
OS Haella chejuensis KCTC 2396.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Haellaceae; Haella.
OX NCBI_TaxID=349521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=KCTC 2396;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.-K., Oh T.K., Kim J.F.;
RT "Genomic blueprint of Haella chejuensis, a marine microbe producing
an algicidal agent.";

Query Match 30.2%; Score 29; DB 1; Length 37;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 EHCNFDVTRLR 16
| : : ||||
Db 15 EHCNFDVTRLR 29

RL Nucleic Acids Res. 33:7066-7073(2005).
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QY 3 HCNF 6
| : : ||||
Db 26 HCNF 29

Query Match 30.2%; Score 29; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCNF 6
| : : ||||
Db 26 HCNF 29

RESULT 62
TOTIA ATRRO
ID TOTIA ATRRO STANDARD; PRT; 37 AA.
AC P83580;
DT 27-JUN-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-MAR-2006, entry version 19.
DE Omega-atracotoxin-Ar1a (Omega-ACTX-Ar1a).
OS Atrax robustus (Funnel-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Hexathelidae; Atrax.
OX NCBI_TaxID=6903;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
SPECTROMETRY.
RC TISSUE=Venom.
RA Hayes J., Wen S., Yang Q., Hains P.G., Broady K.R., Nicholson G.M.;
RL Submitted (MAY-2003) to Swiss-Prot.
CC -!- FUNCTION: Potent inhibitor of insect, but not mammalian, voltage-
gated calcium channel currents (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=4003; METHOD=Electrospray; RANGE=1-37;
NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the omega-atracotoxin type 1 family.
CC
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QY 3 HCNF 6
| : : ||||
Db 26 HCNF 29

Query Match 30.2%; Score 29; DB 1; Length 37;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 6; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 EHCNFDVTRLR 16
| : : ||||
Db 15 EHCNFDVTRLR 29

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RESULT 61
Q91XM5_RAT
ID Q91XM5_RAT PRELIMINARY; PRT; 38 AA.
AC Q91XM5;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Homeodomain protein PAX3 (Fragment).
GN Name=Pax3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=U;WU; TISSUE=Dorsal root ganglion;
RA Vogelaar C.F., Smits S.M., Brakkee J.H., Gispén W.H., Smidt M.P.,
RA Schrama L.H., Hoekman M.P.M., Burbach J.P.H.;
RT "Homeobox gene repertoire in adult rat dorsal root ganglia.";
RL Neurosci. Res. Commun. 32:49-59(2003).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC EMBL; AF390074; AAK70501.1; -; mRNA.
CC HSP5; P06601; 1FJL.
CC Ensembl; ENSRNOG00000013670; Rattus norvegicus.
CC GDI; G20431; Pax3.
CC GO; GO:0003700; P:transcription factor activity; NAS.
CC GO; GO:0042063; P:glucogenesis; NAS.
CC GO; GO:0042063; P:glucogenesis; NAS.
CC InterPro; IPR01356; Homeobox.
CC InterPro; IPR012287; Homeodomain-rel.
CC Pfam; PF00046; Homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC PROSITE; PSS0071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
FT NON TER 38
SQ SEQUENCE 38 AA; 4590 MW; CE354E53B338D358 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 38;
Best Local Similarity 41.7%; Pred. No. 3.2e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTR 12
DB 11 FERTHYFDIVTR 22
|||:|:|:|
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RESULT 62
Q79DP5_BACTU
ID Q79DP5_BACTU PRELIMINARY; PRT; 39 AA.
AC Q79DP5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Crystall protein (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=thompsoni;
RX MEDLINE=94075234; PubMed=7504667;
RA Brown K.L.;
RT "Transcriptional regulation of the Bacillus thuringiensis subsp.
RL J. Bacteriol. 175:7951-7957(1993).
-----
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-----
CC EMBL; AF390074; AAK70501.1; -; mRNA.
CC HSP5; P06601; 1FJL.
CC Ensembl; ENSRNOG00000013670; Rattus norvegicus.
CC GDI; G20431; Pax3.
CC GO; GO:0003700; P:transcription factor activity; NAS.
CC GO; GO:0042063; P:glucogenesis; NAS.
CC GO; GO:0042063; P:glucogenesis; NAS.
CC InterPro; IPR01356; Homeobox.
CC InterPro; IPR012287; Homeodomain-rel.
CC Pfam; PF00046; Homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC PROSITE; PSS0071; HOMEBOX 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON TER 1
FT NON TER 38
SQ SEQUENCE 38 AA; 4590 MW; CE354E53B338D358 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 38;
Best Local Similarity 41.7%; Pred. No. 3.2e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTR 12
DB 11 FERTHYFDIVTR 22
|||:|:|:|
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RESULT 63
Q5HEUL_STAAC
ID Q5HEUL_STAAC PRELIMINARY; PRT; 36 AA.
AC Q5HEUL;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN OrderedLocusNames=SACOL1890;
OS Staphylococcus aureus (Strain COL).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uitterlinden T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain."
RL J. Bacteriol. 187:2426-2438(2005).
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CC EMBL; CP000046; AAW36903.1; -; Genomic_DNA.
CC TIGR; SACOL1890; -.
CC Complete proteome; Hypothetical protein.
SQ SEQUENCE 36 AA; 4319 MW; DA051C886C404139 CRC64;

Query Match 29.7%; Score 28.5; DB 2; Length 36;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 4 CNFNDV-TTRELRENE 17
DB 4 CQFYDIYLLKIRTNE 18
|||:|:|:|
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RESULT 64
O40249_9HIV1
ID O40249_9HIV1 PRELIMINARY; PRT; 39 AA.
AC O40249;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
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CC EMBL; M90843; AAA16229.1; -; Unassigned_DNA.
CC NON TER 39
SQ SEQUENCE 39 AA; 4420 MW; 4DC469A548CE6DD9 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 39;
Best Local Similarity 36.4%; Pred. No. 3.3e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 NFNNDVTVTRLE 15
DB 2 NFNNTGNFKD 12
|||:|:|:|
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RESULT 65
Q5HEUL_STAAC
ID Q5HEUL_STAAC PRELIMINARY; PRT; 36 AA.
AC Q5HEUL;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein.
GN OrderedLocusNames=SACOL1890;
OS Staphylococcus aureus (Strain COL).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uitterlinden T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain."
RL J. Bacteriol. 187:2426-2438(2005).
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-----
CC EMBL; CP000046; AAW36903.1; -; Genomic_DNA.
CC TIGR; SACOL1890; -.
CC Complete proteome; Hypothetical protein.
SQ SEQUENCE 36 AA; 4319 MW; DA051C886C404139 CRC64;

Query Match 29.7%; Score 28.5; DB 2; Length 36;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 4 CNFNDV-TTRELRENE 17
DB 4 CQFYDIYLLKIRTNE 18
|||:|:|:|
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RESULT 66
O40249_9HIV1
ID O40249_9HIV1 PRELIMINARY; PRT; 39 AA.
AC O40249;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
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Matches	4;	Conservative	2;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	1	FEHCNFNDVT 10							
		:							
Db	4	FRCQYFNPI S 13							
RESULT 66									
ID	Q7BW21_9ZZZZ	PRELIMINARY; PRT; 16 AA.							
AC	Q7BW21;								
DT	05-JUL-2004,	integrated into UniProtKB/TrEMBL.							
DT	05-JUL-2004,	sequence version 1.							
DT	07-FEB-2006,	entry version 6.							
DE	TrailH (Fragment).								
GN	Name=trailH;								
OS	Incn plasmid pKM101.								
OC	other sequences;	broad host range plasmids.							
OX	NCBI_TaxID=192122;								
[1]									
RN	NNUCLEOTIDE SEQUENCE.								
RA	Woodgate R.;								
RL	Submitted (APR-1997)	to the EMBL/GenBank/DBJ databases.							
CC	-----								
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CC	-----								
EMBL:	AF000361;	AAB58710.1; -; Genomic_DNA.							
NON TER	16								
FT	SEQUENCE	16 AA;	1791 MW;	49BCB8E5ECBD5CE7	CRC64;				
SQ									
Query Match	29.2%;	Score	28;	DB	2;	Length	16;		
Best Local Similarity	55.6%;	Pred. No.	1.8e+03;						
Matches	5;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	8	DVITRLREN 16							
		: :							
Db	3	DITITTRON 11							
RESULT 67									
QRTM9_HUMAN									
ID	Q7RTM9_HUMAN	PRELIMINARY; PRT; 19 AA.							
AC	Q7RTM9;								
DT	15-DEC-2003,	integrated into UniProtKB/TrEMBL.							
DT	15-DEC-2003,	sequence version 1.							
DT	07-FEB-2006,	entry version 8.							
DE	Truncated RTN2-A2.								
GN	Name=RTN2;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Bukariyoka; Mammalia;	Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;							
OC	HOMO								
OX	NCBI_TaxID=9606;								
[1]									
RN	NNUCLEOTIDE SEQUENCE.								
RP	MEDLINE=22715887;	PubMed=12832288; DOI=10.1096/fj.02-1166hyp;							
RX	Oertle T., Klinger M., Stuermer C.A.O., Schwab M.E.;								
RT	"A reticular rhapsody: phylogenetic evolution and nomenclature of the								
RTN/Nogo gene family.";									
RL	FASEB J. 17:1238-1247(2003).								
CC	- - MISCELLANEOUS: The sequence shown here is derived from an								
CC	EMBL/GenBank/DBJ third party annotation (TPA) entry.								
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CC	-----								
EMBL:	BK001690;	DAA01935.1; -; mRNA.							
DR	SEQUENCE	19 AA;	2044 MW;	B910DB1ACD7F5B8A	CRC64;				
SQ									
Query Match	29.2%;	Score	28;	DB	2;	Length	19;		
Best Local Similarity	80.0%;	Pred. No.	2.2e+03;						
Matches	4;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;

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QY      1 FEHCN 5
      | | | |
Db      8 FAHCN 12

RESULT 68
Q4X533_PLACH PRELIMINARY; PRT; 21 AA.
AC Q4X533;
DT 03-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC105576.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5925;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAJ01009880; CAH8051.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 21 AA; 2629 MW; E36657CDDAE031FA CRC64;

Query Match 29.2%; Score 28; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 HCNFNDVTTR 12
      | | | |
Db      2 HVYNNITNR 11

RESULT 69
Q8X365_ECO57 PRELIMINARY; PRT; 22 AA.
AC Q8X365;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Putative transcriptional regulator.
GN OrderedLocNames=ECs2938;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX SFRAIN=O157:H7 / Sakai / RMD 0509952 / EHEC;
RC MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -----
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CC -----
DR EMBL; BAO00007; BAB36361.1; -; Genomic_DNA.
DR PIR; B90996; B90996.
DR BioCyc; ECOL83334-1:EC52938-MONOMER; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000551; HTH MerR.
DR PROSITE; PS50937; HTH MERR_2; 1.
SQ SEQUENCE 22 AA; 2377 MW; A12244C773A97E36 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 22;
Best Local Similarity 55.6%; Pred. No. 2.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4 CMFNDVTTR 12
      | | | |
Db      13 CDINPVTLR 21

RESULT 70
Q4YLA7_PLABE PRELIMINARY; PRT; 24 AA.
AC Q4YLA7;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PB401123.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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CC -----
DR EMBL; CAA101003950; CAI01204.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 24 AA; 2763 MW; CA2B5AD0BC442901 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 FEHCNENDVT 10
      | | | |
Db      13 YTFCSFNLVT 22

RESULT 71

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Q6QVF8 PHAVU
ID Q6QVF8 PHAVU PRELIMINARY; PRT; 25 AA.
AC Q6QVF8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ribonuclease H (Fragment).
GN Name=RNase H;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15060605; DOI=10.1139/g03-102;
RA Galindo L.M., Gaitan E., Baccam P., Tohme J.;
RT "Isolation and characterization of RNase-LTR sequences of Tyl-copia
retrotransposons in common bean (Phaseolus vulgaris L.).";
RL Genome 47:84-95(2004).
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CC -----
DR EMBL; AY524241; AAS18538.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2892 MW; 03E67DF735BDF384 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHC 4
DB 13 FEHC 16

RESULT 72
Q6QVG1 PHAVU
ID Q6QVG1 PHAVU PRELIMINARY; PRT; 25 AA.
AC Q6QVG1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ribonuclease H (Fragment).
GN Name=RNase H;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15060605; DOI=10.1139/g03-102;
RA Galindo L.M., Gaitan E., Baccam P., Tohme J.;
RT "Isolation and characterization of RNase-LTR sequences of Tyl-copia
retrotransposons in common bean (Phaseolus vulgaris L.).";
RL Genome 47:84-95(2004).
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CC -----
DR EMBL; AY524238; AAS18535.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2893 MW; A23C4DF735BDE4E8 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHC 4
DB 13 FEHC 16

RESULT 73
Q6QVK5 PHAVU
ID Q6QVK5 PHAVU PRELIMINARY; PRT; 25 AA.
AC Q6QVK5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ribonuclease H (Fragment).
GN Name=RNase H;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15060605; DOI=10.1139/g03-102;
RA Galindo L.M., Gaitan E., Baccam P., Tohme J.;
RT "Isolation and characterization of RNase-LTR sequences of Tyl-copia
retrotransposons in common bean (Phaseolus vulgaris L.).";
RL Genome 47:84-95(2004).
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CC -----
DR EMBL; AY524194; AAS18491.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2910 MW; B7E67DF735BDF4E9 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHC 4
DB 13 FEHC 16

RESULT 74
Q6QVK8 PHAVU
ID Q6QVK8 PHAVU PRELIMINARY; PRT; 25 AA.
AC Q6QVK8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ribonuclease H (Fragment).
GN Name=RNase H;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15060605; DOI=10.1139/g03-102;
RA Galindo L.M., Gaitan E., Baccam P., Tohme J.;
RT "Isolation and characterization of RNase-LTR sequences of Tyl-copia
retrotransposons in common bean (Phaseolus vulgaris L.).";
RL Genome 47:84-95(2004).
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CC -----
DR EMBL; AY524191; AAS18488.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2880 MW; B7E67DF735BDE4E8 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHC 4
DB 13 FEHC 16

RESULT 75
Q6QVK5 PHAVU
ID Q6QVK5 PHAVU PRELIMINARY; PRT; 25 AA.
AC Q6QVK5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ribonuclease H (Fragment).
GN Name=RNase H;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15060605; DOI=10.1139/g03-102;
RA Galindo L.M., Gaitan E., Baccam P., Tohme J.;
RT "Isolation and characterization of RNase-LTR sequences of Tyl-copia
retrotransposons in common bean (Phaseolus vulgaris L.).";
RL Genome 47:84-95(2004).
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CC -----
DR EMBL; AY524191; AAS18488.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 25 AA; 2880 MW; B7E67DF735BDE4E8 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHC 4
DB 13 FEHC 16

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Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHC 4
Db 13 FEHC 16

RESULT 75

Q6QVK9_PHAVU
ID Q6QVK9_PHAVU PRELIMINARY; PRT; 25 AA.
AC Q6QVK9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ribonuclease H (Fragment).
GN Name=RNase H;
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15060605; DOI=10.1139/g03-102;
RA Galindo J.M., Gaitan E., Baccam P., Tohme J.;
RT "Isolation and characterization of RNase-LTR sequences of Tyl-copia
RT retrotransposons in common bean (Phaseolus vulgaris L.).";
RL Genome 47:84-95(2004).
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CC -----
DR EMBL; AY524190; AAS18487.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 25 AA; 2914 MW; B7B67DF735B08988 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHC 4
Db 13 FEHC 16

RESULT 76

Q76K95_SERQU
ID Q76K95_SERQU PRELIMINARY; PRT; 25 AA.
AC Q76K95;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein ANTI-RAFI.
GN Name=ANTI-RAFI;
OS Seriola quinqueradiata (Five-ray yellowtail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciformes; Carangoidae;
OC Carangidae; Seriola.
OX NCBI_TaxID=8161;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Heart;
RA Abe S., Chiba S., Doi M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AB094039; BAC99064.1; -; Other_RNA.

KW Hypothetical protein.
SQ SEQUENCE 25 AA; 2977 MW; ABD418F304E4519D CRC64;

Query Match 29.2%; Score 28; DB 2; Length 25;
Best Local Similarity 44.4%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNFNDV 9
Db 4 FETCDSEI 12

RESULT 77

Q9UCG8_HUMAN
ID Q9UCG8_HUMAN PRELIMINARY; PRT; 28 AA.
AC Q9UCG8;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Urinary gonadotrophin peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9329246; PubMed=8471426;
RA Kardana A., Bagshaw K.D., Coles B., Read D., Taylor M.;
RT "Characterisation of UGP and its relationship with beta-core
RT fragment.";
RL Br. J. Cancer 67:686-692(1993).
CC -----
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CC -----
DR HSSP; P01233; 1HCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR PANTHER; PTHR11515; Gly_hormoneB; 1.
DR Pfam; PF00007; Cys_knot; 1.
SQ SEQUENCE 28 AA; 3150 MW; EF76A484C83D9071 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CNFNDV 9
Db 3 CNYRDV 8

RESULT 78

Q4YC14_PLABE
ID Q4YC14_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YC14;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PBL04664.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florsen L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

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RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R. III,  
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,  
RA Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcripomic, and proteomic analyses";  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC -----  
DR EMBL; CAI01006725; CAI04541.1; -; Genomic_DNA.  
KW Hypothetical protein.  
FT NON_TER 1  
FT NON_TER 28  
SQ SEQUENCE 28 AA; 3269 MW; CD40C0B7A760D179 CRC64;  
  
Query Match 29.2%; Score 28; DB 2; Length 28;  
Best Local Similarity 30.8%; Pred. No. 3.4e+03;  
Matches 4; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
  
QY 5 NFNDVTVTLRENE 17  
:|::|:|:|:  
Db 14 HFNELTKNKESK 26  
  
RESULT 79  
Q9BJES_9MYRI PRELIMINARY; PRT; 28 AA.  
AC Q9BJES;  
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2001, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE Labial-like protein (Fragment).  
OS Paupopus sp. Wye-1996.  
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Pauropoda; Pauropodidae;  
OC Paupopus.  
OX NCBI_TaxID=146863;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21272202; PubMed=11378385; DOI=10.1016/S0960-9822(01)00222-6;  
RA Cook C.E., Smith M.L., Telford M.J., Bastianello A., Akam M.;  
RT "Hox genes and the phylogeny of the arthropods";  
RL Curr. Biol. 11:759-763(2001).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
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CC -----  
DR EMBL; AF335458; AAK28137.1; -; Genomic_DNA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR012287; Homeodomain-rel.  
DR Pfam; PF00046; Homeobox.1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON_TER 1  
FT NON_TER 28  
SQ SEQUENCE 28 AA; 3389 MW; 9B40DA4D734BA25D CRC64;  
  
Query Match 29.2%; Score 28; DB 2; Length 28;  
Best Local Similarity 46.2%; Pred. No. 3.4e+03;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
QY 5 NFNDVTVTLRENE 17  
:|::|:|:|:  
Db 2 HFNKYLTVRRRIE 14
```

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RESULT 80  
Q96KT2_HUMAN PRELIMINARY; PRT; 29 AA.  
AC Q96KT2;  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE Hypothetical protein C8orf8 (Fragment).  
GN Name=C8orf8;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Appel S., Bergheim A., Reichwald K., Reis A., Rosenthal A., Ramsay M.,  
RA Hennies H.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; AJ301561; CAC82737.1; -; mRNA.  
DR Ensembl; ENSG00000196848; Homo sapiens.  
DR HGNC; HGNC:15544; C8orf8.  
KW Hypothetical protein.  
FT NON_TER 29  
FT NON_TER 29  
SQ SEQUENCE 29 AA; 3538 MW; 48FCCE2A6F1F36F8 CRC64;  
  
Query Match 29.2%; Score 28; DB 2; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 HCNFNDVTVTR 12  
|:|::|:|:  
Db 14 HMEFSELTSR 23  
  
RESULT 81  
Q3EPA2_BACTI PRELIMINARY; PRT; 29 AA.  
AC Q3EPA2;  
DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.  
DT 08-NOV-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Heptaprenyl diphosphate synthase component I (EC 2.5.1.30).  
GN ORFNames=RBTH_09230;  
OS Bacillus thuringiensis serovar israelensis ATCC 35646.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI_TaxID=339854;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 35646;  
RA Anderson I., Sorokin A., Kapatral V., Reznik G., Bhattacharya A.,  
RA Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,  
RA D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,  
RA Goldsman E., Chu L., Feinstein M., Ehrlich D., Overbeek R.,  
RA Kyrpides N., Ivanova N.;  
RT "Comparative genome analysis of Bacillus cereus group genomes with  
RT Bacillus subtilis";  
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC -----  
DR EMBL; AAJW01000296; EA053146.1; -; Genomic_DNA.  
DR GO; GO:0000010; F:trans-hexaprenyltransferase activity; IEA.
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DR GO: GO:0016740; F:transferase activity; IEA.
KW Transferase.
SQ SEQUENCE 29 AA; 3500 MW; 7C1DD8A7474CEED49 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 29;
Best Local Similarity 30.8%; Pred. No. 3.5e+03;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 HCNFNDVTRRLRE 15
| : | : | : | :
DB 16 HIDINEINSLVD 28

RESULT 82
Q5K622_HUMAN
ID Q5K622_HUMAN PRELIMINARY; PRT; 31 AA.
AC Q5K622;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE C12orf7 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schulz H.L., Stoehr H.B., Weber B.H.F.;
RT "Retina-abundant C12orf7 gene.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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-----
DR EMBL; AF517114; AAQ07993.1; -; mRNA.
DR Ensembl; ENSG00000167612; Homo sapiens.
DR InterPro; IPR002110; ANK.
FT NON_TER 1
FT NON_TER 31
SQ SEQUENCE 31 AA; 3214 MW; 1D3050F2079EBDF6 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 31;
Best Local Similarity 71.4%; Pred. No. 3.8e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HCNFNDV 9
| : | : | :
DB 8 HCPFLDV 14

RESULT 83
Q4X5L9_PLACH
ID Q4X5L9_PLACH PRELIMINARY; PRT; 33 AA.
AC Q4X5L9;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC100007.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;

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RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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-----
DR EMBL; CAAJ01009767; CAH87808.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 33
SQ SEQUENCE 33 AA; 4041 MW; 3A918363259C56ED CRC64;

Query Match 29.2%; Score 28; DB 2; Length 33;
Best Local Similarity 57.1%; Pred. No. 4.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNEN 7
| : | : | :
DB 26 FFHCSPS 32

RESULT 84
Q54AR6_DICDI
ID Q54AR6_DICDI PRELIMINARY; PRT; 33 AA.
AC Q54AR6;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
DE ORFNames=DOB0215123;
GN Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero P.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louisedge H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.C.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuepa A.;
RL "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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-----
DR EMBL; AAFI01000314; EAL60357.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 33 AA; 3924 MW; B1AAFBF70320F0E9 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 33;
Best Local Similarity 57.1%; Pred. No. 4.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 FEHCNPN 7
   ||||
Db 14 YESCRPN 20

RESULT 85
Q76K97_SERQU PRELIMINARY; PRT; 34 AA.
AC Q76K97
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein ANTI-RAPI.
GN Name=ANTI-RAPI;
OS Seriola quinqueradiata (Five-ray yellowtail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Carangidae;
OC Carangidae; Seriola.
OX NCBI_TaxID=8161;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Abe S., Chiba S., Doi M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AB094038; BAC99061.1; -; Other_RNA.
KW Hypothetical protein.
SQ SEQUENCE 34 AA; 4009 MW; 05E1A8D0A8F3F0F1 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 34;
Best Local Similarity 44.4%; Pred. No. 4.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNPN 9
   ||||
Db 4 FETCDSEI 12

RESULT 86
Q47W92_COLP3 PRELIMINARY; PRT; 35 AA.
AC Q47W92
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN OrderedLocNames=CPS_4280;
OS Colwellia psychrerythraea (strain 34H / ATCC BAA-681) (Vibrio
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Colwelliaceae; Colwellia.
OX NCBI_TaxID=167879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16043709; DOI=10.1073/pnas.0504766102;
RA Methe B.A., Nelson K.E., Deming J.W., Momen B., Melamud E., Zhang X.,
RA Mout R.J., Madupu R., Nelson W.C., Dodson R.J., Brinkac L.M.,
RA Daugherty S.C., Durkin A.S., DeBoy R.T., Kolonay J.F., Sullivan S.A.,
RA Zhou L., Davidson T.M., Wu M., Huston A.L., Lewis M., Weaver B.,
RA Weidman J.F., Khouri H., Utterback T.R., Feldblyum T.V., Fraser C.M.;
RA "The psychrophilic lifestyle as revealed by the genome sequence of
RT Colwellia psychrerythraea 34H through genomic and proteomic
analyses.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:10913-10918(2005).
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DR EMBL; CP000083; AA227601.1; -; Genomic_DNA.
DR TIGR; CPS_4280; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 35 AA; 4161 MW; 354095496D861868 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 35;
Best Local Similarity 40.0%; Pred. No. 4.3e+03;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 HCNFNDVTTRLRENE 17
   ||||
Db 18 HCSKNETIEREYIE 32

RESULT 87
Q73JCO_TREDE PRELIMINARY; PRT; 35 AA.
AC Q73JCO
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Hypothetical protein.
GN OrderedLocNames=TDE2655; ORFNames=TDE_2655;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selunko J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Derunk S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregorgis E., Geer K., Tsengaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McNeill T.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashishth P., Tiedge M., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
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CC -----
DR EMBL; AE017226; AAS13172.1; -; Genomic_DNA.
DR TIGR; TDE2655; -.
DR BioCyc; TDE2655-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 35 AA; 4252 MW; DF1E86AF106802D8 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 35;
Best Local Similarity 42.1%; Pred. No. 4.3e+03;
Matches 8; Conservative 1; Mismatches 2; Indels 8; Gaps 1;

QY 5 NFNDVT-----TRLRE 15
   ||||
Db 12 NFNSLTGLDFQYKFLRLRE 30

RESULT 88
Q8EY54_LEPIN PRELIMINARY; PRT; 35 AA.
AC Q8EY54
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Hypothetical protein.
GN OrderedLocNames=LB004; ORFNames=LB_004;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interogens revealed by whole-genome sequencing.";
RL Nature 422:988-993(2003).
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CC -----
DR EMBL; AE010301; AAN51562.1; -; Genomic_DNA.
DR GenomeReviews; AE010301.GR; LB004.
DR BioCyc; LINT189518.LB004-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 35 AA; 4081 MW; D532DF883D2EC707 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EHCNFDVTT 11
Db ||| | | |
26 EHQNLPILT 35

RESULT 89
ID Q76K89 SERQU PRELIMINARY; PRT; 35 AA.
AC Q76K89;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein ANTI-RAFI.
GN Name=ANTI-RAFI;
OS Seriola quinqueradiata (Five-ray yellowtail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Carangidae;
OC Carangidae; Seriola.
OX NCBI_TaxID=8161;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Abe S., Chiba S., Doi M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AB094041; BAC99070.1; -; Other_RNA.
KW Hypothetical protein.
SQ SEQUENCE 35 AA; 4156 MW; B801129BC73E6203 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 35;
Best Local Similarity 44.4%; Pred. No. 4.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FEHCNFDV 9
Db ||| | | |
4 FETCDSEI 12

RESULT 90
Q7SLD8_9HIV1
ID Q7SLD8_9HIV1 PRELIMINARY; PRT; 35 AA.
AC Q7SLD8;
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DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15117457; DOI=10.1089/08992204322996572;
RA Hamano T., Sawanpanyalert P., Yanai H., Piyaworawong S., Hara T.,
RA Sapsutthipas S., Phromjai J., Yamazaki S., Yamamoto N., Warachit P.,
RA Honda M., Matsuo K.;
RT "Determination of HIV Type 1 CRF01_AB gag p17 and env-V3 Consensus
RT Sequences for HIV/AIDS Vaccine Design.";
RL AIDS Res. Hum. Retroviruses 20:337-340(2004).
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CC -----
DR EMBL; AB115842; BAC81275.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 4004 MW; B37C90F6A9A481A4 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 35;
Best Local Similarity 62.5%; Pred. No. 4.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FNDVTTRL 13
Db ||| | | |
5 FNNVTRRM 12

RESULT 91
Q9JAE3_9HIV1
ID Q5J4E3_9HIV1 PRELIMINARY; PRT; 35 AA.
AC Q5J4E3;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Envelope protein V3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20491829; PubMed=11035611;
RA Collins K.R., Mayanja-Kizza H., Sullivan B.A., Quinones-Mateu M.E.,
RA Toossi Z., Arts E.J.;
RT "Greater diversity of HIV-1 quaspecies in HIV-infected individuals
RT with active tuberculosis.";
RL J. Acquir. Immune Defic. Syndr. 24:408-417(2000).
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CC -----
DR EMBL; AF201859; AAF71204.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
```

```

FT NON_TER 35 35
SQ SEQUENCE 35 AA; 4021 MW; BD0590F889A90B54 CRC64;

Query Match
Best Local Similarity 29.2%; Score 28; DB 2; Length 35;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FNDVTTRL 13
Db 5 FNNVTRTM 12

RESULT 92
Q4X2A2 PLACH PRELIMINARY; PRT; 36 AA.
AC Q4X2A2;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DE Hypothetical protein (Fragment).
GN ORFNames=PC106864.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; CAJ01010679; CAB89233.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 36 AA; 4277 MW; 332A0546B48DFC8 CRC64;

Query Match
Best Local Similarity 29.2%; Score 28; DB 2; Length 36;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNP 6
Db 21 FTYCNP 26

RESULT 93
Q6WJCO_9TURB PRELIMINARY; PRT; 36 AA.
AC Q6WJCO;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE Posterior Hox protein PostA (Fragment).
OS Paratomella rubra.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Acoelomorpha;
OC Acoela; Paratomellidae; Paratomella.
OX NCBI_TaxID=90914;
RN [1]
RP PubMed=1509302; DOI=10.1111/j.1525-142X.2004.04020.x;
RT NUCLEOTIDE SEQUENCE.

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RA Cook C.E., Jimenez E., Akam M., Salo E.;
RT "The Hox gene complement of acoel flatworms, a basal bilaterian
RT clade.";
RL Evol. Dev. 6:154-163(2004).
CC -!- SURCELLULAR LOCATION: Nuclear (By similarity).
CC -----
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CC -----
DR EMBL; AY282606; AAQ18801.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; E:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH lambdarepressor.
DR Pfam; PF000046; Homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox_1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 36
SQ SEQUENCE 36 AA; 4375 MW; CB4930590C336713 CRC64;

Query Match
Best Local Similarity 29.2%; Score 28; DB 2; Length 36;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 FNDVTTRLRENE 17
Db 7 FNNYTRRRGE 18

RESULT 94
Q2T8M9 BURTH PRELIMINARY; PRT; 36 AA.
AC Q2T8M9;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Isr807-transposase protein.
GN ORFNames=BTH_I10268;
OS Burkholderia thailandensis E264.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=271848;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E264;
RA Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Palmer N., Dodson R.,
RA Hickey E.K., Gwinn M., Dougherty B., Fleischmann R.D., Richardson D.,
RA Peterson J., Ravilavag A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van-Vugt R., Adams M.D., Gocayne J.D., Weidman J., Utterback T.,
RA Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C.,
RA Cotton M.D., Horst K., Tomb J.-F., Roberts K., Hatch B., Smith H.O.,
RA Venter J.C.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000085; ABC35995.1; -; Genomic DNA.
SQ SEQUENCE 36 AA; 4174 MW; DF52EAF03BE92CB3 CRC64;

Query Match
Best Local Similarity 29.2%; Score 28; DB 2; Length 36;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FNDVTTR 12
Db 7 FNNYTRRRGE 18

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Db 4 FNDLKR 10

RESULT 95
Q8EYJ2_LEPIN
ID Q8EYJ2_LEPIN PRELIMINARY; PRT; 36 AA.
AC Q8EYJ2;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Hypothetical protein.
GN OrderedLocusNames=LA4222; ORFNames=LA_4222;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Zhang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
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CC -----
DR EMBL; AE010300; AAN51420.1; -; Genomic_DNA.
DR GenomeReviews; AE010300 GR; LA4222.
DR BioCyc; LINT189518:LA4221-MONOMER; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 36 AA; 4418 MW; 3016EF434EF316B9 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 36;
Best Local Similarity 45.5%; Pred. No. 4.5e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CNFNDVTVTLR 14
| : : : |
Db 24 CSFEPRRLR 34

RESULT 96
Q6LE94_HUMAN
ID Q6LE94_HUMAN PRELIMINARY; PRT; 37 AA.
AC Q6LE94;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Aggregran epidermal growth factor-like domain-1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cartilage proteoglycan;
RA MEDLINE=97079270; PubMed=8921002;
RA Fulop C., Cs-Szabo G., Glant T.T.;
RT "Species-specific alternative splicing of the epidermal growth factor-
RT like domain 1 of cartilage aggrecan.";
RL Biochem. J. 319:935-940(1996).
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CC -----
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DR EMBL; L29488; AAB48068.1; -; Genomic_DNA.
DR Ensembl; ENSG00000157766; Homo sapiens.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR001438; EGF_2.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR Pfam; PF00008; EGF_1.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF_1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 3834 MW; 5E749D755570B81D CRC64;

Query Match 29.2%; Score 28; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EHCN 5
| : : |
Db 33 EHCN 36

RESULT 97
Q5C316_SCHJA
ID Q5C316_SCHJA PRELIMINARY; PRT; 37 AA.
AC Q5C316;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY809900; AAX25789.1; -; mRNA.
DR Hypothetical protein.
SQ SEQUENCE 37 AA; 4447 MW; 9EC17E5B2D2CA628 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 37;
Best Local Similarity 41.7%; Pred. No. 4.6e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 FEHCNENDVTVTR 12
| : : : |
Db 21 FIETNYNKITDR 32

RESULT 98
Q5DVA0_9DIPT
ID Q5DVA0_9DIPT PRELIMINARY; PRT; 37 AA.
AC Q5DVA0;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acetylcholinesterase (Fragment).
GN Name=ace-1;
OS Simulium ornatum.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Simuliidae; Simulium.
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OX NCBI_TaxID=304233;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR03;
RA Huchard E., Martinez M., Douzery E., Alout H., Berthomieu A.,
RA Berticat C., Raymond M., Weill M.;
RT "True flies don't have it. . .";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC -----
DR EMBL; AJ865836; CAI29768.1; -; mRNA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR Pfam; PF00135; Coesterase; 1.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 4608 MW; 582F99EED392D1C9 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 37;
Best Local Similarity 41.7%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 CNFNDVTTLRLE 15
Db |||:|
4 CNVNEFAQRYAE 15

RESULT 99
QSDVAL_9DIPT PRELIMINARY; PRT; 37 AA.
AC QSDVAL;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Acetylcholinesterase (Fragment).
GN Name=ace-1;
OS Culex annulirostris.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Culicinae; Culicini; Culex; Culex.
OX NCBI_TaxID=162997;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR01;
RA Huchard E., Martinez M., Douzery E., Alout H., Berthomieu A.,
RA Berticat C., Raymond M., Weill M.;
RT "True flies don't have it. . .";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC -----
DR EMBL; AJ865835; CAI29767.1; -; mRNA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR Pfam; PF00135; Coesterase; 1.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 4564 MW; 654349EED392D1DE CRC64;

Query Match 29.2%; Score 28; DB 2; Length 37;
Best Local Similarity 41.7%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 CNFNDVTTLRLE 15
Db |||:|
4 CNVNEFAQRYAE 15

RESULT 100
QSGN35_9DIPT
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ID QSGN35_9DIPT PRELIMINARY; PRT; 37 AA.
AC QSGN35;
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Acetylcholinesterase (Fragment).
DE Name=ace-1;
OS Chironomidae sp. OR02.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae.
OX NCBI_TaxID=305540;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Huchard E., Martinez M., Douzery E.J.P., Alout H., Berthomieu A.,
RA Berticat C., Raymond M., Weill M.;
RT "True flies don't have it. . .";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC -----
DR EMBL; AJ866990; CAI29272.1; -; mRNA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR PANTHER; PTHR11559; CarboxylesteraseB; 1.
DR Pfam; PF00135; Coesterase; 1.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 4660 MW; 732F99EED382CD1E CRC64;

Query Match 29.2%; Score 28; DB 2; Length 37;
Best Local Similarity 41.7%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 CNFNDVTTLRLE 15
Db |||:|
4 CNVNEFAQRYAE 15

Search completed: July 15, 2006, 00:24:25
Job time : 322 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 15, 2006, 00:15:25 ; Search time 193 Seconds
(without alignments)
40.273 Million cell updates/sec

Title: US-09-020-393b-3_copy_42_58
Perfect score: 96
Sequence: 1 FEHCNFDVTRLRENE 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1170880

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	23	9	Adx69810 Human K41
2	96	100.0	26	9	Adx69816 Human K41
3	96	100.0	30	9	Adx69811 Human K41
4	96	100.0	36	10	Aee66127 Human CD5
5	96	100.0	36	10	Aef63782 Human CD5
6	91	94.8	18	9	Adx69809 Human K41
7	80	83.3	18	9	Adx69815 Human K41
8	77	80.2	25	9	Adx69837 Human K65
9	71	74.0	12	8	Adt77352 Human car
10	71	74.0	12	8	Adt61251 Human ant
11	71	74.0	12	8	Adul4952 Human Car
12	71	74.0	12	8	ADU15085 Human Car
13	71	74.0	12	8	ADU74235 Human car
14	71	74.0	12	9	ADV09024 Human car
15	62	64.6	21	9	Adx69841 Human K65
16	52	54.2	13	9	Adx69800 Human CD5
17	52	54.2	16	9	Adx69812 Human K41
18	52	54.2	18	9	Adx69818 Human K41
19	48	50.0	14	9	Adx69819 Human K41
20	46	47.9	18	9	Adx69820 Human K41
21	44	45.8	21	9	Adx69840 Human K65
22	43	44.8	14	9	Adx69799 Human KS-
23	43	44.8	14	9	Adx69806 Human KS-

97	32	33.3	20	5	AAU75603	Aau75603 Human typ	170	30	31.2	8	3	AAV61736	Aay61736 Cadherin-
98	32	33.3	20	6	ADA20267	Ada20267 Human tum	171	30	31.2	8	9	AEC42258	Aec42258 Cadherin-
99	32	33.3	20	7	ADC17688	Adc17688 Type IV c	172	30	31.2	9	3	AAW43797	Aaw43797 Specific
100	32	33.3	20	7	ADC17688	Adc17688 Type IV c	173	30	31.2	9	3	AAW43799	Aay61739 Cadherin-
101	32	33.3	20	8	ADRI19210	Adri19210 Monomer-m	174	30	31.2	9	7	AEC42261	Aec42261 Cadherin-
102	32	33.3	20	8	ADRI19206	Adri19206 Monomer-m	175	30	31.2	10	7	ADC17691	Adc17691 Type IV c
103	32	33.3	20	9	ADY81247	Ady81247 Peptide b	176	30	31.2	10	8	ADRI19213	Adri19213 Type IV c
104	32	33.3	23	2	RAE84341	Are84341 Plant aco	177	30	31.2	12	4	ADRI19213	Adri19213 Type IV c
105	32	33.3	25	10	AEF22625	Aef22625 Recombina	178	30	31.2	14	10	AEF43261	Aef43261 Human Mul
106	32	33.3	28	5	ADH68794	Adh68794 Synthetic	179	30	31.2	15	2	AAW41168	Aaw41168 Metal-reg
107	32	33.3	32	8	ADL97607	Adl97607 Protein e	180	30	31.2	15	5	AAW47726	Aam47726 Peptide B
108	32	33.3	33	8	ADK70565	Adk70565 Human ery	181	30	31.2	15	8	ADP26440	Adp26440 Plasmodiu
109	32	33.3	33	10	AEF37612	Aee37612 Human ser	182	30	31.2	16	2	AAW41167	Aaw41167 Metal-reg
110	32	33.3	36	8	ADT39170	Adt39170 hSARS vir	183	30	31.2	16	6	ABP59517	Abp59517 Frd3 prot
111	32	33.3	36	8	ADS78590	Ads78590 SARS viru	184	30	31.2	16	8	ADT06039	Adt06039 Soil rest
112	32	33.3	36	8	ADT36700	Adt36700 hSARS vir	185	30	31.2	18	7	ADC17654	Adc17654 Type IV c
113	32	33.3	36	8	ABY00203	AbY00203 SARS coro	186	30	31.2	18	7	ADC17658	Adc17658 Type IV c
114	32	33.3	39	10	AEF22639	Aef22639 Carbamyla	187	30	31.2	18	8	ADRI19176	Adri19176 Inter-CDS
115	32	33.3	40	2	AAW92906	Aaw92906 Pseudomon	188	30	31.2	18	8	ADRI19180	Adri19180 Inter-CDS
116	32	33.3	40	2	AAW92920	Aaw92920 Pseudomon	189	30	31.2	18	10	AEF34021	Aef34021 Human cor
117	32	33.3	40	3	AAI98340	Aay98340 Alpha D p	190	30	31.2	21	7	ABR61484	AbR61484 Fowlpox v
118	31.5	32.8	26	10	AEF22614	Aef22614 Recombina	191	30	31.2	21	9	ADV55896	Adv55896 G protein
119	31	32.3	10	7	ADE28574	Ade28574 Human CD1	192	30	31.2	21	9	ADV55338	Adv55338 G protein
120	31	32.3	10	9	ADZ77605	Adz77605 Human MHC	193	30	31.2	22	7	ADC17660	Adc17660 Type IV c
121	31	32.3	14	4	AAW97385	Aaw97385 Human pep	194	30	31.2	22	7	ADC17664	Adc17664 Type IV c
122	31	32.3	15	5	ABB83992	Abb83992 Human pho	195	30	31.2	22	8	ADRI19186	Adri19186 SR, inter
123	31	32.3	15	5	ABJ04349	AbJ04349 Human col	196	30	31.2	22	8	ADRI19182	Adri19182 SR, inter
124	31	32.3	15	8	ADK70657	Adk70657 Human ery	197	30	31.2	23	8	ADT40777	Adt40777 hSARS vir
125	31	32.3	15	8	ADK70611	Adk70611 Human ery	198	30	31.2	23	8	ADS80193	Ads80193 SARS viru
126	31	32.3	15	8	ADK70590	Adk70590 Human ery	199	30	31.2	23	8	ADT38307	Adt38307 hSARS vir
127	31	32.3	15	8	ADK70575	Adk70575 Human ery	200	30	31.2	24	10	ABE28209	Aee28209 Human CSI
128	31	32.3	17	5	ADE03016	Ade03016 Hybrid po	201	30	31.2	25	2	AAW03364	Aaw03364 Influenza
129	31	32.3	18	7	ADC17656	Adc17656 Type IV c	202	30	31.2	27	7	ADF28427	Adf28427 Complemen
130	31	32.3	18	7	ADRI19178	Adri19178 Inter-CDS	203	30	31.2	27	7	ADF28404	Adf28404 Complemen
131	31	32.3	19	10	ABE38966	Aee38966 Human ser	204	30	31.2	27	8	ADP84401	Adp84401 Core pept
132	31	32.3	19	10	ABE35903	Aee35903 Human ser	205	30	31.2	28	2	AAW06123	Aaw06123 Guinea Pi
133	31	32.3	20	3	AAV67749	Aay67749 Peptide #	206	30	31.2	28	4	AAW06123	Aaw06123 Guinea Pi
134	31	32.3	21	5	ABJ01102	Abj01102 Ovary cel	207	30	31.2	28	4	AAW06123	Aaw06123 Guinea Pi
135	31	32.3	21	8	ADK70595	Adk70595 Human ery	208	30	31.2	28	5	ABG93961	Abg93961 Human vas
136	31	32.3	21	9	ADV56328	Adv56328 G protein	209	30	31.2	28	5	ABG94064	Abg94064 Human vas
137	31	32.3	21	9	ADV55511	Adv55511 G protein	210	30	31.2	28	5	ABG93962	Abg93962 Human vas
138	31	32.3	21	9	ADV54141	Adv54141 G protein	211	30	31.2	28	9	ADV55343	Adv55343 G protein
139	31	32.3	21	9	ADW99292	Adw99292 Yeast imm	212	30	31.2	28	9	ADV55901	Adv55901 G protein
140	31	32.3	21	9	AEA36631	Aea36631 Target pr	213	30	31.2	29	4	AAW21718	Aam21718 Peptide #
141	31	32.3	22	7	ADC17662	Adc17662 Type IV c	214	30	31.2	29	4	ABM44086	Abm44086 Peptide #
142	31	32.3	22	7	ADRI19184	Adri19184 SR, inter	215	30	31.2	29	4	ABB26977	Abb26977 Peptide #
143	31	32.3	25	6	ADA20237	Ada20237 T7 mutant	216	30	31.2	29	4	ABM77814	Abm77814 Human bon
144	31	32.3	26	2	AAW31069	Aaw31069 Mugwort p	217	30	31.2	29	4	AAW65107	Aam65107 Human bra
145	31	32.3	26	4	AAE01708	Aae01708 Human gen	218	30	31.2	29	4	ABG59468	Abg59468 Human liv
146	31	32.3	26	5	ABG63948	Abg63948 Human alb	219	30	31.2	29	5	ABG46845	Abg46845 Human pep
147	31	32.3	26	6	ADA41283	Ada41283 Human sec	220	30	31.2	34	5	AAO21771	Aao21771 Lung-epic
148	31	32.3	26	7	ADB91743	Adb91743 Human sec	221	30	31.2	34	6	ADA95279	Ada95279 Protein d
149	31	32.3	26	8	ADL77213	Adl77213 Albumin f	222	30	31.2	34	8	ADP84194	Adp84194 Human AAA
150	31	32.3	28	4	RAAG70495	Rag70495 Insulin s	223	30	31.2	35	2	AAW25701	Aaw25701 VIP. 1/19
151	31	32.3	28	5	ABG94062	Abg94062 Human vas	224	30	31.2	35	8	ADG45844	Adg45844 Staphyloc
152	31	32.3	28	9	ADY90847	Ady90847 Glucagon-	225	30	31.2	35	8	ADT76680	Adt76680 Antiviral
153	31	32.3	28	9	ADY40359	Ady40359 Glucose-d	226	30	31.2	40	4	ABM58894	Abm58894 Drosophil
154	31	32.3	28	9	ABE62635	Aee62635 VPAC2-rec	227	29.5	30.7	17	9	ADV59054	Adv59054 G protein
155	31	32.3	28	9	ABE35601	Aee35601 VPAC2-rec	228	29.5	30.7	17	9	ADV58112	Adv58112 G protein
156	31	32.3	28	10	AEF32974	Aef32974 Insulin r	229	29.5	30.7	18	10	AEF10815	Aef10815 Vaccinia
157	31	32.3	29	8	ADK68035	Adk68035 Interleuk	230	29.5	30.7	20	9	ADV58138	Adv58138 G protein
158	31	32.3	30	9	ADZ77604	Adz77604 Human MHC	231	29.5	30.7	20	9	ADV59080	Adv59080 G protein
159	31	32.3	33	3	AAW20680	Aaw20680 Type I PK	232	29.5	30.7	25	10	ABE38959	Aee38959 Human ser
160	31	32.3	33	7	ADC78962	Adc78962 N-termina	233	29.5	30.7	29	4	AAU86502	Aau86502 Novel hum
161	31	32.3	33	7	ADN01215	Adn01215 Modular p	234	29.5	30.7	29	7	ABM59836	Abm59836 Connectiv
162	31	32.3	34	6	ADA95152	Ada95152 Protein d	235	29.5	30.7	29	8	ADK83267	Adk83267 Human 191
163	31	32.3	35	8	ABO54179	AbO54179 Human gen	236	29	30.2	9	2	AAW49475	Aaw49475 Human leu
164	31	32.3	37	5	AAE23064	Aae23064 Synthetic	237	29	30.2	10	7	ADC17694	Adc17694 Type IV c
165	31	32.3	37	5	AAU93767	Aau93767 Synthetic	238	29	30.2	10	8	ADRI19216	Adri19216 Type IV c
166	31	32.3	37	5	AAE23437	Aae23437 Synthetic	239	29	30.2	12	7	ADF10462	Adf10462 Serum alb
167	31	32.3	38	3	AAW20677	Aaw20677 Type I PK	240	29	30.2	12	8	ADJ50665	Adj50665 Human ser
168	31	32.3	38	7	ADC78959	Adc78959 N-termina	241	29	30.2	12	9	ADW15812	Adw15812 Novel hum
169	31	32.3	38	7	ADN01212	Adn01212 Modular p	242	29	30.2	12	10	ABE31823	Aef31823 Human cor

243	29	30.2	13	7	ABW01377	Abw01377 Human HEA	316	29	30.2	37	9	ADM10185	Adw10185 Human Thy
244	29	30.2	14	2	AAR71732	Aar71732 Meroeoin m	317	29	30.2	39	4	AAO05320	Aao05320 Human pol
245	29	30.2	14	2	ADC17403	Adc17403 Type IV c	318	29	30.2	39	6	ABR43606	Abt43606 Human bot
246	29	30.2	15	8	ADR18925	Adr18925 Human typ	319	29	30.2	40	4	ABB40927	Abb40927 Peptide #
247	29	30.2	15	8	ADK70589	Adk70589 Human ery	320	29	30.2	40	4	AAW34699	Aaw34699 Peptide #
248	29	30.2	15	8	ADK70610	Adk70610 Human ery	321	29	30.2	40	4	AAW74587	Aam74587 Human bon
249	29	30.2	15	8	ADK70656	Adk70656 Human ery	322	29	30.2	40	4	AAW61789	Aam61789 Human bra
250	29	30.2	15	8	ADK70574	Adk70574 Human ery	323	29	30.2	40	4	ABG56374	Abg56374 Human liv
251	29	30.2	16	3	AAW36539	Aaw36539 Human ser	324	29	30.2	40	5	ABG44426	Abg44426 Human pep
252	29	30.2	16	3	AAW36546	Aaw36546 Human ser	325	29	30.2	40	5	AEC04876	Aec04876 Human bre
253	29	30.2	16	9	ADV59801	Adv59801 G protein	326	29	30.2	40	9	ABD71282	Abd71282 Corynebac
254	29	30.2	16	9	ADV56758	Adv56758 G protein	327	28.5	29.7	15	6	AAE35188	Aae35188 HIV helpe
255	29	30.2	16	9	ADV59913	Adv59913 G protein	328	28.5	29.7	15	7	ADN14069	Adn14069 HIV helpe
256	29	30.2	16	9	ADV57067	Adv57067 G protein	329	28.5	29.7	15	9	ADV22028	Adv22028 SHIV env
257	29	30.2	16	9	ADV58347	Adv58347 G protein	330	28.5	29.7	15	9	ADZ82213	Adz82213 Synthetic
258	29	30.2	16	9	ADV58747	Adv58747 G protein	331	28.5	29.7	18	6	ABP82551	Abp82551 G protein
259	29	30.2	16	9	ADW69834	Adw69834 Human K65	332	28.5	29.7	20	2	AAW43304	Aaw43304 C108G epi
260	29	30.2	17	10	AAE30469	Aae30469 Represent	333	28.5	29.7	21	8	ADR41065	Adr41065 Cyclic KD
261	29	30.2	17	10	AEF52085	Aef52085 Interfaci	334	28.5	29.7	21	8	ADR51113	Adr51113 Duo bindi
262	29	30.2	18	7	ADC17650	Adc17650 Type IV c	335	28.5	29.7	21	8	ADU40108	Adu40108 Kinase do
263	29	30.2	18	8	ADR19172	Adr19172 Type IV c	336	28.5	29.7	23	1	AAW91434	Aaw91434 Peptide f
264	29	30.2	18	9	ADY97092	Ady97092 VIP recep	337	28.5	29.7	23	2	AAW57832	Aaw57832 Peptide w
265	29	30.2	19	8	ADK52275	Adk52275 Murine VS	338	28.5	29.7	25	2	AAW30023	Aaw30023 Gp120-12,
266	29	30.2	20	7	ADC17685	Adc17685 Type IV c	339	28.5	29.7	25	2	AAW63814	Aaw63814 HIV-1 gp1
267	29	30.2	20	8	ADR19207	Adr19207 Monomer-m	340	28.5	29.7	25	2	AAW74604	Aaw74604 HIV-1 gp1
268	29	30.2	20	8	ADU79253	Adu79253 Human pep	341	28.5	29.7	25	2	AAW35461	Aaw35461 Immunogen
269	29	30.2	21	5	AAU88586	Aau88586 Insulin/i	342	28.5	29.7	25	2	ADW99188	Adw99188 Novel ant
270	29	30.2	21	6	ADA03432	Ada03432 Insulin r	343	28.5	29.7	25	9	ADW98779	Adw98779 Novel ant
271	29	30.2	21	7	ADH94645	Adh94645 Insulin r	344	28.5	29.7	27	2	AAW23070	Aaw23070 Peptide c
272	29	30.2	21	8	ADL67336	Adl67336 IGF-1R/IR	345	28.5	29.7	27	2	ADV55493	Adv55493 G protein
273	29	30.2	22	4	ADM37181	Adm37181 Anti-IR f	346	28.5	29.7	32	9	ADV55507	Adv55507 G protein
274	29	30.2	22	4	AAW87426	Aaw87426 Human gen	347	28.5	29.7	35	9	ADV55504	Adv55504 G protein
275	29	30.2	22	4	AAW87425	Aaw87425 Human gen	348	28.5	29.7	36	6	ABW71103	Abw71103 Staphyloc
276	29	30.2	22	9	ADY97093	Ady97093 VIP recep	349	28.5	29.7	40	3	AAW49314	Aaw49314 Human ZPI
277	29	30.2	24	6	AAW30300	Aaw30300 Human LP3	350	28	29.2	6	1	AAW20158	Aaw20158 Hexapepti
278	29	30.2	26	2	AAW27729	Aaw27729 Amino aci	351	28	29.2	7	9	ADY04105	Ady04105 Peptide d
279	29	30.2	26	2	AAW27730	Aaw27730 Amino aci	352	28	29.2	9	2	ADY20456	Ady20456 Human mic
280	29	30.2	28	5	ADH68837	Adh68837 Synthetic	353	28	29.2	9	8	ADI38425	Adi38425 beta-hCG
281	29	30.2	28	5	ADH68778	Adh68778 Synthetic	354	28	29.2	9	8	ADI38431	Adi38431 beta-hCG
282	29	30.2	29	5	AAU76067	Aau76067 C. elegan	355	28	29.2	9	8	ADI38437	Adi38437 beta-hCG
283	29	30.2	30	2	AAW53245	Aaw53245 Exo-alpha	356	28	29.2	9	8	ADI38443	Adi38443 beta-hCG
284	29	30.2	31	5	AAW49660	Aaw49660 Human bet	357	28	29.2	9	9	ADW69821	Adw69821 Human K41
285	29	30.2	34	4	AAW15150	Aaw15150 Peptide #	358	28	29.2	10	4	AAW43078	Aaw43078 Mycoplasm
286	29	30.2	34	4	ABB34142	Abb34142 Peptide #	359	28	29.2	10	7	ADK24181	Adk24181 Human 98P
287	29	30.2	34	4	AAW27606	Aaw27606 Peptide #	360	28	29.2	10	7	ADK25050	Adk25050 Human 98P
288	29	30.2	34	4	ABW28975	Abw28975 Peptide #	361	28	29.2	10	7	ADW62292	Adw62292 Human 98P
289	29	30.2	34	4	AAW64752	Aaw64752 Gene 36 h	362	28	29.2	10	7	ADW58207	Adw58207 Human 98P
290	29	30.2	34	4	ABB19584	Abb19584 Protein #	363	28	29.2	10	7	ADW61621	Adw61621 Human 98P
291	29	30.2	34	4	AAW67314	Aaw67314 Human bon	364	28	29.2	10	7	ADW62120	Adw62120 Human 98P
292	29	30.2	34	4	AAW54933	Aaw54933 Human bra	365	28	29.2	10	7	ADW57537	Adw57537 Human 98P
293	29	30.2	34	4	ABG48975	Abg48975 Human liv	366	28	29.2	10	7	ADW56212	Adw56212 Human 98P
294	29	30.2	34	4	AAW02890	Aaw02890 Peptide #	367	28	29.2	10	7	ADW62544	Adw62544 Human 98P
295	29	30.2	34	5	ADR41533	Adr41533 Human CD-	368	28	29.2	10	7	ADW56870	Adw56870 Human 98P
296	29	30.2	36	6	ADA95239	Ada95239 Protein d	369	28	29.2	10	7	ADW55533	Adw55533 Human 98P
297	29	30.2	36	6	ADA95293	Ada95293 Protein d	370	28	29.2	12	7	ADC97785	Adc97785 Gene regu
298	29	30.2	34	6	ADA95273	Ada95273 Protein d	371	28	29.2	12	9	ADX17307	Adx17307 Human ser
299	29	30.2	34	7	ADL12078	Adl12078 Human sec	372	28	29.2	13	3	AAW57800	Aaw57800 TRAM-inte
300	29	30.2	34	7	ADJ81457	Adj81457 Plant ret	373	28	29.2	13	5	ASG60330	Asg60330 Selective
301	29	30.2	35	4	AAO10530	Aao10530 Human pol	374	28	29.2	13	5	AAW50781	Aaw50781 Human cho
302	29	30.2	35	6	ABR43536	Abt43536 Human bet	375	28	29.2	14	7	ADC17401	Adc17401 Type IV c
303	29	30.2	35	6	ADQ75498	Adq75498 PTH/PTHrP	376	28	29.2	14	8	ADR18923	Adr18923 Human typ
304	29	30.2	35	8	ADQ75500	Adq75500 PTH/PTHrP	377	28	29.2	15	2	AAW11465	Aaw11465 Leptidopte
305	29	30.2	35	8	ADQ75499	Adq75499 PTH/PTHrP	378	28	29.2	15	6	ABP72616	Abp72616 Manduca s
306	29	30.2	35	8	ADQ75497	Adq75497 PTH/PTHrP	379	28	29.2	15	6	ABR37851	Abt37851 Human can
307	29	30.2	35	8	ADQ97619	Adq97619 Chromogra	380	28	29.2	15	6	ABR37871	Abt37871 Human can
308	29	30.2	36	2	AAW07774	Aaw07774 Human sec	381	28	29.2	15	7	ADE14702	Adel14702 DMGPR b1
309	29	30.2	36	4	AAW33675	Aaw33675 Peptide #	382	28	29.2	15	7	ADL83598	Adl83598 Manducta
310	29	30.2	36	4	AAW73477	Aaw73477 Human bon	383	28	29.2	15	7	ADW63757	Adw63757 Human 98P
311	29	30.2	36	4	AAW60800	Aaw60800 Human bra	384	28	29.2	15	7	ADW63480	Adw63480 Human 98P
312	29	30.2	36	4	ABG55200	Abg55200 Human liv	385	28	29.2	15	7	ADW63755	Adw63755 Human 98P
313	29	30.2	36	5	ABG43336	Abg43336 Human pep	386	28	29.2	15	7	ADW62890	Adw62890 Human 98P
314	29	30.2	37	2	AAW39316	Aaw39316 MRI toxin	387	28	29.2	15	7	ADW63486	Adw63486 Human 98P
315	29	30.2	37	2	AAW78460	Aaw78460 Insectici	388	28	29.2	15	7	ADW63173	Adw63173 Human 98P

389	28	29.2	15	7	ADW63488	Adw63488 Human 98P	462	28	29.2	29	10	AEF09486	Aef09486 pegylated
390	28	29.2	15	7	ADW63484	Adw63484 Human 98P	463	28	29.2	29	10	AEF09410	Aef09410 Pegylated
391	28	29.2	15	7	ADW63485	Adw63485 Human 98P	464	28	29.2	30	2	AAW92254	Aaw92254 BL172 pol
392	28	29.2	15	7	ADW63178	Adw63178 Human 98P	465	28	29.2	30	6	ABP77098	Abp77098 N. gonorr
393	28	29.2	15	7	ADW62889	Adw62889 Human 98P	466	28	29.2	30	7	AAE39147	Aae39147 BL172 pro
394	28	29.2	15	7	ADW62891	Adw62891 Human 98P	467	28	29.2	30	8	ADI24004	Adi24004 VPAC2 rec
395	28	29.2	15	8	ADH04830	Adh04830 TDFRP pep	468	28	29.2	30	8	ADI24018	Adi24018 VPAC2 rec
396	28	29.2	15	9	ADH69833	Adh69833 Human K38	469	28	29.2	30	8	ADI24019	Adi24019 VPAC2 rec
397	28	29.2	16	7	ADC97788	Adc97788 Gene regu	470	28	29.2	30	8	ADI24087	Adi24087 VPAC2 rec
398	28	29.2	16	7	ADC97786	Adc97786 Gene regu	471	28	29.2	30	8	ADI24083	Adi24083 VPAC2 rec
399	28	29.2	16	7	ADC97784	Adc97784 Gene regu	472	28	29.2	30	8	ADI24097	Adi24097 VPAC2 rec
400	28	29.2	18	7	ADC17648	Adc17648 Type IV c	473	28	29.2	30	8	ADI24103	Adi24103 VPAC2 rec
401	28	29.2	18	7	ADF14572	Adf14572 Gluten-de	474	28	29.2	30	8	ADI24006	Adi24006 VPAC2 rec
402	28	29.2	18	8	ADR19170	Adr19170 Type IV c	475	28	29.2	30	8	ADI24010	Adi24010 VPAC2 rec
403	28	29.2	20	2	AAW50065	Aaw50065 Human cho	476	28	29.2	30	8	ADI24021	Adi24021 VPAC2 rec
404	28	29.2	20	2	AAW47505	Aaw47505 Human bet	477	28	29.2	30	8	ADI24099	Adi24099 VPAC2 rec
405	28	29.2	20	2	AAW50100	Aaw50100 Human cho	478	28	29.2	30	8	ADI24007	Adi24007 VPAC2 rec
406	28	29.2	20	4	AAW71778	Aaw71778 Beta-huma	479	28	29.2	30	8	ADI24011	Adi24011 VPAC2 rec
407	28	29.2	20	5	AAU83027	Aau83027 Beta-huma	480	28	29.2	30	8	ADI24089	Adi24089 VPAC2 rec
408	28	29.2	20	7	ADP17683	Adp17683 Type IV c	481	28	29.2	30	8	ADI24100	Adi24100 VPAC2 rec
409	28	29.2	20	7	ADF72657	Adf72657 B. burgdo	482	28	29.2	30	8	ADI24003	Adi24003 VPAC2 rec
410	28	29.2	20	7	ADM64564	Adm64564 Beta-huma	483	28	29.2	30	8	ADI24015	Adi24015 VPAC2 rec
411	28	29.2	20	8	ADH52626	Adh52626 Human cho	484	28	29.2	30	8	ADI24022	Adi24022 VPAC2 rec
412	28	29.2	20	8	ADH52589	Adh52589 Human cho	485	28	29.2	30	8	ADI24090	Adi24090 VPAC2 rec
413	28	29.2	20	8	ADK39777	Adk39777 Human cho	486	28	29.2	30	8	ADI24002	Adi24002 VPAC2 rec
414	28	29.2	20	8	ADR19205	Adr19205 Monomer-m	487	28	29.2	30	8	ADI24017	Adi24017 VPAC2 rec
415	28	29.2	20	8	ADT90969	Adt90969 Human bet	488	28	29.2	30	8	ADI24014	Adi24014 VPAC2 rec
416	28	29.2	20	10	AEF09705	Aef09705 Monkeypox	489	28	29.2	30	8	ADI24025	Adi24025 VPAC2 rec
417	28	29.2	21	5	ABG90959	Abg90959 Human col	490	28	29.2	30	8	ADI24088	Adi24088 VPAC2 rec
418	28	29.2	21	5	ABJ04336	Abj04336 Human col	491	28	29.2	30	8	ADI24072	Adi24072 VPAC2 rec
419	28	29.2	21	6	ABR52557	Abrr52557 Group A s	492	28	29.2	30	8	ADI24080	Adi24080 VPAC2 rec
420	28	29.2	22	2	AAW48546	Aar48546 Sequence	493	28	29.2	30	8	ADI24084	Adi24084 VPAC2 rec
421	28	29.2	23	6	ABOI12880	Aboi12880 Human zin	494	28	29.2	30	8	ADI24102	Adi24102 VPAC2 rec
422	28	29.2	23	6	ABOI13428	Aboi13428 Mouse zin	495	28	29.2	30	8	ADI24107	Adi24107 VPAC2 rec
423	28	29.2	23	6	ABOI13429	Aboi13429 Mouse zin	496	28	29.2	30	8	ADI24020	Adi24020 VPAC2 rec
424	28	29.2	23	6	ABOI12881	Aboi12881 Human zin	497	28	29.2	30	8	ADI24027	Adi24027 VPAC2 rec
425	28	29.2	23	6	ABOI11741	Aboi11741 Human zin	498	28	29.2	30	8	ADI24081	Adi24081 VPAC2 rec
426	28	29.2	24	8	ABO54318	Abos4318 Human gen	499	28	29.2	30	8	ADI24082	Adi24082 VPAC2 rec
427	28	29.2	24	8	ADT39505	Adt39505 hSARS vir	500	28	29.2	30	8	ADI24092	Adi24092 VPAC2 rec
428	28	29.2	24	8	ADS78924	Ads78924 SARS viru	501	28	29.2	30	8	ADI24005	Adi24005 VPAC2 rec
429	28	29.2	24	8	ADT37035	Adt37035 hSARS vir	502	28	29.2	30	8	ADI24077	Adi24077 VPAC2 rec
430	28	29.2	24	9	ADW43386	Adw43386 Prostate	503	28	29.2	30	8	ADI24083	Adi24083 VPAC2 rec
431	28	29.2	25	2	AAW95881	Aar95881 p67 signa	504	28	29.2	30	8	ADI24093	Adi24093 VPAC2 rec
432	28	29.2	25	2	AAW26456	Aay26456 Erythrope	505	28	29.2	30	8	ADI24101	Adi24101 VPAC2 rec
433	28	29.2	25	2	AAW75943	Aaw75943 Skn7 poly	506	28	29.2	30	8	ADI23996	Adi23996 VPAC2 rec
434	28	29.2	25	5	ABG62417	Abg62417 Eubacteri	507	28	29.2	30	8	ADI24013	Adi24013 VPAC2 rec
435	28	29.2	26	2	AAW95882	Aar95882 p67 signa	508	28	29.2	30	8	ADI24091	Adi24091 VPAC2 rec
436	28	29.2	26	2	AAW95883	Aar95883 p67 signa	509	28	29.2	30	8	ADI24094	Adi24094 VPAC2 rec
437	28	29.2	27	9	ADV54353	Adv54353 G protein	510	28	29.2	30	8	ADI24095	Adi24095 VPAC2 rec
438	28	29.2	28	5	ABG94060	Abg94060 Human vas	511	28	29.2	30	8	ADI24026	Adi24026 VPAC2 rec
439	28	29.2	28	5	ABG94113	Abg94113 Human vas	512	28	29.2	30	8	ADI24016	Adi24016 VPAC2 rec
440	28	29.2	28	5	ABG94107	Abg94107 Human vas	513	28	29.2	30	8	ADI24014	Adi24014 VPAC2 rec
441	28	29.2	28	5	ABG94061	Abg94061 Human vas	514	28	29.2	30	8	ADI24078	Adi24078 VPAC2 rec
442	28	29.2	28	5	ABG94063	Abg94063 Human vas	515	28	29.2	30	8	ADI24079	Adi24079 VPAC2 rec
443	28	29.2	28	5	ABG94054	Abg94054 Human vas	516	28	29.2	30	8	ADI24096	Adi24096 VPAC2 rec
444	28	29.2	28	5	ABG94071	Abg94071 Human vas	517	28	29.2	30	8	ADI24098	Adi24098 VPAC2 rec
445	28	29.2	28	5	ABB07014	Abb07014 Neurite i	518	28	29.2	30	8	ADI24001	Adi24001 VPAC2 rec
446	28	29.2	28	5	ABB07016	Abb07016 Neurite i	519	28	29.2	30	8	ADI24008	Adi24008 VPAC2 rec
447	28	29.2	28	5	ADH68835	Adh68835 Synthetic	520	28	29.2	30	8	ADI24009	Adi24009 VPAC2 rec
448	28	29.2	28	7	ADBF61600	Adbf61600 Conformat	521	28	29.2	30	8	ADI24012	Adi24012 VPAC2 rec
449	28	29.2	28	8	ADP54723	Adp54723 Neurotoxi	522	28	29.2	30	8	ADI24085	Adi24085 VPAC2 rec
450	28	29.2	28	8	ADJ11286	Adj11286 Peptide f	523	28	29.2	30	9	ADZ86123	Adz86123 Rabbit be
451	28	29.2	29	4	AAW71799	Aaw71799 Beta-hCG	524	28	29.2	30	9	ABE90807	Aeb90807 Human BL1
452	28	29.2	29	5	ABP42947	Abp42947 Human ova	525	28	29.2	30	9	ABE88030	Aeb88030 VPAC 2 ag
453	28	29.2	29	7	ADC22287	Adc22287 Protein b	526	28	29.2	30	9	ABE88049	Aeb88049 VPAC 2 ag
454	28	29.2	29	8	ADI23993	Adi23993 VPAC2 rec	527	28	29.2	30	9	ABE87972	Aeb87972 VPAC 2 ag
455	28	29.2	29	8	ADI24069	Adi24069 VPAC2 rec	528	28	29.2	30	9	ABE88035	Aeb88035 VPAC 2 ag
456	28	29.2	29	9	ABE87946	Aeb87946 VPAC 2 ag	529	28	29.2	30	9	ABE88040	Aeb88040 VPAC 2 ag
457	28	29.2	29	9	ABE88020	AbE88020 VPAC 2 ag	530	28	29.2	30	9	ABE87956	Aeb87956 VPAC 2 ag
458	28	29.2	29	9	ABE62722	Aee62722 VPAC2-rec	531	28	29.2	30	9	ABE87959	Aeb87959 VPAC 2 ag
459	28	29.2	29	9	ABE62646	Aee62646 VPAC2-rec	532	28	29.2	30	9	ABE87974	Aeb87974 VPAC 2 ag
460	28	29.2	29	9	ABE35612	Aee35612 VPAC2 rec	533	28	29.2	30	9	ABE88053	Aeb88053 VPAC 2 ag
461	28	29.2	29	9	ABE35688	Aee35688 VPAC2 rec	534	28	29.2	30	9	ABE88053	Aeb88053 VPAC 2 ag

535	28	29.2	30	9	AEB87968	Aeb87968	VPAC 2 ag	608	28	29.2	30	9	AEB62679	Aee62679	VPAC2-rec
536	28	29.2	30	9	AEB88033	Aeb88033	VPAC 2 ag	609	28	29.2	30	9	AEB62680	Aee62680	VPAC2-rec
537	28	29.2	30	9	AEB87955	Aeb87955	VPAC 2 ag	610	28	29.2	30	9	AEB62730	Aee62730	VPAC2-rec
538	28	29.2	30	9	AEB87978	Aeb87978	VPAC 2 ag	611	28	29.2	30	9	AEB62743	Aee62743	VPAC2-rec
539	28	29.2	30	9	AEB88043	Aeb88043	VPAC 2 ag	612	28	29.2	30	9	AEB62649	Aee62649	VPAC2-rec
540	28	29.2	30	9	AEB88047	Aeb88047	VPAC 2 ag	613	28	29.2	30	9	AEB62662	Aee62662	VPAC2-rec
541	28	29.2	30	9	AEB88039	Aeb88039	VPAC 2 ag	614	28	29.2	30	9	AEB62745	Aee62745	VPAC2-rec
542	28	29.2	30	9	AEB88032	Aeb88032	VPAC 2 ag	615	28	29.2	30	9	AEB62667	Aee62667	VPAC2-rec
543	28	29.2	30	9	AEB88051	Aeb88051	VPAC 2 ag	616	28	29.2	30	9	AEB62675	Aee62675	VPAC2-rec
544	28	29.2	30	9	AEB87963	Aeb87963	VPAC 2 ag	617	28	29.2	30	9	AEB62725	Aee62725	VPAC2-rec
545	28	29.2	30	9	AEB87964	Aeb87964	VPAC 2 ag	618	28	29.2	30	9	AEB62744	Aee62744	VPAC2-rec
546	28	29.2	30	9	AEB87965	Aeb87965	VPAC 2 ag	619	28	29.2	30	9	AEB62751	Aee62751	VPAC2-rec
547	28	29.2	30	9	AEB88042	Aeb88042	VPAC 2 ag	620	28	29.2	30	9	AEB62657	Aee62657	VPAC2-rec
548	28	29.2	30	9	AEB88045	Aeb88045	VPAC 2 ag	621	28	29.2	30	9	AEB62660	Aee62660	VPAC2-rec
549	28	29.2	30	9	AEB87949	Aeb87949	VPAC 2 ag	622	28	29.2	30	9	AEB62664	Aee62664	VPAC2-rec
550	28	29.2	30	9	AEB87975	Aeb87975	VPAC 2 ag	623	28	29.2	30	9	AEB62670	Aee62670	VPAC2-rec
551	28	29.2	30	9	AEB87977	Aeb87977	VPAC 2 ag	624	28	29.2	30	9	AEB62738	Aee62738	VPAC2-rec
552	28	29.2	30	9	AEB88041	Aeb88041	VPAC 2 ag	625	28	29.2	30	9	AEB62734	Aee62734	VPAC2-rec
553	28	29.2	30	9	AEB88034	Aeb88034	VPAC 2 ag	626	28	29.2	30	9	AEB62748	Aee62748	VPAC2-rec
554	28	29.2	30	9	AEB87958	Aeb87958	VPAC 2 ag	627	28	29.2	30	9	AEB62754	Aee62754	VPAC2-rec
555	28	29.2	30	9	AEB87960	Aeb87960	VPAC 2 ag	628	28	29.2	30	9	AEB62760	Aee62760	VPAC2-rec
556	28	29.2	30	9	AEB87967	Aeb87967	VPAC 2 ag	629	28	29.2	30	9	AEB62674	Aee62674	VPAC2-rec
557	28	29.2	30	9	AEB87979	Aeb87979	VPAC 2 ag	630	28	29.2	30	9	AEB62735	Aee62735	VPAC2-rec
558	28	29.2	30	9	AEB88028	Aeb88028	VPAC 2 ag	631	28	29.2	30	9	AEB62741	Aee62741	VPAC2-rec
559	28	29.2	30	9	AEB88031	Aeb88031	VPAC 2 ag	632	28	29.2	30	9	AEB62672	Aee62672	VPAC2-rec
560	28	29.2	30	9	AEB88044	Aeb88044	VPAC 2 ag	633	28	29.2	30	9	AEB62676	Aee62676	VPAC2-rec
561	28	29.2	30	9	AEB88052	Aeb88052	VPAC 2 ag	634	28	29.2	30	9	AEB62731	Aee62731	VPAC2-rec
562	28	29.2	30	9	AEB87957	Aeb87957	VPAC 2 ag	635	28	29.2	30	9	AEB62733	Aee62733	VPAC2-rec
563	28	29.2	30	9	AEB87966	Aeb87966	VPAC 2 ag	636	28	29.2	30	9	AEB62749	Aee62749	VPAC2-rec
564	28	29.2	30	9	AEB87973	Aeb87973	VPAC 2 ag	637	28	29.2	30	9	AEB62750	Aee62750	VPAC2-rec
565	28	29.2	30	9	AEB88057	Aeb88057	VPAC 2 ag	638	28	29.2	30	9	AEB62656	Aee62656	VPAC2-rec
566	28	29.2	30	9	AEB88023	Aeb88023	VPAC 2 ag	639	28	29.2	30	9	AEB62677	Aee62677	VPAC2-rec
567	28	29.2	30	9	AEB88034	Aeb88034	VPAC 2 ag	640	28	29.2	30	9	AEB35622	Aee35622	VPAC2-rec
568	28	29.2	30	9	AEB88048	Aeb88048	VPAC 2 ag	641	28	29.2	30	9	AEB35712	Aee35712	VPAC2-rec
569	28	29.2	30	9	AEB88050	Aeb88050	VPAC 2 ag	642	28	29.2	30	9	AEB35716	Aee35716	VPAC2-rec
570	28	29.2	30	9	AEB87961	Aeb87961	VPAC 2 ag	643	28	29.2	30	9	AEB35632	Aee35632	VPAC2-rec
571	28	29.2	30	9	AEB87980	Aeb87980	VPAC 2 ag	644	28	29.2	30	9	AEB35640	Aee35640	VPAC2-rec
572	28	29.2	30	9	AEB88038	Aeb88038	VPAC 2 ag	645	28	29.2	30	9	AEB35696	Aee35696	VPAC2-rec
573	28	29.2	30	9	AEB87962	Aeb87962	VPAC 2 ag	646	28	29.2	30	9	AEB35714	Aee35714	VPAC2-rec
574	28	29.2	30	9	AEB88037	Aeb88037	VPAC 2 ag	647	28	29.2	30	9	AEB35624	Aee35624	VPAC2-rec
575	28	29.2	30	9	AEB88046	Aeb88046	VPAC 2 ag	648	28	29.2	30	9	AEB35634	Aee35634	VPAC2-rec
576	28	29.2	30	9	AEB87970	Aeb87970	VPAC 2 ag	649	28	29.2	30	9	AEB35700	Aee35700	VPAC2-rec
577	28	29.2	30	9	AEB87971	Aeb87971	VPAC 2 ag	650	28	29.2	30	9	AEB35719	Aee35719	VPAC2-rec
578	28	29.2	30	9	AEB88036	Aeb88036	VPAC 2 ag	651	28	29.2	30	9	AEB35721	Aee35721	VPAC2-rec
579	28	29.2	30	9	AEB87954	Aeb87954	VPAC 2 ag	652	28	29.2	30	9	AEB35707	Aee35707	VPAC2-rec
580	28	29.2	30	9	AEB87969	Aeb87969	VPAC 2 ag	653	28	29.2	30	9	AEB35621	Aee35621	VPAC2-rec
581	28	29.2	30	9	AEB87976	Aeb87976	VPAC 2 ag	654	28	29.2	30	9	AEB35623	Aee35623	VPAC2-rec
582	28	29.2	30	9	AEB88039	Aeb88039	VPAC 2 ag	655	28	29.2	30	9	AEB35625	Aee35625	VPAC2-rec
583	28	29.2	30	9	AEB62655	Aee62655	VPAC2-rec	656	28	29.2	30	9	AEB35718	Aee35718	VPAC2-rec
584	28	29.2	30	9	AEB62666	Aee62666	VPAC2-rec	657	28	29.2	30	9	AEB35620	Aee35620	VPAC2-rec
585	28	29.2	30	9	AEB62668	Aee62668	VPAC2-rec	658	28	29.2	30	9	AEB35626	Aee35626	VPAC2-rec
586	28	29.2	30	9	AEB62678	Aee62678	VPAC2-rec	659	28	29.2	30	9	AEB35633	Aee35633	VPAC2-rec
587	28	29.2	30	9	AEB62736	Aee62736	VPAC2-rec	660	28	29.2	30	9	AEB35639	Aee35639	VPAC2-rec
588	28	29.2	30	9	AEB62753	Aee62753	VPAC2-rec	661	28	29.2	30	9	AEB35709	Aee35709	VPAC2-rec
589	28	29.2	30	9	AEB62665	Aee62665	VPAC2-rec	662	28	29.2	30	9	AEB35615	Aee35615	VPAC2-rec
590	28	29.2	30	9	AEB62671	Aee62671	VPAC2-rec	663	28	29.2	30	9	AEB35630	Aee35630	VPAC2-rec
591	28	29.2	30	9	AEB62740	Aee62740	VPAC2-rec	664	28	29.2	30	9	AEB35638	Aee35638	VPAC2-rec
592	28	29.2	30	9	AEB62658	Aee62658	VPAC2-rec	665	28	29.2	30	9	AEB35641	Aee35641	VPAC2-rec
593	28	29.2	30	9	AEB62661	Aee62661	VPAC2-rec	666	28	29.2	30	9	AEB35717	Aee35717	VPAC2-rec
594	28	29.2	30	9	AEB62742	Aee62742	VPAC2-rec	667	28	29.2	30	9	AEB35628	Aee35628	VPAC2-rec
595	28	29.2	30	9	AEB62746	Aee62746	VPAC2-rec	668	28	29.2	30	9	AEB35636	Aee35636	VPAC2-rec
596	28	29.2	30	9	AEB62747	Aee62747	VPAC2-rec	669	28	29.2	30	9	AEB35715	Aee35715	VPAC2-rec
597	28	29.2	30	9	AEB62752	Aee62752	VPAC2-rec	670	28	29.2	30	9	AEB35629	Aee35629	VPAC2-rec
598	28	29.2	30	9	AEB62654	Aee62654	VPAC2-rec	671	28	29.2	30	9	AEB35642	Aee35642	VPAC2-rec
599	28	29.2	30	9	AEB62732	Aee62732	VPAC2-rec	672	28	29.2	30	9	AEB35643	Aee35643	VPAC2-rec
600	28	29.2	30	9	AEB62673	Aee62673	VPAC2-rec	673	28	29.2	30	9	AEB35644	Aee35644	VPAC2-rec
601	28	29.2	30	9	AEB62739	Aee62739	VPAC2-rec	674	28	29.2	30	9	AEB35645	Aee35645	VPAC2-rec
602	28	29.2	30	9	AEB62755	Aee62755	VPAC2-rec	675	28	29.2	30	9	AEB35691	Aee35691	VPAC2-rec
603	28	29.2	30	9	AEB62737	Aee62737	VPAC2-rec	676	28	29.2	30	9	AEB35705	Aee35705	VPAC2-rec
604	28	29.2	30	9	AEB62756	Aee62756	VPAC2-rec	677	28	29.2	30	9	AEB35697	Aee35697	VPAC2-rec
605	28	29.2	30	9	AEB62659	Aee62659	VPAC2-rec	678	28	29.2	30	9	AEB35704	Aee35704	VPAC2-rec
606	28	29.2	30	9	AEB62663	Aee62663	VPAC2-rec	679	28	29.2	30	9	AEB35706	Aee35706	VPAC2-rec
607	28	29.2	30	9	AEB62669	Aee62669	VPAC2-rec	680	28	29.2	30	9	AEB35711	Aee35711	VPAC2-rec

681	28	29.2	30	9	ABE35637	Aee35637 VPAC2 rec	754	28	29.2	31	4	AAG99874	Aag99874 ERA bindi
682	28	29.2	30	9	ABE35646	Aee35646 VPAC2 rec	755	28	29.2	31	4	AAG99877	Aag99877 ERA bindi
683	28	29.2	30	9	ABE35698	Aee35698 VPAC2 rec	756	28	29.2	31	4	AAG99883	Aag99883 Insulin s
684	28	29.2	30	9	ABE35702	Aee35702 VPAC2 rec	757	28	29.2	31	4	AAG70532	Aag70532 Insulin s
685	28	29.2	30	9	ABE35631	Aee35631 VPAC2 rec	758	28	29.2	31	4	AAG70537	Aag70537 Insulin s
686	28	29.2	30	9	ABE35701	Aee35701 VPAC2 rec	759	28	29.2	31	4	AAG70536	Aag70536 Insulin s
687	28	29.2	30	9	ABE35713	Aee35713 VPAC2 rec	760	28	29.2	31	4	AAG70533	Aag70533 Insulin s
688	28	29.2	30	9	ABE35720	Aee35720 VPAC2 rec	761	28	29.2	31	8	ADI23991	Adi23991 VPAC2 rec
689	28	29.2	30	9	ABE35699	Aee35699 VPAC2 rec	762	28	29.2	31	8	ADI24119	Adi24119 VPAC2 rec
690	28	29.2	30	9	ABE35710	Aee35710 VPAC2 rec	763	28	29.2	31	8	ADI24123	Adi24123 VPAC2 rec
691	28	29.2	30	9	ABE35722	Aee35722 VPAC2 rec	764	28	29.2	31	8	ADI24129	Adi24129 VPAC2 rec
692	28	29.2	30	9	ABE35726	Aee35726 VPAC2 rec	765	28	29.2	31	8	ADI24134	Adi24134 VPAC2 rec
693	28	29.2	30	9	ABE35627	Aee35627 VPAC2 rec	766	28	29.2	31	8	ADI24128	Adi24128 VPAC2 rec
694	28	29.2	30	9	ABE35635	Aee35635 VPAC2 rec	767	28	29.2	31	8	ADI24138	Adi24138 VPAC2 rec
695	28	29.2	30	9	ABE35703	Aee35703 VPAC2 rec	768	28	29.2	31	8	ADI23994	Adi23994 VPAC2 rec
696	28	29.2	30	9	ABE35708	Aee35708 VPAC2 rec	769	28	29.2	31	8	ADI24118	Adi24118 VPAC2 rec
697	28	29.2	30	10	AEF09440	Aef09440 Pegylated	770	28	29.2	31	8	ADI24131	Adi24131 VPAC2 rec
698	28	29.2	30	10	AEF09442	Aef09442 Pegylated	771	28	29.2	31	8	ADI24131	Adi24131 VPAC2 rec
699	28	29.2	30	10	AEF09444	Aef09444 Pegylated	772	28	29.2	31	8	ADI23992	Adi23992 VPAC2 rec
700	28	29.2	30	10	AEF09437	Aef09437 Pegylated	773	28	29.2	31	8	ADI24073	Adi24073 VPAC2 rec
701	28	29.2	30	10	AEF09424	Aef09424 Pegylated	774	28	29.2	31	8	ADI24074	Adi24074 VPAC2 rec
702	28	29.2	30	10	AEF09433	Aef09433 Pegylated	775	28	29.2	31	8	ADI24116	Adi24116 VPAC2 rec
703	28	29.2	30	10	AEF09512	Aef09512 Pegylated	776	28	29.2	31	8	ADI24127	Adi24127 VPAC2 rec
704	28	29.2	30	10	AEF09439	Aef09439 Pegylated	777	28	29.2	31	8	ADI23997	Adi23997 VPAC2 rec
705	28	29.2	30	10	AEF09439	Aef09439 Pegylated	778	28	29.2	31	8	ADI24122	Adi24122 VPAC2 rec
706	28	29.2	30	10	AEF09518	Aef09518 Pegylated	779	28	29.2	31	8	ADI24137	Adi24137 VPAC2 rec
707	28	29.2	30	10	AEF09519	Aef09519 Pegylated	780	28	29.2	31	8	ADI24068	Adi24068 VPAC2 rec
708	28	29.2	30	10	AEF09420	Aef09420 Pegylated	781	28	29.2	31	8	ADI24135	Adi24135 VPAC2 rec
709	28	29.2	30	10	AEF09422	Aef09422 Pegylated	782	28	29.2	31	8	ADI24066	Adi24066 VPAC2 rec
710	28	29.2	30	10	AEF09428	Aef09428 Pegylated	783	28	29.2	31	8	ADI24075	Adi24075 VPAC2 rec
711	28	29.2	30	10	AEF09431	Aef09431 Pegylated	784	28	29.2	31	8	ADI24110	Adi24110 VPAC2 rec
712	28	29.2	30	10	AEF09505	Aef09505 Pegylated	785	28	29.2	31	8	ADI24115	Adi24115 VPAC2 rec
713	28	29.2	30	10	AEF09511	Aef09511 Pegylated	786	28	29.2	31	8	ADI24121	Adi24121 VPAC2 rec
714	28	29.2	30	10	AEF09430	Aef09430 Pegylated	787	28	29.2	31	8	ADI24133	Adi24133 VPAC2 rec
715	28	29.2	30	10	AEF09438	Aef09438 Pegylated	788	28	29.2	31	8	ADI24140	Adi24140 VPAC2 rec
716	28	29.2	30	10	AEF09441	Aef09441 Pegylated	789	28	29.2	31	8	ADI24000	Adi24000 VPAC2 rec
717	28	29.2	30	10	AEF09494	Aef09494 Pegylated	790	28	29.2	31	8	ADI24071	Adi24071 VPAC2 rec
718	28	29.2	30	10	AEF09502	Aef09502 Pegylated	791	28	29.2	31	8	ADI24071	Adi24071 VPAC2 rec
719	28	29.2	30	10	AEF09504	Aef09504 Pegylated	792	28	29.2	31	8	ADI24117	Adi24117 VPAC2 rec
720	28	29.2	30	10	AEF09426	Aef09426 Pegylated	793	28	29.2	31	8	ADI24132	Adi24132 VPAC2 rec
721	28	29.2	30	10	AEF09495	Aef09495 Pegylated	794	28	29.2	31	8	ADI24141	Adi24141 VPAC2 rec
722	28	29.2	30	10	AEF09496	Aef09496 Pegylated	795	28	29.2	31	8	ADI23995	Adi23995 VPAC2 rec
723	28	29.2	30	10	AEF09514	Aef09514 Pegylated	796	28	29.2	31	8	ADI24136	Adi24136 VPAC2 rec
724	28	29.2	30	10	AEF09517	Aef09517 Pegylated	797	28	29.2	31	8	ADI23998	Adi23998 VPAC2 rec
725	28	29.2	30	10	AEF09418	Aef09418 Pegylated	798	28	29.2	31	8	ADI23999	Adi23999 VPAC2 rec
726	28	29.2	30	10	AEF09437	Aef09437 Pegylated	799	28	29.2	31	8	ADI24139	Adi24139 VPAC2 rec
727	28	29.2	30	10	AEF09497	Aef09497 Pegylated	800	28	29.2	31	8	ADI24067	Adi24067 VPAC2 rec
728	28	29.2	30	10	AEF09432	Aef09432 Pegylated	801	28	29.2	31	8	ADI24076	Adi24076 VPAC2 rec
729	28	29.2	30	10	AEF09432	Aef09432 Pegylated	802	28	29.2	31	8	ADI24126	Adi24126 VPAC2 rec
730	28	29.2	30	10	AEF09427	Aef09427 Pegylated	803	28	29.2	31	8	ADI24130	Adi24130 VPAC2 rec
731	28	29.2	30	10	AEF09489	Aef09489 Pegylated	804	28	29.2	31	8	ADI23990	Adi23990 VPAC2 rec
732	28	29.2	30	10	AEF09509	Aef09509 Pegylated	805	28	29.2	31	8	ADI24070	Adi24070 VPAC2 rec
733	28	29.2	30	10	AEF09515	Aef09515 Pegylated	806	28	29.2	31	8	ADI24120	Adi24120 VPAC2 rec
734	28	29.2	30	10	AEF09516	Aef09516 Pegylated	807	28	29.2	31	8	ADI24124	Adi24124 VPAC2 rec
735	28	29.2	30	10	AEF09421	Aef09421 Pegylated	808	28	29.2	31	9	ADV90888	Adv90888 Glucagon-
736	28	29.2	30	10	AEF09436	Aef09436 Pegylated	809	28	29.2	31	9	ADV90889	Adv90889 Glucagon-
737	28	29.2	30	10	AEF09506	Aef09506 Pegylated	810	28	29.2	31	9	ADV90885	Adv90885 Glucagon-
738	28	29.2	30	10	AEF09513	Aef09513 Pegylated	811	28	29.2	31	9	ADV90884	Adv90884 Glucagon-
739	28	29.2	30	10	AEF09413	Aef09413 Pegylated	812	28	29.2	31	9	ADY40404	Ady40404 Glucose-d
740	28	29.2	30	10	AEF09443	Aef09443 Pegylated	813	28	29.2	31	9	ADY40399	Ady40399 Glucose-d
741	28	29.2	30	10	AEF09501	Aef09501 Pegylated	814	28	29.2	31	9	ADY40403	Ady40403 Glucose-d
742	28	29.2	30	10	AEF09503	Aef09503 Pegylated	815	28	29.2	31	9	ADY40400	Ady40400 Glucose-d
743	28	29.2	30	10	AEF09425	Aef09425 Pegylated	816	28	29.2	31	9	AEB87947	Aeb87947 VPAC 2 ag
744	28	29.2	30	10	AEF09434	Aef09434 Pegylated	817	28	29.2	31	9	AEB88021	Aeb88021 VPAC 2 ag
745	28	29.2	30	10	AEF09498	Aef09498 Pegylated	818	28	29.2	31	9	AEB87952	Aeb87952 VPAC 2 ag
746	28	29.2	30	10	AEF09500	Aef09500 Pegylated	819	28	29.2	31	9	AEB88075	Aeb88075 VPAC 2 ag
747	28	29.2	30	10	AEF09507	Aef09507 Pegylated	820	28	29.2	31	9	AEB87950	Aeb87950 VPAC 2 ag
748	28	29.2	30	10	AEF09508	Aef09508 Pegylated	821	28	29.2	31	9	AEB88026	Aeb88026 VPAC 2 ag
749	28	29.2	30	10	AEF09510	Aef09510 Pegylated	822	28	29.2	31	9	AEB88065	Aeb88065 VPAC 2 ag
750	28	29.2	30	10	AEF09419	Aef09419 Pegylated	823	28	29.2	31	9	AEB88072	Aeb88072 VPAC 2 ag
751	28	29.2	30	10	AEF09429	Aef09429 Pegylated	824	28	29.2	31	9	AEB88073	Aeb88073 VPAC 2 ag
752	28	29.2	30	10	AEF09435	Aef09435 Pegylated	825	28	29.2	31	9	AEB88085	Aeb88085 VPAC 2 ag
753	28	29.2	30	10	AEF09520	Aef09520 Pegylated	826	28	29.2	31	9	AEB88091	Aeb88091 VPAC 2 ag
												AEb87951	AEb87951 VPAC 2 ag

827	28	29.2	31	9	AEB88022	Aeb88022	VPAC 2 ag	900	28	29.2	31	9	AEE62721	Aee62721	VPAC2-rec
828	28	29.2	31	9	AEB88060	Aeb88060	VPAC 2 ag	901	28	29.2	31	9	AEE62727	Aee62727	VPAC2-rec
829	28	29.2	31	9	AEB88079	Aeb88079	VPAC 2 ag	902	28	29.2	31	9	AEE62785	Aee62785	VPAC2-rec
830	28	29.2	31	9	AEB88025	Aeb88025	VPAC 2 ag	903	28	29.2	31	9	AEE62510	Aee62510	VPAC2-rec
831	28	29.2	31	9	AEB88077	Aeb88077	VPAC 2 ag	904	28	29.2	31	9	AEE62724	Aee62724	VPAC2-rec
832	28	29.2	31	9	AEB88067	Aeb88067	VPAC 2 ag	905	28	29.2	31	9	AEE62776	Aee62776	VPAC2-rec
833	28	29.2	31	9	AEB88086	Aeb88086	VPAC 2 ag	906	28	29.2	31	9	AEE62507	Aee62507	VPAC2-rec
834	28	29.2	31	9	AEB88095	Aeb88095	VPAC 2 ag	907	28	29.2	31	9	AEE62768	Aee62768	VPAC2-rec
835	28	29.2	31	9	AEB87953	Aeb87953	VPAC 2 ag	908	28	29.2	31	9	AEE62770	Aee62770	VPAC2-rec
836	28	29.2	31	9	AEB88068	Aeb88068	VPAC 2 ag	909	28	29.2	31	9	AEE62781	Aee62781	VPAC2-rec
837	28	29.2	31	9	AEB88070	Aeb88070	VPAC 2 ag	910	28	29.2	31	9	AEE62788	Aee62788	VPAC2-rec
838	28	29.2	31	9	AEB88080	Aeb88080	VPAC 2 ag	911	28	29.2	31	9	AEE35477	Aee35477	VPAC2-rec
839	28	29.2	31	9	AEB88083	Aeb88083	VPAC 2 ag	912	28	29.2	31	9	AEE35611	Aee35611	VPAC2-rec
840	28	29.2	31	9	AEB88089	Aeb88089	VPAC 2 ag	913	28	29.2	31	9	AEE35729	Aee35729	VPAC2-rec
841	28	29.2	31	9	AEB88019	Aeb88019	VPAC 2 ag	914	28	29.2	31	9	AEE35756	Aee35756	VPAC2-rec
842	28	29.2	31	9	AEB88024	Aeb88024	VPAC 2 ag	915	28	29.2	31	9	AEE35476	Aee35476	VPAC2-rec
843	28	29.2	31	9	AEB88082	Aeb88082	VPAC 2 ag	916	28	29.2	31	9	AEE35616	Aee35616	VPAC2-rec
844	28	29.2	31	9	AEB88066	Aeb88066	VPAC 2 ag	917	28	29.2	31	9	AEE35690	Aee35690	VPAC2-rec
845	28	29.2	31	9	AEB88081	Aeb88081	VPAC 2 ag	918	28	29.2	31	9	AEE35693	Aee35693	VPAC2-rec
846	28	29.2	31	9	AEB88090	Aeb88090	VPAC 2 ag	919	28	29.2	31	9	AEE35736	Aee35736	VPAC2-rec
847	28	29.2	31	9	AEB88018	Aeb88018	VPAC 2 ag	920	28	29.2	31	9	AEE35742	Aee35742	VPAC2-rec
848	28	29.2	31	9	AEB88027	Aeb88027	VPAC 2 ag	921	28	29.2	31	9	AEE35747	Aee35747	VPAC2-rec
849	28	29.2	31	9	AEB88069	Aeb88069	VPAC 2 ag	922	28	29.2	31	9	AEE35737	Aee35737	VPAC2-rec
850	28	29.2	31	9	AEB88074	Aeb88074	VPAC 2 ag	923	28	29.2	31	9	AEE35740	Aee35740	VPAC2-rec
851	28	29.2	31	9	AEB88076	Aeb88076	VPAC 2 ag	924	28	29.2	31	9	AEE35741	Aee35741	VPAC2-rec
852	28	29.2	31	9	AEB88084	Aeb88084	VPAC 2 ag	925	28	29.2	31	9	AEE35749	Aee35749	VPAC2-rec
853	28	29.2	31	9	AEB88078	Aeb88078	VPAC 2 ag	926	28	29.2	31	9	AEE35755	Aee35755	VPAC2-rec
854	28	29.2	31	9	AEB88096	Aeb88096	VPAC 2 ag	927	28	29.2	31	9	AEE35686	Aee35686	VPAC2-rec
855	28	29.2	31	9	AEB87944	Aeb87944	VPAC 2 ag	928	28	29.2	31	9	AEE35618	Aee35618	VPAC2-rec
856	28	29.2	31	9	AEB88071	Aeb88071	VPAC 2 ag	929	28	29.2	31	9	AEE35689	Aee35689	VPAC2-rec
857	28	29.2	31	9	AEB88087	Aeb88087	VPAC 2 ag	930	28	29.2	31	9	AEE35609	Aee35609	VPAC2-rec
858	28	29.2	31	9	AEB88088	Aeb88088	VPAC 2 ag	931	28	29.2	31	9	AEE35757	Aee35757	VPAC2-rec
859	28	29.2	31	9	AEB87945	Aeb87945	VPAC 2 ag	932	28	29.2	31	9	AEE35613	Aee35613	VPAC2-rec
860	28	29.2	31	9	AEB87948	Aeb87948	VPAC 2 ag	933	28	29.2	31	9	AEE35738	Aee35738	VPAC2-rec
861	28	29.2	31	9	AEB62773	Aee62773	VPAC2-rec	934	28	29.2	31	9	AEE35754	Aee35754	VPAC2-rec
862	28	29.2	31	9	AEB62778	Aee62778	VPAC2-rec	935	28	29.2	31	9	AEE35694	Aee35694	VPAC2-rec
863	28	29.2	31	9	AEB62780	Aee62780	VPAC2-rec	936	28	29.2	31	9	AEE35734	Aee35734	VPAC2-rec
864	28	29.2	31	9	AEB62769	Aee62769	VPAC2-rec	937	28	29.2	31	9	AEE35735	Aee35735	VPAC2-rec
865	28	29.2	31	9	AEB62771	Aee62771	VPAC2-rec	938	28	29.2	31	9	AEE35743	Aee35743	VPAC2-rec
866	28	29.2	31	9	AEB62774	Aee62774	VPAC2-rec	939	28	29.2	31	9	AEE35692	Aee35692	VPAC2-rec
867	28	29.2	31	9	AEB62787	Aee62787	VPAC2-rec	940	28	29.2	31	9	AEE35695	Aee35695	VPAC2-rec
868	28	29.2	31	9	AEB62643	Aee62643	VPAC2-rec	941	28	29.2	31	9	AEE35748	Aee35748	VPAC2-rec
869	28	29.2	31	9	AEB62650	Aee62650	VPAC2-rec	942	28	29.2	31	9	AEE35758	Aee35758	VPAC2-rec
870	28	29.2	31	9	AEB62653	Aee62653	VPAC2-rec	943	28	29.2	31	9	AEE35473	Aee35473	VPAC2-rec
871	28	29.2	31	9	AEB62782	Aee62782	VPAC2-rec	944	28	29.2	31	9	AEE35739	Aee35739	VPAC2-rec
872	28	29.2	31	9	AEB62723	Aee62723	VPAC2-rec	945	28	29.2	31	9	AEE35744	Aee35744	VPAC2-rec
873	28	29.2	31	9	AEB62729	Aee62729	VPAC2-rec	946	28	29.2	31	9	AEE35753	Aee35753	VPAC2-rec
874	28	29.2	31	9	AEB62763	Aee62763	VPAC2-rec	947	28	29.2	31	9	AEE35610	Aee35610	VPAC2-rec
875	28	29.2	31	9	AEB62606	Aee62606	VPAC2-rec	948	28	29.2	31	9	AEE35745	Aee35745	VPAC2-rec
876	28	29.2	31	9	AEB62645	Aee62645	VPAC2-rec	949	28	29.2	31	9	AEE35759	Aee35759	VPAC2-rec
877	28	29.2	31	9	AEB62652	Aee62652	VPAC2-rec	950	28	29.2	31	9	AEE35760	Aee35760	VPAC2-rec
878	28	29.2	31	9	AEB62728	Aee62728	VPAC2-rec	951	28	29.2	31	9	AEE35751	Aee35751	VPAC2-rec
879	28	29.2	31	9	AEB62772	Aee62772	VPAC2-rec	952	28	29.2	31	9	AEE35614	Aee35614	VPAC2-rec
880	28	29.2	31	9	AEB62779	Aee62779	VPAC2-rec	953	28	29.2	31	9	AEE35746	Aee35746	VPAC2-rec
881	28	29.2	31	9	AEB62647	Aee62647	VPAC2-rec	954	28	29.2	31	9	AEE35472	Aee35472	VPAC2-rec
882	28	29.2	31	9	AEB62648	Aee62648	VPAC2-rec	955	28	29.2	31	9	AEE35617	Aee35617	VPAC2-rec
883	28	29.2	31	9	AEB62777	Aee62777	VPAC2-rec	956	28	29.2	31	9	AEE35687	Aee35687	VPAC2-rec
884	28	29.2	31	9	AEB62784	Aee62784	VPAC2-rec	957	28	29.2	31	9	AEE35750	Aee35750	VPAC2-rec
885	28	29.2	31	9	AEB62794	Aee62794	VPAC2-rec	958	28	29.2	31	9	AEE35752	Aee35752	VPAC2-rec
886	28	29.2	31	9	AEB62644	Aee62644	VPAC2-rec	959	28	29.2	31	9	AEE35619	Aee35619	VPAC2-rec
887	28	29.2	31	9	AEB62720	Aee62720	VPAC2-rec	960	28	29.2	31	9	AEE35685	Aee35685	VPAC2-rec
888	28	29.2	31	9	AEB62790	Aee62790	VPAC2-rec	961	28	29.2	31	10	AEE33015	Aee33015	Insulin r
889	28	29.2	31	9	AEB62775	Aee62775	VPAC2-rec	962	28	29.2	31	10	AEE33018	Aee33018	Insulin r
890	28	29.2	31	9	AEB62719	Aee62719	VPAC2-rec	963	28	29.2	31	10	AEE33019	Aee33019	Insulin r
891	28	29.2	31	9	AEB62789	Aee62789	VPAC2-rec	964	28	29.2	31	10	AEE33014	Aee33014	Insulin r
892	28	29.2	31	9	AEB62793	Aee62793	VPAC2-rec	965	28	29.2	31	10	AEEF09408	AeeF09408	Pegylated
893	28	29.2	31	9	AEB62726	Aee62726	VPAC2-rec	966	28	29.2	31	10	AEEF09491	AeeF09491	Pegylated
894	28	29.2	31	9	AEB62792	Aee62792	VPAC2-rec	967	28	29.2	31	10	AEEF09553	AeeF09553	Pegylated
895	28	29.2	31	9	AEB62511	Aee62511	VPAC2-rec	968	28	29.2	31	10	AEEF09547	AeeF09547	Pegylated
896	28	29.2	31	9	AEB62651	Aee62651	VPAC2-rec	969	28	29.2	31	10	AEEF09548	AeeF09548	Pegylated
897	28	29.2	31	9	AEB62783	Aee62783	VPAC2-rec	970	28	29.2	31	10	AEEF09411	AeeF09411	Pegylated
898	28	29.2	31	9	AEB62786	Aee62786	VPAC2-rec	971	28	29.2	31	10	AEEF09546	AeeF09546	Pegylated
899	28	29.2	31	9	AEB62791	Aee62791	VPAC2-rec	972	28	29.2	31	10	AEEF09555	AeeF09555	Pegylated

973 Aef09558 Pegylated
 974 Aef09414 Pegylated
 975 Aef09534 Pegylated
 976 Aef09549 Pegylated
 977 Aef09554 Pegylated
 978 Aef09556 Pegylated
 979 Aef09416 Pegylated
 980 Aef09535 Pegylated
 981 Aef09543 Pegylated
 982 Aef09409 Pegylated
 983 Aef09412 Pegylated
 984 Aef09415 Pegylated
 985 Aef09488 Pegylated
 986 Aef09527 Pegylated
 987 Aef09533 Pegylated
 988 Aef09536 Pegylated
 989 Aef09550 Pegylated
 990 Aef09551 Pegylated
 991 Aef09485 Pegylated
 992 Aef09490 Pegylated
 993 Aef09537 Pegylated
 994 Aef09557 Pegylated
 995 Aef09417 Pegylated
 996 Aef09532 Pegylated
 997 Aef09542 Pegylated
 998 Aef09493 Pegylated
 999 Aef09539 Pegylated
 1000 Aef09540 Pegylated

ALIGNMENTS

RESULT 1
 ADX69810
 ID ADX69810 standard; peptide; 23 AA.
 AC ADX69810;
 DT 21-APR-2005 (first entry)
 XX Human K41-glycated CD59 immunogenic peptide, seqid:14.
 XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Modified-site 3 /note= "Lys is glycated"
 XX US2005032128-A1.
 XX 10-FEB-2005.
 XX 17-JUN-2004; 2004US-00870342.
 XX 08-MAY-2000; 2000US-0203254P.
 XX 16-APR-2001; 2001US-00835752.
 XX (HARD) HARVARD COLLEGE.
 XX Halperin J;
 XX WPI; 2005-161655/17.

PT Novel isolated antibody or its antigen-binding fragment, binding specifically to glycated epitope of glycated CD59, in which epitope including glycated lysine, useful for diagnosing and treating diabetic conditions.
 PT
 PT
 XX Disclosure; SEQ ID NO 14; 41pp; English.
 XX The present invention relates to an antibody or its antigen-binding fragment, binding specifically to a glycated epitope of glycated CD59, where the epitope including a glycated lysine. The invention is useful for diagnosing and treating diabetic conditions and diabetic-associated conditions, where the diabetes includes juvenile diabetes (Type 1 diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes and any other conditions of insulin deficiency or reduction in the ability to metabolize glucose. The invention is also useful in treatments and/or medications to reduce glycated CD59 levels, thus reducing, for e.g., subject's risk of complications including diabetic nephropathy, diabetic retinopathy, macro-vascular disease, micro-vascular disease and diabetic neuropathy. The antibody is useful for isolating and identifying CD59 protein and in screening patients for diseases associated with the presence of elevated levels of glycated CD59, to differentiate whether or not a subject has a diabetic condition. The present sequence is the human K41-glycated CD59 immunogenic peptide. K41 represents the lysine position in full-length mature CD59 protein.
 XX Sequence 23 AA;
 SQ
 Query Match 100.0%; Score 96; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 7.3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FEHCNFDVTTLRENE 17
 DB 4 FEHCNFDVTTLRENE 20
 RESULT 2
 ADX69816
 ID ADX69816 standard; peptide; 26 AA.
 XX
 AC ADX69816;
 XX
 DT 21-APR-2005 (first entry)
 XX Human K41-glycated CD59 immunogenic peptide, seqid:20.
 DE
 XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4 /note= "Lys is glycated"
 XX US2005032128-A1.
 XX 10-FEB-2005.
 XX 17-JUN-2004; 2004US-00870342.
 XX 08-MAY-2000; 2000US-0203254P.
 XX 16-APR-2001; 2001US-00835752.
 XX (HARD) HARVARD COLLEGE.
 XX Halperin J;
 PI

XX WPI; 2005-161655/17.
XX
XX Novel isolated antibody or its antigen-binding fragment, binding
PT specifically to glycosylated epitope of glycosylated CD59, in which epitope
PT including glycosylated lysine, useful for diagnosing and treating diabetic
PT conditions.
XX
XX Disclosure; SEQ ID NO 20; 41pp; English.
XX
XX The present invention relates to an antibody or its antigen-binding
CC fragment, binding specifically to a glycosylated epitope of glycosylated CD59,
CC where the epitope including a glycosylated lysine. The invention is useful
CC for diagnosing and treating diabetic conditions and diabetic-associated
CC conditions, where the diabetes includes juvenile diabetes (Type 1
CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
CC and any other conditions of insulin deficiency or reduction in the
CC ability to metabolize glucose. The invention is also useful in treatments
CC and/or medications to reduce glycosylated CD59 levels, thus reducing, for
CC e.g., subject's risk of complications including diabetic nephropathy,
CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
CC diabetic neuropathy. The antibody is useful for isolating and identifying
CC CD59 protein and in screening patients for diseases associated with the
CC presence of elevated levels of glycosylated CD59, to differentiate whether or
CC not a subject has a diabetic condition. The present sequence is the human
CC K41-glycosylated CD59 immunogenic peptide. K41 represents the lysine position
CC in full-length mature CD59 protein.
XX
XX Sequence 26 AA;
SQ
Query Match 100.0%; Score 96; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTTRENE 17
Db 5 FEHCNFDVTTRENE 21
RESULT 3
ADX69811
ID ADX69811 standard; peptide; 30 AA.
XX AC ADX69811;
XX
XX 21-APR-2005 (first entry)
XX
XX Human K41-glycosylated CD59 immunogenic peptide, seqid:15.
XX
XX Antibody production; antigen; diagnosis; pharmaceutical;
KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
KW endocrine disease; gastrointestinal disease; metabolic disorder;
KW non-insulin dependent diabetes; diabetic nephropathy;
KW genitourinary disease; nephrotropic; diabetic retinopathy;
KW ophthalmological; cardiovascular disease; ocular disease;
KW diabetic neuropathy; neuroprotective; neurological disease;
KW vascular disease; vasotropic; cd59.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 11
FT /note= "Lys is glycosylated"
FT
XX US2005032128-A1.
XX
XX 10-FEB-2005.
XX
XX 17-JUN-2004; 2004US-00870342.
XX
XX 08-MAY-2000; 2000US-0203254P.
PR 16-APR-2001; 2001US-00835752.
XX

PA (HARD) HARVARD COLLEGE.
XX Halperin J;
XX WPI; 2005-161655/17.
XX
XX Novel isolated antibody or its antigen-binding fragment, binding
PT specifically to glycosylated epitope of glycosylated CD59, in which epitope
PT including glycosylated lysine, useful for diagnosing and treating diabetic
PT conditions.
XX
XX Disclosure; SEQ ID NO 15; 41pp; English.
XX
XX The present invention relates to an antibody or its antigen-binding
CC fragment, binding specifically to a glycosylated epitope of glycosylated CD59,
CC where the epitope including a glycosylated lysine. The invention is useful
CC for diagnosing and treating diabetic conditions and diabetic-associated
CC conditions, where the diabetes includes juvenile diabetes (Type 1
CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
CC and any other conditions of insulin deficiency or reduction in the
CC ability to metabolize glucose. The invention is also useful in treatments
CC and/or medications to reduce glycosylated CD59 levels, thus reducing, for
CC e.g., subject's risk of complications including diabetic nephropathy,
CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
CC diabetic neuropathy. The antibody is useful for isolating and identifying
CC CD59 protein and in screening patients for diseases associated with the
CC presence of elevated levels of glycosylated CD59, to differentiate whether or
CC not a subject has a diabetic condition. The present sequence is the human
CC K41-glycosylated CD59 immunogenic peptide. K41 represents the lysine position
CC in full-length mature CD59 protein.
XX
XX Sequence 30 AA;
SQ
Query Match 100.0%; Score 96; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTTRENE 17
Db 12 FEHCNFDVTTRENE 28
RESULT 4
AEE66127
ID AEE66127 standard; peptide; 36 AA.
XX AC AEE66127;
XX
XX 09-FEB-2006 (first entry)
XX
XX Human CD59 peptide (amino acids 67-104) SEQ ID: 44 #1.
XX Protein detection; pesticide; biological warfare; cd59.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Binding-site 11
FT /note= "glycosylphosphatidylinositol (GPI) attachment
FT site"
FT /note= "This position corresponds to position 77 of the
FT full length human CD59 protein"
XX US2005272114-A1.
XX
XX 08-DEC-2005.
XX
XX 06-DEC-2004; 2004US-00006031.
XX
XX 31-JAN-2003; 2003US-0444094P.
PR 30-MAY-2003; 2003US-0474659P.
PR 30-JAN-2004; 2004US-00768976.
PR 30-JUL-2004; 2004US-0592499P.
PR

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 PA (ENCE/) ENCELL L.
 PA (JOHN/) JOHNSON T.
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 PA (LGEO/) LOS GEORGYI V.
 PA (MCDO/) MCDUGALL M.
 PA (WOOD/) WOOD K V.
 PA (WOOD/) WOOD M G.
 PA (ZIMP/) ZIMPRICH C.
 XX Darzins A, Encell L, Johnson T, Klaubert D, Los Georgyi V;
 PI McDougall M, Wood KV, Wood MG, Zimprich C;
 XX WPI; 2006-044483/05.
 XX Compound useful for detecting molecules of interest e.g. protein in
 PT sample or labeling animal, having functional groups, multiatom straight
 PT or branched chain, substrate for dehalogenase and halogen.
 XX Example 11; SEQ ID NO 44; 121pp; English.
 XX The present invention provides methods, compositions and kits for
 CC tethering (linking), e.g., via a covalent or otherwise stable bond, one
 CC or more functional groups to a protein of the invention or to a fusion
 CC protein (chimera) which includes a protein of the invention. A protein of
 CC the invention is a mutant hydrolase having atleast two amino acid
 CC substitutions relative to the wild-type hydrolase (e.g. haloalkane
 CC dehalogenase; Dna enzyme which catalyzes the irreversible hydrolysis of a
 CC variety of haloalkanes). The mutant hydrolase binds a substrate of the
 CC corresponding wild-type hydrolase but lacks or has reduced catalytic
 CC activity relative to the wild-type hydrolase. The invention also provides
 CC hydrolase substrates comprising one or more functional groups and fusion
 CC proteins capable of forming a stable bond with the substrate and cells
 CC which express the fusion proteins. The invention is useful for isolating
 CC a molecule of interest, detecting one or more molecules of interest in a
 CC sample (e.g. physiological sample) where the molecule of interest is
 CC specific for one or more infectious agents, labeling cells in a
 CC transgenic animal, labeling an animal, selectively inhibiting one or more
 CC proteins of interest or cellular activities in a cell, labeling proteins
 CC and for detecting pesticides, industrial toxic compounds, infectious
 CC agents and bio weapons. The present sequence is a human CD59 peptide
 CC (amino acids 67-104). This sequence contains the
 CC glycosylphosphatidylinositols (GPI) attachment site at residue 77. This
 CC sequence is used to generate a GPI-anchored DhaA mutant for cell surface
 CC display. Note: The present sequence is the SEQ ID NO: 44 which is given
 CC in the sequence listing. This sequence differs from the SEQ ID NO: 44
 CC shown on example 8 (page 52) of the specification (see AEB66165).
 XX SQ Sequence 36 AA;

Query Match 100.0%; Score 96; DB 10; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FEHCNFNDVTVTLRENE 17
 |||||
 Db 1 FEHCNFNDVTVTLRENE 17

RESULT 5
 AEF63782
 ID AEF63782 standard; peptide; 36 AA.
 XX
 AC AEF63782;
 XX
 DT 06-APR-2006 (first entry)
 XX Human CD59 amino acids 67 to 102 SEQ ID NO:44.
 DE
 XX mutant; dehalogenase; hydrolase; protein engineering; CD59.
 KW
 XX Homo sapiens.
 OS

XX US2006024808-A1.
 XX 02-FEB-2006.
 XX 29-JUL-2005; 2005US-00194110.
 XX 30-JUL-2004; 2004US-0592499P.
 XX (DARZ/) DARZINS A.
 PA (ENCE/) ENCELL L.
 PA (KLAU/) KLAUBERT D.
 PA (LGEO/) LOS GEORGYI V.
 PA (MCDO/) MCDUGALL M.
 PA (WOOD/) WOOD K V.
 PA (WOOD/) WOOD M G.
 PA (ZIMP/) ZIMPRICH C.
 XX Darzins A, Encell L, Klaubert D, Los Georgyi V, McDougall M;
 PI Wood KV, Wood MG, Zimprich C;
 XX WPI; 2006-135434/14.

XX New mutant dehalogenase comprising at least two amino acid substitutions
 PT relative to a corresponding wild-type dehalogenase, useful for isolating,
 PT detecting, identifying, imaging, displaying, or localizing molecules of
 PT interest.

XX Example 11; SEQ ID NO 44; 170pp; English.

XX The invention relates to a mutant dehalogenase comprising at least two
 PS amino acid substitutions relative to a corresponding wild-type
 CC dehalogenase, where the mutant dehalogenase forms a bond with a
 CC dehalogenase substrate which comprises one or more functional groups,
 CC which bond is more stable than the bond formed between the corresponding
 CC wild-type dehalogenase and the substrate. Also described: (1) a method
 CC for detecting or determining the presence or amount of a mutant hydrolase
 CC ; (2) a method for isolating a molecule, cell or sub-cellular organelle
 CC of interest in a sample; (3) a method for labeling a cell; (4) a method
 CC for labeling a cell; (5) a polynucleotide encoding the mutant hydrolase;
 CC (6) a mutant hydrolase comprising at least two amino acid substitutions
 CC relative to a corresponding wild-type hydrolase, where one substitution
 CC is at a position corresponding to amino acid residue 272 of a Rhodococcus
 CC rhodochrous dehalogenase or at a position corresponding to amino acid
 CC residue 106 of a Rhodococcus rhodochrous dehalogenase, and a second
 CC substitution is at an amino acid residue corresponding to position 175,
 CC 176 or 273 of a Rhodococcus rhodochrous dehalogenase; and (7) a
 CC thermostable mutant dehalogenase comprising at least one substitution
 CC a position corresponding to amino acid residue 175 of a Rhodococcus
 CC rhodochrous dehalogenase, which substitution is correlated with enhanced
 CC thermostability relative to a corresponding mutant dehalogenase without
 CC the substitution at the position corresponding to amino acid residue 175.
 CC The mutant dehalogenase is useful for isolating, detecting, identifying,
 CC imaging, displaying, or localizing molecules of interest; labeling cells,
 CC including live cell imaging; or labeling proteins in vitro and/or in
 CC vivo. The present sequence represents a human CD59 peptide of amino acids
 CC 67 to 102 containing the GPI attachment site at residue 77, which is used
 CC in an example from the present invention.

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 96; DB 10; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNFNDVTVTLRENE 17
 |||||
 Db 1 FEHCNFNDVTVTLRENE 17

RESULT 6
 ADX69809
 ID ADX69809 standard; peptide; 18 AA.

XX AC ADX69809;
XX DT 21-APR-2005 (first entry)
XX DE Human K41-glycated CD59 immunogenic peptide, seqid:13.
XX KW Antibody production; antigen; diagnosis; pharmaceutical;
KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
KW endocrine disease; gastrointestinal disease; metabolic disorder;
KW non-insulin dependent diabetes; diabetic nephropathy;
KW genitourinary disease; nephrotropic; diabetic retinopathy;
KW ophthalmological; cardiovascular disease; ocular disease;
KW diabetic neuropathy; neuroprotective; neurological disease;
KW vascular disease; vasotrophic; cd59.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Lys is glycated"
XX PN US2005032128-A1.
XX PD 10-FEB-2005.
XX PF 17-JUN-2004; 2004US-00870342.
XX PR 08-MAY-2000; 2000US-0203254P.
XX PR 16-APR-2001; 2001US-00835752.
XX PA (HARD) HARVARD COLLEGE.
XX PI Halperin J;
XX DR WPI; 2005-161655/17.
XX PT Novel isolated antibody or its antigen-binding fragment, binding
PT specifically to glycated epitope of glycated CD59, in which epitope
PT including glycated lysine, useful for diagnosing and treating diabetic
PT conditions.
XX PS Disclosure; SEQ ID NO 13; 41pp; English.
XX CC The present invention relates to an antibody or its antigen-binding
CC fragment, binding specifically to a glycated epitope of glycated CD59,
CC where the epitope including a glycated lysine. The invention is useful
CC for diagnosing and treating diabetic conditions and diabetic-associated
CC conditions, where the diabetes includes juvenile diabetes (Type 1
CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
CC and any other conditions of insulin deficiency or reduction in the
CC ability to metabolize glucose. The invention is also useful in treatments
CC and/or medications to reduce glycated CD59 levels, thus reducing, for
CC e.g., subject's risk of complications including diabetic nephropathy,
CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
CC diabetic neuropathy. The antibody is useful for isolating and identifying
CC CD59 protein and in screening patients for diseases associated with the
CC presence of elevated levels of glycated CD59, to differentiate whether or
CC not a subject has a diabetic condition. The present sequence is the human
CC K41-glycated CD59 immunogenic peptide. K41 represents the lysine position
CC in full-length mature CD59 protein.
XX SQ Sequence 18 AA;
Query Match 94.8%; Score 91; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTTLRN 16
Db 3 FEHCNFDVTTLRN 18
|||||

RESULT 7
ADX69815
ID ADX69815 standard; peptide; 18 AA.
XX AC ADX69815;
XX DT 21-APR-2005 (first entry)
XX DE Human K41-glycated CD59 immunogenic peptide, seqid:19.
XX KW Antibody production; antigen; diagnosis; pharmaceutical;
KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
KW endocrine disease; gastrointestinal disease; metabolic disorder;
KW non-insulin dependent diabetes; diabetic nephropathy;
KW genitourinary disease; nephrotropic; diabetic retinopathy;
KW ophthalmological; cardiovascular disease; ocular disease;
KW diabetic neuropathy; neuroprotective; neurological disease;
KW vascular disease; vasotrophic; cd59.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 4 /note= "Lys is glycated"
XX PN US2005032128-A1.
XX PD 10-FEB-2005.
XX PF 17-JUN-2004; 2004US-00870342.
XX PR 08-MAY-2000; 2000US-0203254P.
XX PR 16-APR-2001; 2001US-00835752.
XX PA (HARD) HARVARD COLLEGE.
XX PI Halperin J;
XX DR WPI; 2005-161655/17.
XX PT Novel isolated antibody or its antigen-binding fragment, binding
PT specifically to glycated epitope of glycated CD59, in which epitope
PT including glycated lysine, useful for diagnosing and treating diabetic
PT conditions.
XX PS Disclosure; SEQ ID NO 19; 41pp; English.
XX CC The present invention relates to an antibody or its antigen-binding
CC fragment, binding specifically to a glycated epitope of glycated CD59,
CC where the epitope including a glycated lysine. The invention is useful
CC for diagnosing and treating diabetic conditions and diabetic-associated
CC conditions, where the diabetes includes juvenile diabetes (Type 1
CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
CC and any other conditions of insulin deficiency or reduction in the
CC ability to metabolize glucose. The invention is also useful in treatments
CC and/or medications to reduce glycated CD59 levels, thus reducing, for
CC e.g., subject's risk of complications including diabetic nephropathy,
CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
CC diabetic neuropathy. The antibody is useful for isolating and identifying
CC CD59 protein and in screening patients for diseases associated with the
CC presence of elevated levels of glycated CD59, to differentiate whether or
CC not a subject has a diabetic condition. The present sequence is the human
CC K41-glycated CD59 immunogenic peptide. K41 represents the lysine position
CC in full-length mature CD59 protein.
XX SQ Sequence 18 AA;
Query Match 83.3%; Score 80; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTTLR 14
|||||

Db 5 FEHCNFNDVTTLR 18

RESULT 8

ADX69837

ID ADX69837 standard; peptide; 25 AA.

XX

AC ADX69837;

XX

DT 21-APR-2005 (first entry)

XX

DE Human K65 and K66-glycated CD59 immunogenic peptide, seqid:41.

XX

DE Antibody production; antigen; diagnosis; pharmaceutical;

KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;

KW endocrine disease; gastrointestinal disease; metabolic disorder;

KW non-insulin dependent diabetes; diabetic nephropathy;

KW genitourinary disease; nephrotropic; diabetic retinopathy;

KW ophthalmological; cardiovascular disease; ocular disease;

KW diabetic neuropathy; neuroprotective; neurological disease;

KW vascular disease; vasotropic; cd59.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Modified-site 21..22

FT /note= "Lys is glycated"

XX

US2005032128-A1.

PN

XX

PD 10-FEB-2005.

XX

XX

PF 17-JUN-2004; 2004US-00870342.

XX

PR 08-MAY-2000; 2000US-0203254P.

PR 16-APR-2001; 2001US-00835752.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Halperin J;

XX

XX

WPI; 2005-161655/17.

DR

XX

PT Novel isolated antibody or its antigen-binding fragment, binding specifically to glycated epitope of glycated CD59, in which epitope including glycated lysine, useful for diagnosing and treating diabetic conditions.

PT

XX

PS Disclosure; SEQ ID NO 41; 41pp; English.

XX

CC The present invention relates to an antibody or its antigen-binding fragment, binding specifically to a glycated epitope of glycated CD59, where the epitope including a glycated lysine. The invention is useful for diagnosing and treating diabetic conditions and diabetic-associated conditions, where the diabetes includes juvenile diabetes (Type 1 diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes and any other conditions of insulin deficiency or reduction in the ability to metabolize glucose. The invention is also useful in treatments and/or medications to reduce glycated CD59 levels, thus reducing, for e.g., subject's risk of complications including diabetic nephropathy, diabetic retinopathy, macro-vascular disease, micro-vascular disease and diabetic neuropathy. The antibody is useful for isolating and identifying CD59 protein and in screening patients for diseases associated with the presence of elevated levels of glycated CD59, to differentiate whether or not a subject has a diabetic condition. The present sequence is the human K65 and K66-glycated CD59 immunogenic peptide. K65 and K66 represents the lysine position in full-length mature CD59 protein.

CC

XX

Sequence 25 AA;

Query Match 80.2%; Score 77; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.8e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db 1 FEHCNFNDVTTLR 18

RESULT 10

QY 4 CNENDVTTLRENE 17

Db 1 CNFNDVTTLRENE 14

RESULT 9

ADT77352

ID ADT77352 standard; peptide; 12 AA.

XX

AC ADT77352;

XX

DT 13-JAN-2005 (first entry)

XX

DE Human cardiovascular disorder plasma polypeptide CPP15 peptide - SEQ 43.

XX

KW cardiovascular disorder; cardiac; vasotropic; cerebroprotective;

KW hypotensive; antiarteriosclerotic; heart disease; vascular disease;

KW cerebral ischaemia; atherosclerosis; hypertension; CPP15.

XX

OS Homo sapiens.

XX

PN WO2004090551-A2.

XX

PD 21-OCT-2004.

XX

PF 07-APR-2004; 2004WO-EP003737.

XX

PR 08-APR-2003; 2003US-0461558P.

PR 08-APR-2003; 2003US-0461623P.

PR 16-MAY-2003; 2003US-0471479P.

PR 30-MAY-2003; 2003US-0474863P.

PR 30-JUN-2003; 2003US-0484140P.

XX

PA (XENO-) XENOVA LTD.

PA (NOVS) NOVARTIS PHARMA GMBH.

XX

PI Aigoud-Puy G, Bederr N, Bougueleret L, Cusin I, Mahe E;

PI Niknejad A, Reffas S;

XX

WPI; 2004-775414/76.

DR

XX

PT New isolated polypeptide, useful for screening for and/or diagnosis of, or predicting a cardiovascular disorder, and for identifying a modulator for treating cardiovascular disorders e.g. atherosclerosis and cerebral ischemia.

PT

XX

PS Disclosure; SEQ ID NO 43; 166pp; English.

XX

CC The invention relates to a novel isolated cardiovascular disorder plasma polypeptide (CPP) comprising an amino acid sequence of SEQ ID NO: 1-5, 6-10, 11-14, 15-23 or 24-28, fully defined in the specification, where the polypeptide is fused to a heterologous polypeptide sequence. The polypeptide of the invention demonstrates cardiovascular, cardiac, vasotrophic, cerebroprotective, hypotensive and antiarteriosclerotic activities and may be useful during diagnosis, prevention and treatment of coronary artery disease, coronary heart disease, peripheral vascular disease, cerebral ischaemia, congestive heart failure, atherosclerosis, hypertension and other cardiovascular diseases. The current sequence is that of a human CPP tryptic peptide of the invention.

CC

XX

Sequence 12 AA;

Query Match 74.0%; Score 71; DB 8; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00032;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db 1 FEHCNFNDVTTR 12

1 FEHCNFNDVTTR 12

ADT61251
ID ADT61251 standard; peptide; 12 AA.
XX
AC ADT61251;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human antileukoprotease 1 tryptic peptide #21.
XX
KW cardiovascular disorder plasma polypeptide; cardiovascular disorder;
KW coronary artery disease; human; antileukoprotease 1.
XX
OS Homo sapiens.
XX
PN WO2004089987-A1.
XX
PD 21-OCT-2004.
XX
PF 07-APR-2004; 2004WO-EP003746.
XX
PR 08-APR-2003; 2003US-0461560P.
XX
PA (XENO-) XENOVA LTD.
PA (NOVS) NOVARTIS PHARMA GMBH.
XX
PI Argoud-Puy G, Bederr N, Bougueleret L, Cusin I, Mahe B;
PI Niknejad A, Reffas S;
XX
DR WPI; 2004-748725/73.
XX
PT New human secreted polypeptides associated with cardiovascular disorders,
PT useful for diagnosing, preventing or treating cardiovascular disorders,
PT for preparing a drug-eluting stent, or for drug screening or drug
PT monitoring.
XX
PS Disclosure; SEQ ID NO 23; 145pp; English.
XX
CC The invention relates to a cardiovascular disorder plasma polypeptide
CC where the polypeptide is fused to a heterologous polypeptide sequence.
CC The polypeptide or its antibody is useful in the preparation of a
CC medicament for the prophylaxis and/or treatment of cardiovascular
CC disorders or in the preparation of a drug-eluting stent. The composition
CC and methods are also used for diagnosing, screening or predicting
CC cardiovascular disorders (e.g. coronary artery disease), for drug
CC screening or for monitoring the efficacy of treatment of cardiovascular
CC disorders. The present sequence represents the amino acid sequence of a
CC human antileukoprotease 1 tryptic peptide.
XX
SQ Sequence 12 AA;
Query Match 74.0%; Score 71; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTR 12
Db 1 FEHCNFDVTR 12
|||||
RESULT 11
ADU14952
ID ADU14952 standard; peptide; 12 AA.
XX
AC ADU14952;
XX
DT 27-JAN-2005 (first entry)
XX
DE Human Cardiovascular disorder Plasma polypeptide, CPP 15 #3.
XX
KW Human; CPP; cardiovascular disorder plasma polypeptide;
KW cardiovascular disorder; drug-eluting stent; coronary artery disease;
KW coronary heart disease; peripheral vascular disease; cerebral ischaemia;
KW stroke; congestive heart failure; atherosclerosis; hypertension;
XX

immunogen.
KW
XX Homo sapiens.
XX
PN WO2004097423-A1.
XX
PD 11-NOV-2004.
XX
PF 23-APR-2004; 2004WO-EP004342.
XX
PR 25-APR-2003; 2003US-0465484P.
XX
PA (XENO-) XENOVA LTD.
PA (NOVS) NOVARTIS PHARMA GMBH.
XX
PI Bougueleret L, Cusin I;
XX
DR WPI; 2004-804848/79.
XX
PT New isolated polypeptide, useful for preparing a medicament for the
PT prophylaxis and/or treatment of cardiovascular disorders such as coronary
PT artery disease, atherosclerosis, or hypertension, or for preparing a drug
PT -eluting stent.
XX
PS Disclosure; SEQ ID NO 27; 146pp; English.
XX
CC The invention relates to an isolated polypeptide comprising human
CC adrenomedullin (precursor, mature, plasma circulating fragment or tryptic
CC peptide) appearing as ADU14926-ADU14931, where the polypeptide is fused
CC to a heterologous polypeptide sequence. Also included are screening for
CC (and/or diagnosing of, or predicting) a cardiovascular disorder in a
CC subject, an anti-Cardiovascular disorder Plasma Polypeptide (CPP)
CC antibody that selectively binds to the polypeptide, binding an antibody
CC to a CPP, identifying a CPP modulator, identifying a modulator of a
CC cardiovascular disorder and monitoring the efficacy of a treatment of a
CC subject having or at risk of developing a cardiovascular disorder with an
CC agent. The polypeptide, its variant with at least 75% sequence identity,
CC having one or more amino acid substitutions, deletions or insertions, or
CC its fragment which is a least ten amino acids long, or the antibody, is
CC useful for preparing a medicament for the prophylaxis and/or treatment of
CC cardiovascular disorders or for preparing a drug-eluting stent. The
CC polypeptide is useful as a diagnostic tool for determining the risk of
CC coronary artery disease, coronary heart disease, peripheral vascular
CC disease, cerebral ischaemia (stroke), congestive heart failure,
CC atherosclerosis, hypertension, and other cardiovascular diseases. The
CC polypeptides are also useful for drug development, diagnosis and
CC prevention of cardiovascular disease. The methods and compositions are
CC useful for screening, diagnosing and prognosing a living individual, but
CC may also be used for postmortem diagnosis in an individual e.g. to
CC identify family members who are at risk of developing the same disorder.
CC Also disclosed are circulating CPP peptides derived from adrenomedullin
CC who are differentially expressed in cardiovascular disorders. The present
CC sequence is a disclosed CPP peptide.
XX
SQ Sequence 12 AA;
Query Match 74.0%; Score 71; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVTR 12
Db 1 FEHCNFDVTR 12
|||||
RESULT 12
ADU15085
ID ADU15085 standard; peptide; 12 AA.
XX
AC ADU15085;
XX
DT 27-JAN-2005 (first entry)
XX

DE Human Cardiovascular disorder Plasma polypeptide, CPP 15 #3.
XX
KW Human; CPP; cardiovascular disorder plasma polypeptide;
KW cardiovascular disorder; drug-eluting stent; coronary artery disease;
KW coronary heart disease; peripheral vascular disease; cerebral ischaemia;
KW stroke; congestive heart failure; atherosclerosis; hypertension;
KW immunogen.
XX
OS Homo sapiens.
XX
FN WO2004097424-A1.
XX
XX 11-NOV-2004.
PD
XX 23-APR-2004; 2004WO-EP004350.
XX
XX 25-APR-2003; 2003US-0465369P.
XX
XX (XENO-) XENOVA LTD.
PA (NOVS) NOVARTIS PHARMA GMBH.
XX
PI Bougueleret L, Refas S;
XX WPI; 2004-804849/79.
DR
XX New isolated polypeptide, useful as a diagnostic tool and for drug
XX development for the treatment of cardiovascular disorders such as
PT coronary artery disease, atherosclerosis, hypertension, and congestive
PT heart failure.
XX
PS Disclosure; SEQ ID NO 23; 138pp; English.
XX
CC The invention relates to an isolated polypeptide comprising human Serine
CC phosphoprotein [precursor, mature, plasma circulating fragment or tryptic
CC peptide] appearing as ADU15063-ADU15070, where the polypeptide is fused
CC to a heterologous polypeptide sequence. Also included are screening for
CC (and/or diagnosing of, or predicting) a cardiovascular disorder in a
CC subject, an anti-Cardiovascular disorder Plasma Polypeptide (CPP)
CC antibody that selectively binds to the polypeptide, binding an antibody
CC to a CPP, identifying a CPP modulator, identifying a modulator of a
CC cardiovascular disorder and monitoring the efficacy of a treatment with a
CC subject having or at risk of developing a cardiovascular disorder with an
CC agent. The polypeptide, its variant with at least 75% sequence identity,
CC having one or more amino acid substitutions, deletions or insertions, or
CC its fragment which is a least ten amino acids long, or the antibody, is
CC useful for preparing a medicament for the prophylaxis and/or treatment of
CC cardiovascular disorders or for preparing a drug-eluting stent. The
CC polypeptide is useful as a diagnostic tool for determining the risk of
CC coronary artery disease, coronary heart disease, peripheral vascular
CC disease, cerebral ischaemia (stroke), congestive heart failure,
CC atherosclerosis, hypertension, and other cardiovascular diseases. The
CC polypeptides are also useful for drug development, diagnosis and
CC prevention of cardiovascular disease. The methods and compositions are
CC useful for screening, diagnosing and prognosing a living individual, but
CC may also be used for postmortem diagnosis in an individual e.g. to
CC identify family members who are at risk of developing the same disorder.
CC Also disclosed are circulating CPP peptides derived from adrenomedullin
CC who are differentially expressed in cardiovascular disorders. The present
CC sequence is a disclosed CPP peptide.
XX
SQ Sequence 12 AA;

Query Match 74.0%; Score 71; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNENDVTR 12
| | | | | | | | | | | |
Db 1 FEHCNENDVTR 12

RESULT 13
ADU74235

ADU74235 standard; peptide; 12 AA.
ADU74235;
10-FEB-2005 (first entry)
Human cardiovascular disorder plasma polypeptide 15 tryptic peptide #3.
Cardiovascular disorder plasma polypeptide; CPP;
liver expressed antimicrobial peptide; diagnosis; cardiovascular disease;
myocardial ischemia; atherosclerosis; angina pectoris; heart arrhythmia;
cerebrovascular ischemia; myocardial infarction; coronary artery disease;
peripheral vascular disease; congestive heart failure; hypertension;
cardiant; vasotropic; antiarrhythmic; cerebroprotective;
Cardiovascular-Gen.; Antiarteriosclerotic.
Homo sapiens.
WO2004101615-A2.
25-NOV-2004.
14-MAY-2004; 2004WO-EP005195.
16-MAY-2003; 2003US-0471061P.
(XENO-) XENOVA LTD.
(NOVS) NOVARTIS PHARMA GMBH.
Bougueleret L, Mahe E;
WPI; 2004-833975/82.
Screening for and/or diagnosing and/or predicting a cardiovascular
disorder comprises detecting and/or quantifying the level of
cardiovascular disorder plasma polypeptide in a biological sample from
the subject.
Disclosure; SEQ ID NO 23; 139pp; English.
The invention relates to screening for and/or diagnosing and/or
predicting a cardiovascular disorder in a subject comprising detecting
and/or quantifying the level of a cardiovascular disorder plasma
polypeptide (CPP) in a biological sample from the subject. Also included
are an isolated CPP14 (also known as liver expressed antimicrobial
peptide, LEAP-2) polypeptide appearing as ADU74213-ADU74216, an anti-
Cardiovascular disorder Plasma Polypeptide (CPP) antibody, a method of
binding an antibody to a CPP, a method of identifying a CPP modulator, a
method of identifying a modulator of a cardiovascular disorder and a
method for monitoring the efficacy of a treatment of a subject having or
at risk of developing a cardiovascular disorder with an agent. The
polypeptide above is useful for preparing a medicament for the
prophylaxis and/or treatment of cardiovascular disorders or for preparing
a drug-eluting stent. The method is useful for screening for and/or
diagnosing and/or predicting a cardiovascular disorder in a subject. The
polypeptide, polynucleotide, composition, and methods are useful for
diagnosing, preventing and/or treating a cardiovascular disorder, i.e.
Coronary Artery Disease (CAD), or atherosclerosis and ischemic diseases.
The present sequence is a tryptic fragment from a CPP protein.
SQ Sequence 12 AA;

Query Match 74.0%; Score 71; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNENDVTR 12
| | | | | | | | | | | |
Db 1 FEHCNENDVTR 12

RESULT 14
ADV09024

ID ADV09024 standard; peptide; 12 AA.
AC ADV09024;
XX
DT 24-FEB-2005 (first entry)
XX
DE Human cardiovascular disorder plasma polypeptide (CPP) #10.
XX
KW Cardiovascular disorder plasma polypeptide; cardiovascular disease;
KW coronary artery disease; heart disease; peripheral vascular disease;
KW cerebrovascular ischemia; congestive heart failure; atherosclerosis;
KW hypertension; cardiovascular-gen.; cardiac; vasotropic;
KW cerebroprotective; antiarteriosclerotic; hypotensive; ELISA;
KW mass spectrometry.
XX
OS Homo sapiens.
XX
XX WO2004106941-A2.
XX
XX 09-DEC-2004.
XX
XX 28-MAY-2004; 2004WO-EP005786.
XX
XX 30-MAY-2003; 2003US-0475082P.
PR 30-MAY-2003; 2003US-0475083P.
PR 30-MAY-2003; 2003US-0475121P.
PR 30-JUN-2003; 2003US-0484102P.
XX
XX (XENO-) XENOVA LTD.
PA (NOVS) NOVARTIS PHARMA GMBH.
XX
XX Bougueleret L;
XX
XX WPI; 2005-048374/05.
XX
XX Novel isolated cardiovascular disorder plasma polypeptides useful for
PT identifying agents capable of treating cardiovascular disorder such as
PT coronary artery disease or cerebral ischemia.
XX
XX Claim 8; SEQ ID NO 10; 150pp; English.
XX
XX The invention relates to an isolated polypeptide comprising one of 25
CC cardiovascular disorder plasma polypeptide (CPP) sequences and fused to a
CC heterologous polypeptide sequence. The invention also relates to a method
CC of screening for and/or diagnosis of a cardiovascular disorder in a
CC subject involving detecting and/or quantifying the level of a polypeptide
CC in a biological sample from the subject and comparing the level to that of
CC a control sample, where an increase in the level relative to that of
CC the control is indicative of a cardiovascular disorder, a method of
CC binding an antibody to a CPP involving contacting an anti-CPP antibody
CC with a biological sample under conditions that permit antibody binding,
CC and removing contaminants, and a method of identifying a CPP modulator
CC involving contacting a test compound with a CPP under sample conditions
CC permissive for at least one CPP biological activity, determining the
CC level of at least one CPP biological activity, comparing the level to
CC that of a control sample lacking the test compound and selecting a test
CC compound which causes the level to change for further testing as a CPP
CC modulator of cardiovascular disorders. The methods and the polypeptides
CC are useful in screening for and/or diagnosis of a cardiovascular disorder
CC such as coronary artery disease (CAD), for predicting a risk of onset of
CC a cardiovascular disorder, for identifying a modulator of a
CC cardiovascular disorder and in monitoring the efficacy of a treatment of
CC a subject having or at risk of developing a cardiovascular disorder. The
CC CPP modulator is useful for preventing or treating disorders associated
CC with aberrant expression or processing of CPPs, such as CAD, coronary
CC heart disease, peripheral vascular disease, cerebral ischemia (stroke),
CC congestive heart failure, atherosclerosis, hypertension and other
CC cardiovascular diseases. This sequence represents a human cardiovascular
CC disorder plasma polypeptide of the invention.
XX
SQ Sequence 12 AA;

Query Match

74.0%; Score 71; DB 9; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFDVVTTR 12
DB 1 FEHCNFDVVTTR 12
RESULT 15
ADK69841
ID ADK69841 standard; peptide; 21 AA.
XX
AC ADK69841;
XX
XX 21-APR-2005 (first entry)
XX
XX Human K65 and K66-glycated CD59 immunogenic peptide, seqid:45.
XX
KW Antibody production; antigen; diagnosis; pharmaceutical;
KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
KW endocrine disease; gastrointestinal disease; metabolic disorder;
KW non-insulin dependent diabetes; diabetic nephropathy;
KW genitourinary disease; nephrotropic; diabetic retinopathy;
KW ophthalmological; cardiovascular disease; ocular disease;
KW diabetic neuropathy; neuroprotective; neurological disease;
KW vascular disease; vasotropic; cd59.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 19..20
FT /note= "Lys is glycated"
XX
XX US2005032128-A1.
XX
XX 10-FEB-2005.
XX
XX 17-JUN-2004; 2004US-00870342.
PR
XX 08-MAY-2000; 2000US-0203254P.
PR 16-APR-2001; 2001US-00835752.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Halperin J;
XX
XX WPI; 2005-161655/17.
XX
XX Novel isolated antibody or its antigen-binding fragment, binding
PT specifically to glycated epitope of glycated CD59, in which epitope
PT including glycated lysine, useful for diagnosing and treating diabetic
PT conditions.
XX
XX Disclosure; SEQ ID NO 45; 41pp; English.
XX
XX The present invention relates to an antibody or its antigen-binding
CC fragment, binding specifically to a glycated epitope of glycated CD59,
CC where the epitope including a glycated lysine. The invention is useful
CC for diagnosing and treating diabetic conditions and diabetic-associated
CC conditions, where the diabetes includes juvenile diabetes (Type 1
CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
CC and any other conditions of insulin deficiency or reduction in the
CC ability to metabolize glucose. The invention is also useful in treatments
CC and/or medications to reduce glycated CD59 levels, thus reducing, for
CC e.g., subject's risk of complications including diabetic nephropathy,
CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
CC diabetic neuropathy. The antibody is useful for isolating and identifying
CC CD59 protein and in screening patients for diseases associated with the
CC presence of elevated levels of glycated CD59, to differentiate whether or
CC not a subject has a diabetic condition. The present sequence is the human
CC K65 and K66-glycated CD59 immunogenic peptide. K65 and K66 represents the
CC lysine position in full-length mature CD59 protein.
XX

SQ Sequence 21 AA;
Query Match 64.6%; Score 62; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 FNDVTTTLRENE 17
| | | | | | | | | | | | | | | | | | | | | |
DB 1 FNDVTTTLRENE 12

RESULT 16
ADX69800
ID ADX69800 standard; peptide; 13 AA.
AC ADX69800;
XX
XX 21-APR-2005 (first entry)
XX
XX Human CD59 immunogenic peptide, seqid:4.
XX Antibody production; antigen; diagnosis; pharmaceutical;
KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
KW endocrine disease; gastrointestinal disease; metabolic disorder;
KW non-insulin dependent diabetes; diabetic nephropathy;
KW genitourinary disease; nephrotropic; diabetic retinopathy;
KW ophthalmological; cardiovascular disease; ocular disease;
KW diabetic neuropathy; neuroprotective; neurological disease;
KW vascular disease; vasotropic; cd59.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 8 /note= "Lys is glycosylated"
FT
XX US2005032128-A1.
XX
XX 10-FEB-2005.
XX
XX 17-JUN-2004; 2004US-00870342.
XX
XX 08-MAY-2000; 2000US-0203254P.
PR 16-APR-2001; 2001US-00835752.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Halperin J;
XX
XX WPI; 2005-161655/17.
XX
XX Novel isolated antibody or its antigen-binding fragment, binding
PT specifically to glycosylated epitope of glycosylated CD59, in which epitope
PT including glycosylated lysine, useful for diagnosing and treating diabetic
PT conditions.
XX
XX Disclosure; SEQ ID NO 4; 41pp; English.
XX
XX The present invention relates to an antibody or its antigen-binding
CC fragment, binding specifically to a glycosylated epitope of glycosylated CD59,
CC where the epitope including a glycosylated lysine. The invention is useful
CC for diagnosing and treating diabetic conditions and diabetic-associated
CC conditions, where the diabetes includes juvenile diabetes (Type 1
CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
CC and any other conditions of insulin deficiency or reduction in the
CC ability to metabolize glucose. The invention is also useful in treatments
CC and/or medications to reduce glycosylated CD59 levels, thus reducing, for
CC e.g., subject's risk of complications including diabetic nephropathy,
CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
CC diabetic neuropathy. The antibody is useful for isolating and identifying
CC CD59 protein and in screening patients for diseases associated with the
CC presence of elevated levels of glycosylated CD59, to differentiate whether or
CC not a subject has a diabetic condition. The present sequence is the human
CC CD59 immunogenic peptide.
XX
XX Sequence 13 AA;

Query Match 54.2%; Score 52; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FEHCNFD 8
| | | | | | | |
DB 6 FEHCNFD 13

RESULT 17
ADX69812
ID ADX69812 standard; peptide; 16 AA.
XX
XX AC ADX69812;
XX
XX DT 21-APR-2005 (first entry)
XX
XX DE Human K41-glycosylated CD59 immunogenic peptide, seqid:16.
XX
XX Antibody production; antigen; diagnosis; pharmaceutical;
KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
KW endocrine disease; gastrointestinal disease; metabolic disorder;
KW non-insulin dependent diabetes; diabetic nephropathy;
KW genitourinary disease; nephrotropic; diabetic retinopathy;
KW ophthalmological; cardiovascular disease; ocular disease;
KW diabetic neuropathy; neuroprotective; neurological disease;
KW vascular disease; vasotropic; cd59.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 8 /note= "Lys is glycosylated"
FT
XX US2005032128-A1.
XX
XX 10-FEB-2005.
XX
XX 17-JUN-2004; 2004US-00870342.
XX
XX 08-MAY-2000; 2000US-0203254P.
PR 16-APR-2001; 2001US-00835752.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX Halperin J;
XX
XX WPI; 2005-161655/17.
XX
XX Novel isolated antibody or its antigen-binding fragment, binding
PT specifically to glycosylated epitope of glycosylated CD59, in which epitope
PT including glycosylated lysine, useful for diagnosing and treating diabetic
PT conditions.
XX
XX Disclosure; SEQ ID NO 16; 41pp; English.
XX
XX The present invention relates to an antibody or its antigen-binding
CC fragment, binding specifically to a glycosylated epitope of glycosylated CD59,
CC where the epitope including a glycosylated lysine. The invention is useful
CC for diagnosing and treating diabetic conditions and diabetic-associated
CC conditions, where the diabetes includes juvenile diabetes (Type 1
CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
CC and any other conditions of insulin deficiency or reduction in the
CC ability to metabolize glucose. The invention is also useful in treatments
CC and/or medications to reduce glycosylated CD59 levels, thus reducing, for
CC e.g., subject's risk of complications including diabetic nephropathy,
CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
CC diabetic neuropathy. The antibody is useful for isolating and identifying
CC CD59 protein and in screening patients for diseases associated with the
CC presence of elevated levels of glycosylated CD59, to differentiate whether or
CC not a subject has a diabetic condition. The present sequence is the human
CC K41-glycosylated CD59 immunogenic peptide. K41 represents the lysine position
CC in full-length mature CD59 protein.

XX SQ Sequence 16 AA;
 Query Match 54.2%; Score 52; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNPNFND 8
 |||||
 Db 9 FEHCNPNFND 16

RESULT 18
 ADX69818
 ID ADX69818 standard; peptide; 18 AA.
 XX
 AC ADX69818;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Human K41-glycated CD59 immunogenic peptide, seqid:22.
 XX
 DE Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 10
 FT /note= "Lys is glycated"
 FT
 XX US2005032128-A1.
 XX
 XX 10-FEB-2005.
 XX
 XX 17-JUN-2004; 2004US-00870342.
 XX
 XX 08-MAY-2000; 2000US-0203254P.
 XX 16-APR-2001; 2001US-00835752.
 XX
 XX (HARD) HARVARD COLLEGE.
 XX
 XX Halperin J;
 XX
 XX WPI; 2005-161655/17.
 XX
 XX Novel isolated antibody or its antigen-binding fragment, binding
 PT specifically to glycated epitope of glycated CD59, in which epitope
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.
 XX
 XX Disclosure; SEQ ID NO 22; 41pp; English.
 XX
 XX The present invention relates to an antibody or its antigen-binding
 CC fragment, binding specifically to a glycated epitope of glycated CD59,
 CC where the epitope including a glycated lysine. The invention is useful
 CC for diagnosing and treating diabetic conditions and diabetic-associated
 CC conditions, where the diabetes includes juvenile diabetes (Type 1
 CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
 CC and any other conditions of insulin deficiency or reduction in the
 CC ability to metabolize glucose. The invention is also useful in treatments
 CC and/or medications to reduce glycated CD59 levels, thus reducing, for
 CC e.g., subject's risk of complications including diabetic nephropathy,
 CC diabetic retinopathy, macro-vascular disease, micro-vascular disease, and
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycated CD59, to differentiate whether or

CC not a subject has a diabetic condition. The present sequence is the human
 CC K41-glycated CD59 immunogenic peptide. K41 represents the lysine position
 CC in full-length mature CD59 protein.

XX SQ Sequence 18 AA;
 Query Match 54.2%; Score 52; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNPNFND 8
 |||||
 Db 11 FEHCNPNFND 18

RESULT 19
 ADX69819
 ID ADX69819 standard; peptide; 14 AA.
 XX
 AC ADX69819;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE Human K41-glycated CD59 immunogenic peptide, seqid:23.
 XX
 DE Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "Lys is glycated"
 FT
 XX US2005032128-A1.
 XX
 XX 10-FEB-2005.
 XX
 XX 17-JUN-2004; 2004US-00870342.
 XX
 XX 08-MAY-2000; 2000US-0203254P.
 XX 16-APR-2001; 2001US-00835752.
 XX
 XX (HARD) HARVARD COLLEGE.
 XX
 XX Halperin J;
 XX
 XX WPI; 2005-161655/17.
 XX
 XX Novel isolated antibody or its antigen-binding fragment, binding
 PT specifically to glycated epitope of glycated CD59, in which epitope
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.
 XX
 XX Disclosure; SEQ ID NO 23; 41pp; English.
 XX
 XX The present invention relates to an antibody or its antigen-binding
 CC fragment, binding specifically to a glycated epitope of glycated CD59,
 CC where the epitope including a glycated lysine. The invention is useful
 CC for diagnosing and treating diabetic conditions and diabetic-associated
 CC conditions, where the diabetes includes juvenile diabetes (Type 1
 CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
 CC and any other conditions of insulin deficiency or reduction in the
 CC ability to metabolize glucose. The invention is also useful in treatments
 CC and/or medications to reduce glycated CD59 levels, thus reducing, for
 CC e.g., subject's risk of complications including diabetic nephropathy,
 CC diabetic retinopathy, macro-vascular disease, micro-vascular disease, and
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycated CD59, to differentiate whether or

CC diabetic neuropathy. The antibody is useful for isolating and identifying
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycated CD59, to differentiate whether or
 CC not a subject has a diabetic condition. The present sequence is the human
 CC K41-glycated CD59 immunogenic peptide. K41 represents the lysine position
 CC in full-length mature CD59 protein.

XX Sequence 14 AA;

Query Match 50.0%; Score 48; DB 9; Length 14;
 Best Local Similarity 87.5%; Pred. No. 1.6;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFD 8
 |||||
 Db 7 FEHCNFE 14

RESULT 20

ADX69820
 ID ADX69820 standard; peptide; 18 AA.

XX AC ADX69820;

XX 21-APR-2005 (first entry)

XX Human K41-glycated CD59 immunogenic peptide, seqid:24.

XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic neuropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 11
 FT /note= "Lys is glycated"

XX US2005032128-A1.

XX 10-FEB-2005.

XX 17-JUN-2004; 2004US-00870342.

XX 08-MAY-2000; 2000US-0203254P.

XX 16-APR-2001; 2001US-00835752.

XX (HARD) HARVARD COLLEGE.

XX Halperin J;

XX WPI; 2005-161655/17.

XX Novel isolated antibody or its antigen-binding fragment, binding
 PT specifically to glycated epitope of glycated CD59, in which epitope
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.

XX Disclosure; SEQ ID NO 24; 4lpp; English.

XX The present invention relates to an antibody or its antigen-binding
 CC fragment, binding specifically to a glycated epitope of glycated CD59,
 CC where the epitope including a glycated lysine. The invention is useful
 CC for diagnosing and treating diabetic conditions and diabetic-associated
 CC conditions, where the diabetes includes juvenile diabetes (Type 1
 CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
 CC and any other conditions of insulin deficiency or reduction in the
 CC ability to metabolize glucose. The invention is also useful in treatments

CC and/or medications to reduce glycated CD59 levels, thus reducing, for
 CC e.g., subject's risk of complications including diabetic nephropathy,
 CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
 CC diabetic neuropathy. The antibody is useful for isolating and identifying
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycated CD59, to differentiate whether or
 CC not a subject has a diabetic condition. The present sequence is the human
 CC K41-glycated CD59 immunogenic peptide. K41 represents the lysine position
 CC in full-length mature CD59 protein.

XX Sequence 18 AA;

Query Match 47.9%; Score 46; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FEHCNFN 7
 |||||
 Db 12 FEHCNFN 18

RESULT 21

ADX69840

ID ADX69840 standard; peptide; 21 AA.

XX AC ADX69840;

XX 21-APR-2005 (first entry)

XX Human K65 and K66-glycated CD59 immunogenic peptide, seqid:44.

XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic neuropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 16..17
 FT /note= "Lys is glycated"

XX US2005032128-A1.

XX 10-FEB-2005.

XX 17-JUN-2004; 2004US-00870342.

XX 08-MAY-2000; 2000US-0203254P.

XX 16-APR-2001; 2001US-00835752.

XX (HARD) HARVARD COLLEGE.

XX Halperin J;

XX WPI; 2005-161655/17.

XX Novel isolated antibody or its antigen-binding fragment, binding
 PT specifically to glycated epitope of glycated CD59, in which epitope
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.

XX Disclosure; SEQ ID NO 44; 4lpp; English.

XX The present invention relates to an antibody or its antigen-binding
 CC fragment, binding specifically to a glycated epitope of glycated CD59,
 CC where the epitope including a glycated lysine. The invention is useful
 CC for diagnosing and treating diabetic conditions and diabetic-associated
 CC conditions, where the diabetes includes juvenile diabetes (Type 1

CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
 CC and any other conditions of insulin deficiency or reduction in the
 CC ability to metabolize glucose. The invention is also useful in treatments
 CC and/or medications to reduce glycated CD59 levels, thus reducing, for
 CC e.g., subject's risk of complications including diabetic nephropathy,
 CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
 CC diabetic neuropathy. The antibody is useful for isolating and identifying
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycated CD59, to differentiate whether or
 CC not a subject has a diabetic condition. The present sequence is the human
 CC K65 and K66-glycated CD59 immunogenic peptide. K65 and K66 represents the
 CC lysine position in full-length mature CD59 protein.
 XX
 SQ Sequence 21 AA;

Query Match 45.8%; Score 44; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VTTRLRENE 17
 |||||
 Db 1 VTTRLRENE 9

RESULT 22

ADX69799
 ID ADX69799 standard; peptide; 14 AA.

XX
 AC ADX69799;

XX
 DT 21-APR-2005 (first entry)

XX
 DE Human K5-glycated CD59 immunogenic peptide, seqid:3.

XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT Modified-site 5 /note= "Lys is glycated"

XX
 PN US2005032128-A1.

XX
 PD 10-FEB-2005.

XX
 PF 17-JUN-2004; 2004US-00870342.

XX
 PR 08-MAY-2000; 2000US-0203254P.

XX
 PR 16-APR-2001; 2001US-00835752.

XX
 PA (HARD) HARVARD COLLEGE.

XX
 XX Halperin J;

XX
 PI WPI; 2005-161655/17.

XX Novel isolated antibody or its antigen-binding fragment, binding
 PT specifically to glycated epitope of glycated CD59, in which epitope
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.

XX
 PS Claim 39; SEQ ID NO 3; 41pp; English.

XX The present invention relates to an antibody or its antigen-binding
 CC fragment, binding specifically to a glycated epitope of glycated CD59,

CC where the epitope including a glycated lysine. The invention is useful
 CC for diagnosing and treating diabetic conditions and diabetic-associated
 CC conditions, where the diabetes includes juvenile diabetes (Type 1
 CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
 CC and any other conditions of insulin deficiency or reduction in the
 CC ability to metabolize glucose. The invention is also useful in treatments
 CC and/or medications to reduce glycated CD59 levels, thus reducing, for
 CC e.g., subject's risk of complications including diabetic nephropathy,
 CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
 CC diabetic neuropathy. The antibody is useful for isolating and identifying
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycated CD59, to differentiate whether or
 CC not a subject has a diabetic condition. The present sequence is the human
 CC K5-glycated CD59 immunogenic peptide.
 XX
 SQ Sequence 14 AA;

Query Match 44.8%; Score 43; DB 9; Length 14;
 Best Local Similarity 87.5%; Pred. No. 9.7;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEHCNPNFND 8
 |||||
 Db 6 PEHCNPNFND 13

RESULT 23

ADX69806

ID ADX69806 standard; peptide; 14 AA.

XX
 AC ADX69806;

XX
 DT 21-APR-2005 (first entry)

XX
 DE Human K5-glycated CD59 immunogenic peptide, seqid:10.

XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT Modified-site 5 /note= "Lys is glycated"

XX
 PN US2005032128-A1.

XX
 PD 10-FEB-2005.

XX
 PF 17-JUN-2004; 2004US-00870342.

XX
 PR 08-MAY-2000; 2000US-0203254P.

XX
 PR 16-APR-2001; 2001US-00835752.

XX
 PA (HARD) HARVARD COLLEGE.

XX
 PI Halperin J;

XX
 DR WPI; 2005-161655/17.

XX Novel isolated antibody or its antigen-binding fragment, binding
 PT specifically to glycated epitope of glycated CD59, in which epitope
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.

XX
 PS Disclosure; SEQ ID NO 10; 41pp; English.

CC The present invention relates to an antibody or its antigen-binding
 CC fragment, binding specifically to a glycosylated epitope of glycosylated CD59,
 CC where the epitope including a glycosylated lysine. The invention is useful
 CC for diagnosing and treating diabetic conditions and diabetic-associated
 CC conditions, where the diabetes includes juvenile diabetes (Type 1
 CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
 CC and any other conditions of insulin deficiency or reduction in the
 CC ability to metabolize glucose. The invention is also useful in treatments
 CC and/or medications to reduce glycosylated CD59 levels, thus reducing, for
 CC e.g., subject's risk of complications including diabetic nephropathy,
 CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
 CC diabetic neuropathy. The antibody is useful for isolating and identifying
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycosylated CD59, to differentiate whether or
 CC not a subject has a diabetic condition. The present sequence is the human
 CC K41-glycosylated CD59 immunogenic peptide.

XX Sequence 14 AA;

Query Match 44.8%; Score 43; DB 9; Length 14;
 Best Local Similarity 87.5%; Pred. No. 9.7;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
 DB 6 FEHANFND 13
 ||| |||||

RESULT 24
 ADR38586
 ID ADR38586 standard; peptide; 15 AA.

XX ADR38586;

XX 18-NOV-2004 (first entry)

XX Human CD59 amino acids 36-50.

XX Human; CD59; protein glycation; diabetes mellitus; urine; immunogen;
 KW blood sugar; glycaemic control.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Modified-site 6 /note= "Optionally Glycosylated"

FT US2004166531-A1.

XX 26-AUG-2004.

XX 16-APR-2001; 2001US-00835752.

XX 08-MAY-2000; 2000US-0203254P.

XX (HALP/) HALPERIN J.

XX Halperin J;

XX WPI; 2004-634394/61.

XX Determining impact of blood sugar level on glycation levels in diabetic
 PT patient involves measuring level of lysine residue at specific position
 PT in glycosylated membrane protein associated with regulation of complement
 PT system.

XX Example 5; SEQ ID NO 1; 18pp; English.

XX The invention relates to determining the impact of blood sugar level on
 CC protein glycation levels in a subject involves measuring a level of
 CC lysine residue at position 41 in a glycosylated membrane protein CD59 (K41-
 CC glycosylated CD59) from a sample (e.g. urine). Also included are
 CC evaluating/selecting a treatment for regulating blood sugar levels (e.g.

CC in a patient suffering from diabetes mellitus), determining regression,
 CC progression or onset of a condition caused by abnormal levels of glycosylated
 CC protein, treating a subject to reduce the risk of or progression of a
 CC disorder associated with abnormally high levels of K41-glycosylated CD59, a
 CC composition comprising isolated, pure or fragment of isolated K41-
 CC glycosylated CD59; and an agent that binds to K41-glycosylated CD59 but not to
 CC K41-nonglycosylated CD59. The method is used to monitor glycaemic control in
 CC a diabetic patient, and to select subject for therapy, to monitor onset,
 CC progression and/or regression of diabetes or other diseases by monitoring
 CC levels of glycosylated CD59 in subject. The method provides direct indication
 CC of the level of the subject's glycaemic control thus effectively
 CC measuring impacts of blood sugar levels or glycation levels. The glycosylated
 CC CD59 can be detected in urine, thus obviating the need for a blood
 CC sample. The present sequence is a peptide used to raise anti-CD59
 CC antibodies, comprising amino acids 36-50 of human CD59.

XX Sequence 15 AA;

Query Match 44.8%; Score 43; DB 8; Length 15;
 Best Local Similarity 87.5%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNFND 8
 DB 7 FEHANFND 14
 ||| |||||

RESULT 25

ADT99253
 ID ADT99253 standard; peptide; 15 AA.

XX ADT99253;

XX 27-JAN-2005 (first entry)

XX Membrane protein CD59 antigenic fragment seqid 1.

XX diabetetic condition; glycosylated membrane protein; CD59; diabetes;
 KW protein glycation.

XX Homo sapiens.

XX US2004219606-A1.

XX 04-NOV-2004.

XX 28-APR-2004; 2004US-00833581.

XX 08-MAY-2000; 2000US-0203254P.

XX 16-APR-2001; 2001US-00835752.

XX (HALP/) HALPERIN J.

XX Halperin J;

XX WPI; 2004-794440/78.

XX Determining onset, progression or regression of diabetic condition by
 PT comparing obtained level of glycosylated membrane protein from human sample
 PT to control level as determination of onset, progression or regression of
 PT diabetic condition.

XX Disclosure; SEQ ID NO 1; 18pp; English.

XX The invention describes onset, progression or regression of a diabetic
 CC condition defined by abnormal levels of glycosylated protein is determined by
 CC obtaining a level of the amount of glycosylated membrane protein (CD59) from
 CC a sample obtained from a human subject and comparing the level of
 CC glycosylated CD59 in the sample to a control level as a determination of
 CC onset, progression or regression of the diabetic condition. Also
 CC described are: a method of measuring the level of glycosylated CD59 in a
 CC sample, comprising contacting the sample with an agent which binds
 CC specifically to glycosylated CD59 but not to non-glycosylated CD59; and measuring

CC the level of glycated CD59 in the sample; a method of assaying a sample,
 CC comprising obtaining a level of the amount of glycated CD59 from the
 CC sample; a method of identifying a subject at risk for a disorder
 CC associated with diabetes, comprising obtaining a level of the amount of
 CC glycated CD59 from a sample obtained from the subject; and comparing the
 CC level of glycated CD59 in the sample to a control level as a
 CC determination of the subject's risk for a disorder associated with
 CC diabetes; a composition of matter, comprising isolated glycated CD59; and
 CC a kit for measuring the level of glycated CD59 in a sample, comprising an
 CC agent that binds specifically to glycated CD59 but not to non-glycated
 CC CD59, and instructions for using the agent to detect the level of
 CC glycated CD59 in the sample. The method is useful for determining onset,
 CC progression, or regression of a diabetic condition defined by abnormal
 CC levels of glycated protein. The method is a simplified and less invasive
 CC method for rapid monitoring of protein glycation levels. This is the
 CC amino acid sequence of a membrane protein CD59 fragment used to raise
 CC antibodies to glycated CD59.

XX Sequence 15 AA;

Query Match 44.8%; Score 43; DB 8; Length 15;
 Best Local Similarity 87.5%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEHCNPNFND 8
 Db |||||
 7 FEHCNPNFND 14

RESULT 26

ADX69817
 ID ADX69817 standard; peptide; 13 AA.

XX ADX69817;

XX 21-APR-2005 (first entry)

XX Human K41-glycated CD59 immunogenic peptide, seqid:21.

XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "Lys is glycated"

FT US2005032128-A1.

XX 10-FEB-2005.

XX 17-JUN-2004; 2004US-00870342.

XX 08-MAY-2000; 2000US-0203254P.

XX 16-APR-2001; 2001US-00835752.

XX (HARD) HARVARD COLLEGE.

XX Halperin J;

XX WPI; 2005-161655/17.

XX Novel isolated antibody or its antigen-binding fragment, binding
 PT specifically to glycated epitope of glycated CD59, in which epitope
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.

XX

PS Disclosure; SEQ ID NO 21; 41pp; English.

XX The present invention relates to an antibody or its antigen-binding
 CC fragment, binding specifically to a glycated epitope of glycated CD59,
 CC where the epitope including a glycated lysine. The invention is useful
 CC for diagnosing and treating diabetic conditions and diabetic-associated
 CC conditions, where the diabetes includes juvenile diabetes (Type 1
 CC diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes
 CC and any other conditions of insulin deficiency or reduction in the
 CC ability to metabolize glucose. The invention is also useful in treatments
 CC and/or medications to reduce glycated CD59 levels, thus reducing, for
 CC e.g., subject's risk of complications including diabetic nephropathy,
 CC diabetic retinopathy, macro-vascular disease, micro-vascular disease and
 CC diabetic neuropathy. The antibody is useful for isolating and identifying
 CC CD59 protein and in screening patients for diseases associated with the
 CC presence of elevated levels of glycated CD59, to differentiate whether or
 CC not a subject has a diabetic condition. The present sequence is the human
 CC K41-glycated CD59 immunogenic peptide. K41 represents the lysine position
 CC in full-length mature CD59 protein.

XX Sequence 13 AA;

Query Match 41.7%; Score 40; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNPF 6

Db |||||
 8 FEHCNPF 13

RESULT 27

ADX69813
 ID ADX69813 standard; peptide; 17 AA.

XX ADX69813;

XX 21-APR-2005 (first entry)

XX Human K41-glycated CD59 immunogenic peptide, seqid:17.

XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 11 /note= "Lys is glycated"

FT US2005032128-A1.

XX 10-FEB-2005.

XX 17-JUN-2004; 2004US-00870342.

XX 08-MAY-2000; 2000US-0203254P.

XX 16-APR-2001; 2001US-00835752.

XX (HARD) HARVARD COLLEGE.

XX Halperin J;

XX WPI; 2005-161655/17.

XX Novel isolated antibody or its antigen-binding fragment, binding
 PT including glycated lysine, useful for diagnosing and treating diabetic
 PT conditions.

specifically to glycosylated epitope of glycosylated CD59, in which epitope including glycosylated lysine, useful for diagnosing and treating diabetic conditions.

Disclosure; SEQ ID NO 17; 41pp; English.

The present invention relates to an antibody or its antigen-binding fragment, binding specifically to a glycosylated epitope of glycosylated CD59, where the epitope including a glycosylated lysine. The invention is useful for diagnosing and treating diabetic conditions and diabetic-associated conditions, where the diabetes includes juvenile diabetes (Type 1 diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes and any other conditions of insulin deficiency or reduction in the ability to metabolize glucose. The invention is also useful in treatments and/or medications to reduce glycosylated CD59 levels, thus reducing, for e.g., subject's risk of complications including diabetic nephropathy, diabetic retinopathy, macro-vascular disease, micro-vascular disease and diabetic neuropathy. The antibody is useful for isolating and identifying CD59 protein and in screening patients for diseases associated with the presence of elevated levels of glycosylated CD59, to differentiate whether or not a subject has a diabetic condition. The present sequence is the human K41-glycosylated CD59 immunogenic peptide. K41 represents the lysine position in full-length mature CD59 protein.

Sequence 17 AA;

Query Match 41.7%; Score 40; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEHCNF 6
 |||||
 Db 12 FEHCNF 17

RESULT 28
 ADX69839
 ID ADX69839 standard; peptide; 19 AA.

AC ADX69839;

XX 21-APR-2005 (first entry)

XX Human K65 and K66-glycosylated CD59 immunogenic peptide, seqid:43.

XX Antibody production; antigen; diagnosis; pharmaceutical;
 KW antibody therapy; diabetes; antidiabetic; insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW non-insulin dependent diabetes; diabetic nephropathy;
 KW genitourinary disease; nephrotropic; diabetic retinopathy;
 KW ophthalmological; cardiovascular disease; ocular disease;
 KW diabetic neuropathy; neuroprotective; neurological disease;
 KW vascular disease; vasotropic; cd59.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 15..16 /note= "Lys is glycosylated"

XX US2005032128-A1.

XX 10-FEB-2005.

XX 17-JUN-2004; 2004US-00870342.

XX 08-MAY-2000; 2000US-0203254P.

XX 16-APR-2001; 2001US-00835752.

XX (HARD) HARVARD COLLEGE.

XX Halperin J;

XX

DR WPI; 2005-161655/17.
 XX Novel isolated antibody or its antigen-binding fragment, binding specifically to glycosylated epitope of glycosylated CD59, in which epitope including glycosylated lysine, useful for diagnosing and treating diabetic conditions.
 PT
 PT
 XX Disclosure; SEQ ID NO 43; 41pp; English.
 XX
 CC The present invention relates to an antibody or its antigen-binding fragment, binding specifically to a glycosylated epitope of glycosylated CD59, where the epitope including a glycosylated lysine. The invention is useful for diagnosing and treating diabetic conditions and diabetic-associated conditions, where the diabetes includes juvenile diabetes (Type 1 diabetes), adult-onset diabetes (Type 2 diabetes), gestational diabetes and any other conditions of insulin deficiency or reduction in the ability to metabolize glucose. The invention is also useful in treatments and/or medications to reduce glycosylated CD59 levels, thus reducing, for e.g., subject's risk of complications including diabetic nephropathy, diabetic retinopathy, macro-vascular disease, micro-vascular disease and diabetic neuropathy. The antibody is useful for isolating and identifying CD59 protein and in screening patients for diseases associated with the presence of elevated levels of glycosylated CD59, to differentiate whether or not a subject has a diabetic condition. The present sequence is the human K65 and K66-glycosylated CD59 immunogenic peptide. K65 and K66 represents the lysine position in full-length mature CD59 protein.

XX Sequence 19 AA;

Query Match 41.7%; Score 40; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TTRLRENE 17
 |||||
 Db 1 TTRLRENE 8

RESULT 29

ADC17659

ID ADC17659 standard; peptide; 18 AA.

XX ADC17659;

XX 18-DEC-2003 (first entry)

XX Type IV collagen NC1 domain related peptide SEQ ID NO:264.

XX crystallised NC1 domain hexamer of type IV collagen;
 KW angiogenesis inhibitor; angiogenesis-mediated disease;
 KW tumour metastasis inhibitor; tumour growth inhibitor;
 KW endothelial cell interaction inhibitor;
 KW basal lamina membrane formation inhibitor; cytotstatic; antipsoriatic;
 KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
 KW endothelial cell adhesion inhibitor;
 KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
 KW blood-borne tumour.

XX Synthetic.

OS Homo sapiens.

XX WO2003012122-A2.

XX 13-FEB-2003.

XX 26-JUL-2002; 2002WO-US023763.

XX 27-JUL-2001; 2001US-0308523P.

XX 29-OCT-2001; 2001US-0351289P.

XX 22-MAR-2002; 2002US-0366854P.

XX 03-JUN-2002; 2002US-0385362P.

XX

PA (UNIV) UNIV KANSAS MEDICAL CENT.
PA (SUND/) SUNDARAMOORTHY M.
PA (HUDS/) HUDSON B.
XX
XX Sundaramoorthy M, Hudson B;
XX WPI; 2003-332730/31.
XX
XX New polypeptide, useful for treating an angiogenesis-mediated disease or
PT condition consisting of glaucoma or blood-borne tumors or for inhibiting
PT basal lamina membrane formation in cell or tissue development.
XX
XX Claim 57; SEQ ID NO 264; 168pp; English.
XX
XX The present invention describes a crystallised NCI domain hexamer of type
CC IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a
CC pharmaceutical composition comprising the polypeptide and a carrier; (3)
CC inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
CC disease or condition in a mammal; (5) inhibiting tumour metastasis or
CC growth; (6) inhibiting endothelial cell interaction with the
CC extracellular matrix in an animal tissue; (6) inhibiting basal lamina
CC membrane formation in cell or tissue development; (7) a crystal of an NCI
CC domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
CC collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
CC crystallised NCI domain hexamer of type IV collagen (I) has cytostatic,
CC antiapoptotic, antiangiogenic, ophthalmological, antiarteriosclerotic and
CC antiulcer activities, and can be used as an inhibitor of angiogenesis,
CC tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
CC cell proliferation, and basal lamina assembly. A (I) polypeptide can be
CC used for treating an angiogenesis-mediated disease or condition
CC consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
CC psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
CC or for inhibiting basal lamina membrane formation in cell or tissue
CC development. The methods are useful for inhibiting angiogenesis in
CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
CC cell interaction with the extracellular matrix in an animal tissue, and
CC identifying inhibitors of type IV collagen assembly. The present sequence
CC represents a peptide which is used in the exemplification of the present
XX invention.
XX
XX Sequence 18 AA;
XX
XX Query Match 40.6%; Score 39; DB 7; Length 18;
XX Best Local Similarity 41.2%; Pred. No. 54;
XX Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 FEHCNFDVTVTLRENE 17
XX :|||:|||:
XX Db 2 FYICNINEVCHVARND 18
XX
XX RESULT 30
XX ADR19181
XX ID ADR19181 standard; peptide; 18 AA.
XX AC ADR19181;
XX
XX DT 04-NOV-2004 (first entry)
XX
XX DE Inter-CDSR plus contiguous hexamer Interface region alpha6 chain peptide.
XX
XX KW angiogenesis; angiogenesis-mediated disease; tumour metastasis;
XX tumour growth; type IV collagen; NCI domain hexamer; angiogenic;
XX cytostatic; antiangiogenic; ophthalmological; antiarthritic;
XX immunosuppressive; antiseborrheic; dermatological; antibacterial;
XX vulnary; antiulcer; fungicide; virucide; proteoacide; anti-HIV;
XX antiinflammatory; antiangiogenic; antiseborrheic; osteopathic; vasotropic;
XX gastrointestinal; antipsoriatic; antiatherosclerotic.
XX
XX OS Homo sapiens.
XX
XX PN WO2004067762-A2.
XX
XX

PD 12-AUG-2004.
XX
XX 27-JAN-2004; 2004WO-US002187.
XX
XX 27-JAN-2003; 2003US-0443133P.
XX
XX (UNIV) UNIV KANSAS MEDICAL CENT.
XX
XX Sundaramoorthy M, Hudson B;
XX WPI; 2004-594218/57.
XX
XX Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions,
PT tumor metastasis, and tumor growth, involves contacting subject with
PT crystallized type IV collagen NCI domain hexamer polypeptide.
XX
XX Disclosure; SEQ ID NO 264; 178pp; English.
XX
XX The invention relates to a novel method for inhibiting angiogenesis,
CC angiogenesis-mediated diseases or conditions, tumour metastasis, and
CC tumour growth, involving contacting a subject with a crystallised type IV
CC collagen NCI domain hexamer polypeptide. A polypeptide of the invention
CC has angiogenic, cytostatic, antiangiogenic, ophthalmological,
CC antirheumatic, antiarthritic, immunosuppressive, antiseborrheic,
CC dermatological, antibacterial, vulnary, antiulcer, fungicide, virucide,
CC proteoacide, anti-HIV, antiinflammatory, antiseborrheic, antipsoriatic, and
CC osteopathic, vasotropic, gastrointestinal, antipsoriatic, and
CC antiatherosclerotic activity. The polypeptide inhibits assembly of type
CC IV collagen heterotrimers and hexamers. The method of the invention is
CC useful for inhibiting angiogenesis, angiogenesis-mediated diseases or
CC conditions, tumour metastasis and tumour growth. The angiogenesis-
CC mediated disease or condition is solid and blood-borne tumours, diabetic
CC retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal
CC neovascularisation, macular degeneration, corneal neovascularisation,
CC retinopathy of prematurity, corneal graft rejection, neovascular
CC glaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis,
CC pterygium keratitis sicca, Sjogren's, acne rosacea, phlyctenulosis,
CC syphilis, Mycobacteria infections, lipid degeneration, chemical burns,
CC bacterial ulcers, fungal ulcers, Herpes simplex infections, Herpes zoster
CC infections, protozoan infections, Kaposi's sarcoma, Mooren ulcer,
CC Terrien's marginal degeneration, marginal keratolysis, trauma, systemic
CC lupus, polyarteritis, Wegeners sarcoidosis, scleritis, Steven's Johnson
CC disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma
CC elasticum, Paget's disease, vein occlusion, artery occlusion, carotid
CC obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease,
CC Eales disease, Bechet's disease, myopia, optic pite, Stargards disease,
CC pars planitis, chronic retinal detachment, hyperviscosity syndromes,
CC toxoplasmosis, post-laser complications, abnormal proliferation of
CC fibrovascular tissue, haemangiomas, Oeler Weber-Rendu, AIDS, ocular
CC neovascular disease, osteoarthritis, chronic inflammation, Crohn's
CC disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid.
CC The present sequence represents a peptide of the invention, derived from
CC type IV collagen crystallised NCI domain hexamer.
XX
XX Sequence 18 AA;
XX
XX Query Match 40.6%; Score 39; DB 8; Length 18;
XX Best Local Similarity 41.2%; Pred. No. 54;
XX Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 FEHCNFDVTVTLRENE 17
XX :|||:|||:
XX Db 2 FYICNINEVCHVARND 18
XX
XX RESULT 31
XX ADR17665
XX ID ADR17665 standard; peptide; 22 AA.
XX AC ADR17665;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX

CC pars planitis, chronic retinal detachment, hyperviscosity syndromes,
 CC toxoplasmosis, post-laser complications, abnormal proliferation of
 CC fibrovascular tissue, haemangiomas, Osler Weber-Rendu, AIDS, ocular
 CC neovascular disease, osteoarthritis, chronic inflammation, Crohn's
 CC disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid.
 CC The present sequence represents a peptide of the invention, derived from
 CC type IV collagen crystallised NCI domain hexamer.
 XX
 SQ Sequence 22 AA;
 Query Match 40.6%; Score 39; DB 8; Length 22;
 Best Local Similarity 41.2%; Pred. No. 66;
 Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 FEHCNFDVTRLRENE 17
 : : : : :
 Db 6 FYICNINECHYARRND 22
 : : : : :
 RESULT 33
 AAB67300
 ID AAB67300 standard; peptide; 16 AA.
 XX AC AAB67300;
 XX DT 20-APR-2001 (first entry)
 XX DE Cytokine peptide #6.
 XX KW Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.
 XX OS Homo sapiens.
 XX PN EP1072609-A2.
 XX PD 31-JAN-2001.
 XX PF 30-JUN-2000; 2000EP-00305504.
 XX PR 30-JUN-1999; 99JP-00185155.
 XX PA (SAKA/) SAKANAKA M.
 PA (TANA/) TANAKA J.
 PA (SATO/) SATO K.
 XX PI Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;
 XX WPI; 2001-204263/21.
 DR Use of prosaposin-related peptides or derivatives as cytoprotective
 PT agents, for suppressing apoptosis or apoptosis-like cell death.
 XX PS Disclosure; Page 12; 41pp; English.
 XX
 CC The present invention relates to use of a prosaposin-related peptide or
 CC derivative, in the production of a medicament for use in preventing or
 CC delaying cell death, or in promoting the expression of cell death
 CC supporting gene product Bcl-XL. The invention is useful for preventing
 CC the death of cells e.g. brain cells, neurons and cardiac muscle cells, in
 CC vitro or ex vivo
 XX
 SQ Sequence 16 AA;
 Query Match 39.6%; Score 38; DB 4; Length 16;
 Best Local Similarity 60.0%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EHCNFDVTRL 11
 : : : : :
 Db 2 EHCNFDVTRL 11
 : : : : :
 RESULT 34

ABB56683
 ID ABB56683 standard; peptide; 14 AA.
 XX AC ABB56683;
 XX DT 05-MAR-2002 (first entry)
 XX DE Human SNP related amino acid sequence SEQ ID NO:1248.
 XX KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
 KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
 KW autoimmune disease; inflammation; cancer; nervous system disease;
 KW infection; polymorphic protein.
 XX OS Homo sapiens.
 XX PN WO200138586-A2.
 XX PD 31-MAY-2001.
 XX PF 22-NOV-2000; 2000WO-US032311.
 XX PR 24-NOV-1999; 99US-0167383P.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Leach M;
 XX DR WPI; 2001-355949/37.
 XX PT Isolated human nucleic acids comprising one or more single nucleotide
 PT polymorphisms, useful for treating a subject suffering from a pathology,
 PT e.g. autoimmune diseases, ascribed to the presence of a sequence
 PT polymorphism.
 XX PS Claim 1; Page 620; 674pp; English.
 XX CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 CC to ABB56903 represent human peptides encoded by some of the SNP
 CC oligonucleotides. The sequences from the present invention can have
 CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
 CC and antibodies from the present invention can be used for treating a
 CC subject suffering from, at risk for, or suspected of, suffering from a
 CC pathology ascribed to the presence of a sequence polymorphism. The
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs
 CC are also useful for determining which forms of a characterised
 CC polymorphism are present in individuals. The antibodies may be used in
 CC the detection, quantitation and/or cellular or tissue localisation of a
 CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
 CC protein within appropriate physiological samples)
 XX
 SQ Sequence 14 AA;
 Query Match 37.5%; Score 36; DB 4; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EHCNFDVTRL 13
 : : : : :
 Db 3 QHCSRNNFTMRL 14
 : : : : :
 RESULT 35
 ADN06337
 ID ADN06337 standard; protein; 29 AA.
 XX AC ADN06337;
 XX DT 17-JUN-2004 (first entry)
 XX

```
DE VSV G stem region deletion mutant Gdelta13.
XX
KW Cytostatic; Vaccine; Immunotherapy; Rhabdovirus; cancer;
KW Glycoprotein stem region; VSV G; mutant; mutein.
XX
OS Vesicular stomatitis virus; strain San Juan.
OS Synthetic.
XX
PN WO2004022716-A2.
XX
PD 18-MAR-2004.
XX
XX 08-SEP-2003; 2003WO-US027934.
XX
XX 09-SEP-2002; 2002US-0408908P.
XX
XX (UYTE-) UNIV TENNESSEE RES FOUND.
XX
XX Whitt MA, Robison CS, Jayakar HR, Miller MA;
XX WPI; 2004-248460/23.
XX
XX New recombinant non-cytopathic Rhabdovirus comprising a nucleic acid of
XX rhabdoviral genome comprising a deletion or a mutation within a region
XX coding a matrix protein (M), useful as a vaccine or gene delivery vector
XX for treating cancer.
XX
XX Example 5; Fig 21; 157pp; English.
XX
XX The present invention relates to a recombinant non-cytopathic Rhabdovirus
XX comprising a nucleic acid of rhabdoviral genome comprising a deletion or
XX a mutation within a region coding a matrix protein. The recombinant non-
XX cytopathic Rhabdovirus is useful as a gene delivery vector or vaccine for
XX treating a subject suffering from a disease associated with a defective
XX gene, e.g. cancer. The present sequence is a Rhabdovirus Vesicular
XX Stomatitis Virus (VSV) glycoprotein (G) stem region mutant. Mutations in
XX the membrane-proximal region of the VSV G ectodomain were found to not
XX affect G protein expression or stability. The N-terminal and C-terminal
XX residues of the present sequence are residues 421 and 462 of the full-
XX length G protein sequence. The present sequence was made by deleting
XX residues 29-41 (residues 449-461 in the full-length sequence).
XX
XX Sequence 29 AA;
XX
XX Query Match 36.5%; Score 35; DB 8; Length 29;
XX Best Local Similarity 35.3%; Pred. No. 3.8e+02;
XX Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 FEHCNFDVTVTLRENE 17
XX ||| : | :| :|
XX 1 FEHPHIQDAASQLPDDE 17
XX
XX Db
XX
XX RESULT 36
XX ADN06336
XX ID ADN06336 standard; protein; 32 AA.
XX
XX AC ADN06336;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE VSV G stem region deletion mutant deltaP440-N449.
XX
XX KW Cytostatic; Vaccine; Immunotherapy; Rhabdovirus; cancer;
XX KW Glycoprotein stem region; VSV G; mutant; mutein.
XX
XX OS Vesicular stomatitis virus; strain San Juan.
XX OS Synthetic.
XX
XX PN WO2004022716-A2.
XX
XX PD 18-MAR-2004.
XX
XX PF Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
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PF 08-SEP-2003; 2003WO-US027934.
XX
XX 09-SEP-2002; 2002US-0408908P.
XX
XX (UYTE-) UNIV TENNESSEE RES FOUND.
XX
XX Whitt MA, Robison CS, Jayakar HR, Miller MA;
XX WPI; 2004-248460/23.
XX
XX New recombinant non-cytopathic Rhabdovirus comprising a nucleic acid of
XX rhabdoviral genome comprising a deletion or a mutation within a region
XX coding a matrix protein (M), useful as a vaccine or gene delivery vector
XX for treating cancer.
XX
XX Example 5; Fig 21; 157pp; English.
XX
XX The present invention relates to a recombinant non-cytopathic Rhabdovirus
XX comprising a nucleic acid of rhabdoviral genome comprising a deletion or
XX a mutation within a region coding a matrix protein. The recombinant non-
XX cytopathic Rhabdovirus is useful as a gene delivery vector or vaccine for
XX treating a subject suffering from a disease associated with a defective
XX gene, e.g. cancer. The present sequence is a Rhabdovirus Vesicular
XX Stomatitis Virus (VSV) glycoprotein (G) stem region mutant. Mutations in
XX the membrane-proximal region of the VSV G ectodomain were found to not
XX affect G protein expression or stability. The N-terminal and C-terminal
XX residues of the present sequence are residues 421 and 462 of the full-
XX length G protein sequence. The present sequence was made by deleting
XX residues 20-29 (residues 440-449 in the full-length sequence).
XX
XX Sequence 32 AA;
XX
XX Query Match 36.5%; Score 35; DB 8; Length 32;
XX Best Local Similarity 35.3%; Pred. No. 4.2e+02;
XX Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 FEHCNFDVTVTLRENE 17
XX ||| : | :| :|
XX 1 FEHPHIQDAASQLPDDE 17
XX
XX Db
XX
XX RESULT 37
XX ABB40890
XX ID ABB40890 standard; peptide; 33 AA.
XX
XX AC ABB40890;
XX
XX DT 04-FEB-2002 (first entry)
XX
XX DE Peptide #8396 encoded by human foetal liver single exon probe.
XX
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX OS Homo sapiens.
XX
XX PN WO200157277-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000669.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX
XX PR 26-MAY-2000; 2000US-0207456P.
XX
XX PR 30-JUN-2000; 2000US-00608408.
XX
XX PR 03-AUG-2000; 2000US-00632366.
XX
XX PR 21-SEP-2000; 2000US-0234687P.
XX
XX PR 27-SEP-2000; 2000US-0236359P.
XX
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX PI
XX
XX
```



```
XX AAW61750;
XX
XX
XX 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 33855.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 33855; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 33 AA;
XX
XX Query Match 36.5%; Score 35; DB 4; Length 33;
XX Best Local Similarity 46.7%; Pred. No. 4.3e+02;
XX Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX
XX Qy 3 HCNFNDVTRLRENE 17
XX ||| : ||| : |||
XX 7 HDNFTASTIRIPENQ 21
XX
XX RESULT 41
XX ADN06339
XX ID ADN06339 standard; protein; 35 AA.
XX
XX AC ADN06339;
XX
XX 17-JUN-2004 (first entry)
XX
XX VSV G stem region deletion mutant Gdelta9.
XX
XX Cytostatic; Vaccine; Immunotherapy; Rhabdovirus; cancer;
XX glycoprotein stem region; VSV G; mutant; mutein.
XX
XX Vesicular stomatitis virus; strain San Juan.
XX
XX Synthetic.
XX
XX WO2004022716-A2.
XX
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XX
XX 18-MAR-2004.
XX
XX 08-SEP-2003; 2003WO-US027934.
XX
XX 09-SEP-2002; 2002US-0408908P.
XX
XX (UYTE-) UNIV TENNESSEE RES FOUND.
XX
XX Whitt MA, Robison CS, Jayakar HR, Miller MA;
XX
XX WPI; 2004-248460/23.
XX
XX New recombinant non-cytopathic Rhabdovirus comprising a nucleic acid of
XX rhabdoviral genome comprising a deletion or a mutation within a region
XX coding a matrix protein (M), useful as a vaccine or gene delivery vector
XX for treating cancer.
XX
XX Example 5; Fig 21; 157pp; English.
XX
XX The present invention relates to a recombinant non-cytopathic Rhabdovirus
XX comprising a nucleic acid of rhabdoviral genome comprising a deletion or
XX a mutation within a region coding a matrix protein. The recombinant non-
XX cytopathic Rhabdovirus is useful as a gene delivery vector or vaccine for
XX treating a subject suffering from a disease associated with a defective
XX gene, e.g. cancer. The present sequence is a Rhabdovirus Vesicular
XX Stomatitis Virus (VSV) glycoprotein (G) stem region mutant. Mutations in
XX the membrane-proximal region of the VSV G ectodomain were found to not
XX affect G protein expression or stability. The N-terminal and C-terminal
XX residues of the present sequence are residues 421 and 464 of the full-
XX length G protein sequence. The present sequence was made by deleting
XX residues 33-41 (residues 453-461 in the full-length sequence).
XX
XX Sequence 35 AA;
XX
XX Query Match 36.5%; Score 35; DB 8; Length 35;
XX Best Local Similarity 35.3%; Pred. No. 4.6e+02;
XX Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
XX
XX Qy 1 FEHCNFDVTRLRENE 17
XX ||| : ||| : |||
XX 1 FEHPHQDAASQLPDDE 17
XX
XX RESULT 42
XX AAW99851
XX ID AAW99851 standard; peptide; 34 AA.
XX
XX AC AAW99851;
XX
XX 17-OCT-2003 (revised)
XX
XX 09-JUN-1999 (first entry)
XX
XX HIV-1 gp120 V1/V2 domain peptide #1.
XX
XX HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;
XX infection; antibody; immunoassay.
XX
XX Human immunodeficiency virus 1.
XX
XX WO9912556-A1.
XX
XX 18-MAR-1999.
XX
XX 08-SEP-1998; 98WO-US018679.
XX
XX 08-SEP-1997; 97US-0058155P.
XX
XX (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
XX (PINT/) PINTER A.
XX
XX Pinter A;
XX
```

DR WPI; 1999-229137/19.
 XX New gp120 V1/V2 fusion proteins.
 XX
 XX Claim 11; Page 42; 64pp; English.
 XX
 CC The present invention describes a novel protein (A) comprising a gp120
 CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain of
 CC an HIV-1 strain, where the protein does not bind CD4, the gp120 V1/V2
 CC domain of the protein displaying an epitope which is recognized by an
 CC antibody which neutralizes at least one HIV-1 primary isolate with a ND90
 CC of at least 100 mu g/ml. The present sequence represents an HIV-1 gp120
 CC V1/V2 domain peptide from the present invention. The novel proteins can
 CC be used for stimulating the formation of antibodies capable of
 CC neutralizing infection by an HIV viral isolate in mammals. They can also
 CC be used for therapeutic treatment of subjects already infected with HIV.
 CC They can also be used in immunoassays for anti-HIV antibodies and for the
 CC production of anti-HIV antiserum. (Updated on 17-OCT-2003 to standardise
 CC OS field)
 XX
 XX Sequence 34 AA;
 SQ
 Query Match 35.9%; Score 34.5; DB 2; Length 34;
 Best Local Similarity 42.9%; Pred. No. 5.3e+02;
 Matches 6; Conservative 6; Mismatches 1; Indels 1; Gaps 1;
 QY 2 EHCNFDVTVRLRE 15
 Db ::|||::|||:
 4 KNCSPN-IYTSRD 16
 RESULT 43
 ADC17655
 ID ADC17655 standard; peptide; 18 AA.
 XX
 AC ADC17655;
 XX
 DT 18-DRC-2003 (first entry)
 XX
 DE Type IV collagen NC1 domain related peptide SEQ ID NO:260.
 XX
 KW crystallised NC1 domain hexamer of type IV collagen;
 KW angiogenesis inhibitor; angiogenesis-mediated disease;
 KW tumour metastasis inhibitor; tumour growth inhibitor;
 KW endothelial cell interaction inhibitor;
 KW basal lamina membrane formation inhibitor; cytostatic; antipsoriatic;
 KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
 KW endothelial cell adhesion inhibitor;
 KW endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;
 KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
 KW blood-borne tumour.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003012122-A2.
 XX
 XX 13-FEB-2003.
 XX
 XX 26-JUL-2002; 2002WO-US023763.
 XX
 XX 27-JUL-2001; 2001US-0308523P.
 PR 29-OCT-2001; 2001US-0351289P.
 PR 22-MAR-2002; 2002US-0366854P.
 PR 03-JUN-2002; 2002US-0385362P.
 XX
 XX (UNIV) UNIV KANSAS MEDICAL CENT.
 PA (SUND/) SUNDARAMOORTHY M.
 PA (HUDS/) HUDSON B.
 XX
 XX Sundaramoorthy M, Hudson B;
 PI
 XX WPI; 2003-332730/31.

XX New polypeptide, useful for treating an angiogenesis-mediated disease or
 PT condition consisting of glaucoma or blood-borne tumors or for inhibiting
 PT basal lamina membrane formation in cell or tissue development.
 XX
 XX Claim 57; SEQ ID NO 260; 168pp; English.
 PS
 XX The present invention describes a crystallised NC1 domain hexamer of type
 CC IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a
 CC pharmaceutical composition comprising the polypeptide and a carrier; (3)
 CC inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
 CC disease or condition in a mammal; (5) inhibiting tumour metastasis or
 CC growth; (5) inhibiting endothelial cell interaction with the
 CC extracellular matrix in an animal tissue; (6) inhibiting basal lamina
 CC membrane formation in cell or tissue development; (7) a crystal of an NC1
 CC domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
 CC collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
 CC crystallised NC1 domain hexamer of type IV collagen (I) has cytostatic,
 CC antipsoriatic, antianaemic, ophthalmological, antiarteriosclerotic and
 CC antiulcer activities, and can be used as an inhibitor of angiogenesis,
 CC tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
 CC cell proliferation, and basal lamina assembly. A (I) polypeptide can be
 CC used for treating an angiogenesis-mediated disease or condition
 CC consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
 CC psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
 CC or for inhibiting basal lamina membrane formation in cell or tissue
 CC development. The methods are useful for inhibiting angiogenesis in
 CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
 CC cell interaction with the extracellular matrix in an animal tissue, and
 CC identifying inhibitors of type IV collagen assembly. The present sequence
 CC represents a peptide which is used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 35.4%; Score 34; DB 7; Length 18;
 Best Local Similarity 41.2%; Pred. No. 3.3e+02;
 Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 QY 1 FEHCNFDVTVRLRE 17
 Db 2 FLFCNVNDVCNFSRND 18
 RESULT 44
 ADR19177
 ID ADR19177 standard; peptide; 18 AA.
 XX
 AC ADR19177;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Inter-CDSR plus contiguous hexamer Interface region alpha3 chain peptide.
 XX
 KW angiogenesis; angiogenesis-mediated disease; tumour metastasis;
 KW tumour growth; type IV collagen; NC1 domain hexamer; angiogenic;
 KW cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic;
 KW immunosuppressive; antiseborrheic; dermatological; antibacterial;
 KW vulnerary; antiulcer; fungicide; virucide; protozoacide; anti-HIV;
 KW antinflammatory; antianaemic; antiskinking; osteopathic; vasotropic;
 KW gastrointestinal; antipsoriatic; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 XX WO2004067762-A2.
 PN
 XX 12-AUG-2004.
 XX
 XX 27-JAN-2004; 2004WO-US002187.
 XX
 XX 27-JAN-2003; 2003US-0443133P.
 XX
 XX (UNIV) UNIV KANSAS MEDICAL CENT.

PI Lichenstein HS, Li L, Ooi CE, Padigar M, Shimkets RA, Zhong M;
 XX WPI; 2004-035474/03.
 XX Inhibiting cell migration, useful in diagnosing and treating disorders
 PT such as cancer, e.g. neuroblastoma, renal carcinoma, fibrosarcoma or
 PT rhabdosarcoma, by contacting a cell with a composition comprising NOVX
 PT polypeptide.
 XX Example 14; SEQ ID NO 11; 197pp; English.
 XX The present invention describes a method for inhibiting cell migration
 CC which comprises contacting a cell with a composition comprising a
 CC polypeptide (I) having at least 95% sequence identity to any of the 22
 CC sequences of 17-1047 amino acids (EVEN SEQ ID NOS: 14-56) or any of the
 CC 22 sequences of 51-4250 base pairs (ODD SEQ ID NOS: 13-55) defined in the
 CC specification, where (I) is a semaphorin-like protein. Also described:
 CC (1) a method of inhibiting angiogenesis of a tissue; (2) a method of
 CC inhibiting actin filament formation in a cell; (3) a method of preventing
 CC or alleviating a symptom of an angiogenic related disorder; (4) a
 CC chimeric protein comprising a first polypeptide (I) and second
 CC polypeptide; and (5) a composition comprising a sequence of 649 or 878
 CC amino acids (see ADP45360 or ADP45364). (I) has cytosolic activity, and
 CC can be used in gene therapy. The method is useful for inhibiting cell
 CC migration. (I) and the polynucleotides encoding them can be used in
 CC diagnosing and treating disorders such as cancer, e.g. neuroblastoma,
 CC renal carcinoma, fibrosarcoma, rhabdosarcoma cell or a pancreatic cancer.
 CC The present sequence is used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 20 AA;
 Query Match 35.4%; Score 34; DB 8; Length 20;
 Best Local Similarity 54.5%; Pred. No. 3.7e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 7 NDTVTRLRENE 17
 Db ||:|:|:
 2 NDISITPLPDNE 12
 RESULT 47
 ADO40255
 ID ADO40255 standard; peptide; 20 AA.
 AC ADO40255;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human semaphorin-like protein NOV2k/s antigenic peptide #3.
 KW Human; semaphorin; NOV2; angiogenesis inhibitor; gene therapy;
 KW cell migration; angiogenesis; actin filament formation;
 KW angiogenic-related disorder; loss of balance; weight loss; slow speech;
 KW jaundice; fatigue; pain; blood in urine; anaemia; swollen bone; cancer;
 KW pancreatic cancer; renal cancer; neuroblastoma; wound healing;
 KW tissue regeneration; antigen; immunogen.
 XX
 OS Homo sapiens.
 XX
 XX US2004018977-A1.
 XX
 XX 29-JAN-2004.
 XX
 XX 30-MAY-2003; 2003US-00449548.
 XX
 XX 09-MAR-1999; 99US-0123667P.
 PR 08-MAR-2000; 2000US-00520781.
 PR 09-APR-2002; 2002US-0371002P.
 PR 30-MAY-2002; 2002US-0384798P.
 PR 09-AUG-2002; 2002US-0402407P.
 PR 28-JAN-2003; 2003US-0443062P.
 PR 31-MAR-2003; 2003US-00403676.

XX (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 XX Alvarez E, Anderson DW, Dhanabal M, Khrantsov NV, Larochelel WJ;
 PI Lichenstein HS, Li L, Ooi CE, Padigar M, Shimkets RA, Zhong M;
 XX WPI; 2004-122082/12.
 XX Inhibiting cell migration, angiogenesis of a tissue or actin filament
 PT formation in a cell, for preventing or treating cancer, e.g. renal
 PT cancer, comprises contacting or introducing a semaphorin-like polypeptide
 PT or nucleic acid.
 XX Example 14; SEQ ID NO 11; 227pp; English.
 PS The invention relates to inhibiting cell migration, angiogenesis of a
 CC tissue or actin filament formation in a cell comprising contacting the
 CC cell with a composition comprising a semaphorin-like polypeptide having
 CC at least 95 % sequence identity to any one of 22 NOV2 (NOVA-NOVU)
 CC proteins (appearing as ADO40258, ADO40260, ADO40262, ADO40264 . . . etc to
 CC ADO40300), or introducing to a cell a composition comprising a nucleic
 CC acid having at least 95 % sequence identity to any one of the 22 nucleic
 CC acids encoding the NOV2 proteins (appearing as ADO40257, ADO40259,
 CC ADO40261, ADO40263 . . . etc to ADO40299. Also included are preventing or
 CC alleviating a symptom of an angiogenic-related disorder comprising
 CC administering to a subject a composition comprising the semaphorin-like
 CC polypeptide cited above, a chimaeric protein comprising a first
 CC polypeptide comprising a NOVX polypeptide and second polypeptide, and a
 CC composition comprising a NOV2s (ADO40294) or NOV2u (ADO40298). The
 CC semaphorin-like proteins or nucleic acids are useful for inhibiting cell
 CC migration, angiogenesis of a tissue or actin filament formation, or for
 CC diagnosing, preventing and treating an angiogenic-related disorder (with
 CC symptoms such as loss of balance, weight loss, slow speech, jaundice,
 CC fatigue, pain, blood in urine, anaemia or swollen bones) such as cancer,
 CC e.g. pancreatic cancer, renal cancer or neuroblastoma, wound healing and
 CC tissue regeneration. The nucleic acid may be used in gene therapy. The
 CC present sequence represents a NOV2 peptide used to raise anti-NOV2
 CC antibodies.
 XX
 SQ Sequence 20 AA;
 Query Match 35.4%; Score 34; DB 8; Length 20;
 Best Local Similarity 54.5%; Pred. No. 3.7e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 7 NDTVTRLRENE 17
 Db ||:|:|:
 2 NDISITPLPDNE 12
 RESULT 48
 ADC17661
 ID ADC17661 standard; peptide; 22 AA.
 XX
 XX ADC17661;
 AC ADC17661;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 XX Type IV collagen NC1 domain related peptide SEQ ID NO:266.
 DE
 DE crystallised NC1 domain hexamer of type IV collagen;
 XX angiogenesis inhibitor; angiogenesis-mediated disease;
 KW tumour metastasis inhibitor; tumour growth inhibitor;
 KW

CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a therapeutic protein
 CC which was fused with human albumin to create a novel albumin fusion
 CC protein of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 25 AA;

Query Match 35.4%; Score 34; DB 7; Length 25;
 Best Local Similarity 41.2%; Pred. No. 4.6e+02;
 Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTLRENE 17
 | | | | |
 Db 4 FLFCNVNDVCNFAFRND 20

RESULT 52
 ADF16664
 ID ADF16664 standard; protein; 25 AA.
 XX
 AC ADF16664;

DT 12-FEB-2004 (first entry)

DE Human albumin fusion protein-related protein SeqID1766.

XX albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.

XX Homo sapiens.

XX WO2003060071-A2.

XX 24-JUL-2003.

XX 23-DEC-2002; 2002WO-US040891.

XX 21-DEC-2001; 2001US-0341811P.

XX 24-JAN-2002; 2002US-0350358P.

XX 28-JAN-2002; 2002US-0351360P.

XX 26-FEB-2002; 2002US-0359370P.

XX 28-FEB-2002; 2002US-0360000P.

XX 27-MAR-2002; 2002US-0367500P.

XX 08-APR-2002; 2002US-0370227P.

XX 10-MAY-2002; 2002US-0378950P.

XX 24-MAY-2002; 2002US-0382617P.

XX 28-MAY-2002; 2002US-0383123P.

XX 05-JUN-2002; 2002US-0385708P.

XX 10-JUL-2002; 2002US-0394625P.

XX 24-JUL-2002; 2002US-0398008P.

XX 09-AUG-2002; 2002US-0402131P.

XX 13-AUG-2002; 2002US-0402708P.

XX 18-SEP-2002; 2002US-0411355P.

XX 02-OCT-2002; 2002US-0414984P.

XX 11-OCT-2002; 2002US-0417611P.

DR WPI; 2003-598517/56.
 DR N-PSDB; ADF16338.
 XX
 PT New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.

PS Example 4; SEQ ID NO 1766; 24pp; English.

XX This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a therapeutic protein
 CC which was fused with human albumin to create a novel albumin fusion
 CC protein of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
 XX

SQ Sequence 25 AA;

Query Match 35.4%; Score 34; DB 7; Length 25;
 Best Local Similarity 41.2%; Pred. No. 4.6e+02;

Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 FEHCNFDVTVTLRENE 17
 | | | | |
 Db 4 FLFCNVNDVCNFAFRND 20

RESULT 53

ADFI6602

ID ADF16602 standard; protein; 25 AA.

XX ADF16602;

DT 12-FEB-2004 (first entry)

DE Human albumin fusion protein-related protein SeqID1704.

XX albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.

XX Homo sapiens.

XX WO2003060071-A2.

XX 24-JUL-2003.

XX 23-DEC-2002; 2002WO-US040891.

XX 21-DEC-2001; 2001US-0341811P.

XX 24-JAN-2002; 2002US-0350358P.

XX 28-JAN-2002; 2002US-0351360P.

XX 26-FEB-2002; 2002US-0359370P.

XX 28-FEB-2002; 2002US-0360000P.

XX 27-MAR-2002; 2002US-0367500P.

XX 08-APR-2002; 2002US-0370227P.

XX 10-MAY-2002; 2002US-0378950P.

XX 24-MAY-2002; 2002US-0382617P.

XX 28-MAY-2002; 2002US-0383123P.

XX 05-JUN-2002; 2002US-0385708P.

XX 10-JUL-2002; 2002US-0394625P.

XX 24-JUL-2002; 2002US-0398008P.

XX 09-AUG-2002; 2002US-0402131P.

XX 13-AUG-2002; 2002US-0402708P.

XX 18-SEP-2002; 2002US-0411355P.

XX 18-SEP-2002; 2002US-0411426P.

PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16279.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1707; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 27 AA;
Query Match 35.4%; Score 34; DB 7; Length 27;
Best Local Similarity 41.2%; Pred. No. 5e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Qy 1 FEHCNFDVTTRLRENE 17
| | | | |
Db 9 FLFCNVNDVCNFAASND 25
RESULT 56
ADFI6665
ID ADF16665 standard; protein; 27 AA.
XX
AC ADF16665;
XX
XX 12-FEB-2004 (first entry)
XX Human albumin fusion protein-related protein SeqID1767.
XX
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
XX Homo sapiens.
OS

XX WO2003060071-A2.
XX 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 26-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16339.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1767; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 27 AA;
Query Match 35.4%; Score 34; DB 7; Length 27;
Best Local Similarity 41.2%; Pred. No. 5e+02;
Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Qy 1 FEHCNFDVTTRLRENE 17
| | | | |
Db 9 FLFCNVNDVCNFAASND 25
RESULT 57
ADFI6603
ID ADF16603 standard; protein; 27 AA.
XX

PD 14-NOV-2002.
 XX PF 07-MAY-2002; 2002WO-US014457.
 XX PR 07-MAY-2001; 2001US-0289179P.
 XX PR 29-AUG-2001; 2001US-0315736P.
 XX (ALPH-) ALPHAGENE INC.
 XX Stark KA, Weaver A, Hoffmann HM, Krauss R, Valenzuela DB;
 PI Saini KS;
 XX WPI; 2003-111965/10.
 DR N-PSDB; AAD50569.
 XX New carcinoembryonic antigen and polynucleotides encoding them, useful
 PT for treating and/or preventing cell adhesion-mediated disease (e.g.
 PT for cancers, solid tumors, tumor metastasis or benign tumors) symptoms.
 XX Claim 17; Page 129; 143pp; English.
 XX The invention relates to novel human carcinoembryonic antigen (CEA)
 CC polypeptides and polynucleotides encoding such polypeptides. CEA genes
 CC are useful as diagnostic and prognostic markers of colon, stomach and
 CC breast cancers. Polypeptides of the invention can be used to diagnose,
 CC treat and/or prevent cell adhesion-mediated disease (e.g. cancers, solid
 CC tumors, tumour metastasis or benign tumors) and to modulate cell-cell
 CC or cell-matrix adhesion in mammalian tissues. The invention is useful in
 CC gene therapy. The present sequence is human CEA exon encoded peptide
 XX Sequence 20 AA;
 SQ
 Query Match 34.4%; Score 33; DB 6; Length 20;
 Best Local Similarity 38.5%; Pred. No. 5.3e+02;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 2 EHCNFDVVTTLR 14
 Db ||||| : : : :
 5 EYCNISQLQGRIR 17
 RESULT 64
 AED84661
 ID AED84661 standard; peptide; 24 AA.
 AC AED84661;
 XX 26-JAN-2006 (first entry)
 DT Human SCCE HLA DR core binding motif, SEQ ID No:136.
 DE vaccine; serine protease; stratum corneum chymotryptic enzyme; SCCE;
 KW human leukocyte antigen; HLA; immunity; immunotherapy; expression;
 KW screening; neoplasm; cancer; ovary tumor; lung tumor; prostate tumor;
 KW colon tumor; cytostatic.
 XX Homo sapiens.
 OS
 XX WO2005110459-A2.
 FN 24-NOV-2005.
 PD 22-APR-2005; 2005WO-US013877.
 XX 23-APR-2004; 2004US-00831075.
 XX (UYAR-) UNIV ARKANSAS.
 PA Obrien T, Cannon MJ, Santin A;
 FI WPI; 2005-786720/80.
 XX Vaccinating an individual against stratum corneum chymotryptic enzyme
 PT

PT (SCCE) for treating cancer such as ovarian cancer, lung cancer, prostate
 PT cancer, and colon cancer comprises inoculating individual with cancer
 with a SCCE peptide.
 XX Claim 5; SEQ ID NO 136; 96pp; English.
 XX The invention relates to a method of vaccinating an individual against
 CC stratum corneum chymotryptic enzyme (SCCE). The method comprises
 CC inoculating an individual with a SCCE peptide that elicits an immune
 CC response in the individual. Also described are: (1) a method of producing
 CC immune-activated cells directed toward SCCE comprising exposing immune
 CC cells to a SCCE protein or its fragment, where the exposure to the SCCE
 CC protein or its fragment activates the immune cells, thus producing immune
 CC -activated cells directed toward SCCE; (2) a method of immunotherapy
 CC targeted toward stratum SCCE in an individual by isolating dendritic
 CC cells from the individual, expressing a SCCE protein or its fragment in
 CC the dendritic cells, and transferring the dendritic cells back to the
 CC individual, where the dendritic cells would activate SCCE-specific immune
 CC responses in the individual, thus generating immunotherapy targeted
 CC toward SCCE in the individual; (3) a method of monitoring the efficacy of
 CC vaccinating an individual with SCCE or SCCE peptide by vaccinating the
 CC individual with the SCCE or SCCE peptide, isolating T cells from the
 CC individual, and measuring immune responses induced by the SCCE or SCCE
 CC peptide, where an increased level of immune responses compared to those
 CC exhibited by cells from normal individual indicates that the individual
 CC has been vaccinated by the SCCE or SCCE peptide; (4) a method of
 CC inhibiting expression of endogenous SCCE in a cell by introducing into
 CC the cell a vector comprising a sequence complementary to human SCCE cDNA
 CC (given as SEQ ID No: 22 in the specification), where expression of the
 CC vector in the cell produces SCCE antisense RNA that hybridizes to
 CC endogenous SCCE mRNA, thus inhibiting expression of endogenous SCCE in
 CC the cell; (5) a method of inhibiting SCCE protein in a cell by
 CC introducing into the cell an antibody specific for SCCE protein or its
 CC fragment, where binding of the antibody to the SCCE protein inhibits the
 CC SCCE protein in the cell; (6) a method of targeted therapy to an
 CC individual, comprising administering a compound to an individual, where
 CC the compound has a therapeutic moiety and a targeting moiety specific for
 CC SCCE; (7) an immunogenic composition, comprising an immunogenic fragment
 CC of a SCCE protein and an appropriate adjuvant; (8) an oligonucleotide
 CC having a sequence complementary to human SCCE cDNA (SEQ ID No: 22); (9) a
 CC composition comprising the oligonucleotide and a physiologically
 CC acceptable carrier; (10) a method of treating a neoplastic state in an
 CC individual in need of such treatment by administering to the individual
 CC an effective dose of the oligonucleotide; and (11) a method of screening
 CC for compounds that inhibit SCCE activity by contacting a sample
 CC comprising SCCE protein with a compound, and assaying for SCCE protease
 CC activity, where a decrease in the SCCE protease activity in the presence
 CC of the compound relative to SCCE protease activity in the absence of the
 CC compound indicates the compound inhibits SCCE activity. The methods and
 CC compositions of the invention are useful for vaccinating an individual
 CC against SCCE. The individual suffers from a disease selected from ovarian
 CC cancer, lung cancer, prostate cancer, and colon cancer. This sequence
 CC represents a core binding motif of human leukocyte antigen (HLA) DR
 XX within the human SCCE protein.
 SQ Sequence 24 AA;
 Query Match 34.4%; Score 33; DB 9; Length 24;
 Best Local Similarity 45.5%; Pred. No. 6.4e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 3 HCNFNDVVTTLR 13
 Db ||||| : : : :
 10 HCKQNEYTVHL 20
 RESULT 65
 ABG94057
 ID ABG94057 standard; peptide; 28 AA.
 XX AC ABG94057;
 XX 27-NOV-2002 (first entry)
 DT

XX DE Human vasoactive intestinal polypeptide (VIP) analogue #105.
 XX KW Vasoactive intestinal polypeptide; VIP; female sexual dysfunction; vulva;
 KW vagina; vaginal atrophy; pain; intercourse; vaginal itching;
 KW vaginal dryness; sexual desire enhancement; female genitalia; frigidity;
 KW sexual aversion; menopausal state; post-menopausal state; sexual desire;
 KW sexual activity; multiple sclerosis; atherosclerosis; diabetes mellitus;
 KW peripheral neuropathy; autonomic neuropathy; anorgasmia; hypoxia;
 KW vaginal muscle tone; vaginal lubrication; collagen misdeposition.
 XX OS Unidentified.
 XX US2002099003-A1.
 XX PD 25-JUL-2002.
 XX PF 13-AUG-2001; 2001US-00929818.
 XX PR 28-OCT-1997; 97US-00959057.
 XX PR 28-OCT-1997; 97US-00959064.
 XX PR 27-OCT-1998; 98US-00181316.
 XX PR 04-FEB-2000; 2000US-00498522.
 XX (WILSON) WILSON L F.
 XX (PLAC) PLACE V A.
 XX PI Wilson LF, Place VA;
 XX WIPI; 2002-697729/75.
 XX DR Treating sexual dysfunction in females comprises administering vasoactive
 XX PT intestinal polypeptide or against to vagina and/or vulvar region.
 XX PS Claim 19; Page; 19pp; English.
 XX CC The invention relates to a method for treating sexual dysfunction in
 CC females comprising administering a formulation comprising a vasoactive
 CC agent comprising a vasoactive intestinal polypeptide and/or agonist to
 CC the vagina and/or vulvar region. The method is used for preventing
 CC vaginal atrophy and pain during intercourse, for treating vaginal itching
 CC and dryness, for enhancing sexual desire and responsiveness in females
 CC and for maintaining improvement of the tissue health of the female
 CC genitalia. The method is also used for treating persistent or recurrent
 CC deficiency or absence of sexual fantasies and desire for sexual activity,
 CC frigidity, sexual aversion, menopausal or post-menopausal state, multiple
 CC sclerosis, atherosclerosis, peripheral neuropathy, autonomic neuropathy,
 CC diabetes mellitus, substance-induced decreases in sexual desire and
 CC responsiveness and primary and secondary anorgasmia. The formulation
 CC improves vaginal muscle tone and tissue health, increases vaginal
 CC lubrication and minimises collagen misdeposition resulting from hypoxia.
 CC This sequence represents a human vasoactive intestinal polypeptide (VIP)
 CC analogue with agonist and/or antagonist activity. Note: The present
 CC sequence is not featured in the printed specification but was derived
 CC from the wild-type peptide shown in ABG93952
 XX SQ Sequence 28 AA;

Query Match 34.4%; Score 33; DB 5; Length 28;
 Best Local Similarity 70.0%; Pred. No. 7.5e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 FNDVTTLRRE 15
 ||| |||:
 Db 6 FNDVTTLRKK 15

RESULT 66
 ABG94074
 ID ABG94074 standard; peptide; 28 AA.
 XX AC ABG94074;
 XX

DT 27-NOV-2002 (first entry)
 XX DE Human vasoactive intestinal polypeptide (VIP) analogue #122.
 XX KW Vasoactive intestinal polypeptide; VIP; female sexual dysfunction; vulva;
 KW vagina; vaginal atrophy; pain; intercourse; vaginal itching;
 KW vaginal dryness; sexual desire enhancement; female genitalia; frigidity;
 KW sexual aversion; menopausal state; post-menopausal state; sexual desire;
 KW sexual activity; multiple sclerosis; atherosclerosis; diabetes mellitus;
 KW peripheral neuropathy; autonomic neuropathy; anorgasmia; hypoxia;
 KW vaginal muscle tone; vaginal lubrication; collagen misdeposition.
 XX OS Unidentified.
 XX US2002099003-A1.
 XX PD 25-JUL-2002.
 XX PF 13-AUG-2001; 2001US-00929818.
 XX PR 28-OCT-1997; 97US-00959057.
 XX PR 28-OCT-1997; 97US-00959064.
 XX PR 27-OCT-1998; 98US-00181316.
 XX PR 04-FEB-2000; 2000US-00498522.
 XX (WILSON) WILSON L F.
 XX (PLAC) PLACE V A.
 XX PI Wilson LF, Place VA;
 XX WIPI; 2002-697729/75.
 XX DR Treating sexual dysfunction in females comprises administering vasoactive
 XX PT intestinal polypeptide or against to vagina and/or vulvar region.
 XX PS Claim 19; Page; 19pp; English.
 XX CC The invention relates to a method for treating sexual dysfunction in
 CC females comprising administering a formulation comprising a vasoactive
 CC agent comprising a vasoactive intestinal polypeptide and/or agonist to
 CC the vagina and/or vulvar region. The method is used for preventing
 CC vaginal atrophy and pain during intercourse, for treating vaginal itching
 CC and dryness, for enhancing sexual desire and responsiveness in females
 CC and for maintaining improvement of the tissue health of the female
 CC genitalia. The method is also used for treating persistent or recurrent
 CC deficiency or absence of sexual fantasies and desire for sexual activity,
 CC frigidity, sexual aversion, menopausal or post-menopausal state, multiple
 CC sclerosis, atherosclerosis, peripheral neuropathy, autonomic neuropathy,
 CC diabetes mellitus, substance-induced decreases in sexual desire and
 CC responsiveness and primary and secondary anorgasmia. The formulation
 CC improves vaginal muscle tone and tissue health, increases vaginal
 CC lubrication and minimises collagen misdeposition resulting from hypoxia.
 CC This sequence represents a human vasoactive intestinal polypeptide (VIP)
 CC analogue with agonist and/or antagonist activity. Note: The present
 CC sequence is not featured in the printed specification but was derived
 CC from the wild-type peptide shown in ABG93952
 XX SQ Sequence 28 AA;

Query Match 34.4%; Score 33; DB 5; Length 28;
 Best Local Similarity 63.6%; Pred. No. 7.5e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 FNDVTTLRRE 16
 ||| |||:
 Db 6 FNDVTTLRKK 16

RESULT 67
 ABE39240
 ID ABE39240 standard; peptide; 31 AA.
 XX AC ABE39240;
 XX

XX 09-FEB-2006 (first entry)
DT Human serum N-linked glycopeptide SEQ ID NO: 3344.
DE
XX Bioinformatics; blood; serum; plasma protein; protein detection;
XX mass spectroscopy; proteomics; glycosylation; diagnosis; cancer;
XX cytosolic; diabetes; antidiabetic; inflammation; antiinflammatory;
KW rheumatoid arthritis; antiarthritic; antirheumatic; psychiatric disorder;
KW neuroleptic; neurological disease; infection; antimicrobial.
XX
OS Homo sapiens.
XX
XX WO2005114221-A2.
PN
XX
XX 01-DEC-2005.
PD
XX
XX 20-MAY-2005; 2005WO-US017842.
PF
XX
XX 21-MAY-2004; 2004US-0573593P.
PR
XX
XX (SYST-) INST SYSTEMS BIOLOGY.
FA
XX
XX Aebersold RH, Zhang H;
PI
XX
XX WPI; 2006-020173/02.
DR
XX
XX Identifying glycopolypeptides in a serum or plasma sample, by identifying
PT released sample glycopeptide fragments that correspond to standard
PT peptides.
PT
XX
XX Claim 1; SEQ ID NO 3344; 193pp; English.
PS
XX
XX The invention relates to identifying glycopolypeptides in a serum or
CC plasma sample comprising immobilizing derivatized sample
CC glycopolypeptides to a solid support, releasing the sample glycopeptide
CC fragments from the solid support, adding to the released sample
CC glycopeptide fragments standard peptides, and identifying released sample
CC glycopeptide fragments that correspond to standard peptides added by mass
CC spectroscopy. Also included are a method for identifying one or more
CC diagnostic markers for a disease, a composition comprising peptides
CC containing the glycosylation sites (AEE35897-AEE39378, where the peptides
CC each correspond to peptide fragments derived by cleavage of polypeptides
CC using the same cleavage reagent) and a kit comprising peptides containing
CC the glycosylation sites (AEE35897-AEE39378). The methods are useful for
CC identifying glycopolypeptides in a serum or plasma sample. The methods
CC can be used for blood serum profiling for the detection of prognostic and
CC diagnostic protein markers. It can also be used to identify and/or
CC validate drug targets and to evaluate drug efficacy, drug dosing, and/or
CC drug toxicity. The methods can also be used for the detection of changes
CC in the state of glycosylation of proteins based on the concurrent
CC application of protein abundance measurement of protein glycosylation on
CC the same sample. The method allows fast throughput and simplicity. It can
CC be readily adapted for high throughput analysis of samples, which can be
CC particularly advantageous for the analysis of clinical specimens. The
CC method can also be automated to facilitate the processing of multiple
CC samples. The present sequence is a human glycopeptide that does not
CC contain an N-linked glycosylation site, suitable for use as a reference
CC peptide in the method of the invention.
XX
XX Sequence 31 AA;
SQ
Query Match 34.4%; Score 33; DB 10; Length 31;
Best Local Similarity 42.9%; Pred. No. 8.3e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 2 EHCNFDVTTLRLE 15
DB 10 DHPTFNKIPNLAE 23
RESULT 68
AAG75971

ID AAG75971 standard; protein; 32 AA.
XX
AC AAG75971;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6735.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
KW
XX Homo sapiens.
OS
XX WO200122920-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 28-SEP-2000; 2000WO-US026524.
PF
XX
XX 29-SEP-1999; 99US-0157137P.
PR
XX 03-NOV-1999; 99US-0163280P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
PI
XX WPI; 2001-235357/24.
DR
XX N-PSDB; AAH35376.
DR
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
PT
XX
XX Claim 11; Page 8198-8200; 9803pp; English.
PS
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
XX Sequence 32 AA;
SQ
Query Match 34.4%; Score 33; DB 4; Length 32;
Best Local Similarity 44.4%; Pred. No. 8.6e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 FEHCNFDV 9
DB 24 FDHCDPEL 32
RESULT 69
ADA95270
ID ADA95270 standard; peptide; 34 AA.
XX
XX ADA95270;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Protein design automation method derived peptide #251.

XX scaffold protein structure; rotamer; pseudo-energy scoring function;
KW optimized protein sequence; protein fold identification;
KW computational screening; peptide library; target identification;
KW cellular physiology; phenotype; signal transduction pathway.
XX Synthetic.
OS WO2003014325-A2.
XX 20-FEB-2003.
XX 12-AUG-2002; 2002WO-US025588.
XX 10-AUG-2001; 2001US-00927790.
PR 10-AUG-2001; 2001US-0311545P.
PR 25-SEP-2001; 2001US-0324899P.
PR 25-JAN-2002; 2002US-0351937P.
PR 25-JAN-2002; 2002US-0352103P.
XX (XENC-) XENCOR.
XX Bentzien J, Dahiyat BI, Desjarlais J, Hayes RJ, Vielmetter J;
PI WPI; 2003-256574/25.
XX
XX Generating computationally prescreened secondary protein libraries, by
PT receiving scaffold protein with residue positions, and analyzing the
PT interaction of rotamers/amino acids with protein to generate protein
PT sequences.
XX Disclosure; Fig 7; 15pp; English.
XX
XX The invention relates to a method, executed by a computer under the
CC control of a program, involving: (i) receiving a scaffold protein
CC structure with residue positions; (ii) selecting a collection of variable
CC residue positions from the residue positions; (iii) establishing a group
CC of potential rotamers or amino acids (aas), for each of the variable
CC residue positions, where a first group for a first variable residue
CC position has a first set of at least two different (aa) side chains, or
CC rotamers from two different (aa) side chains, and where a second group
CC for a second variable residue position has a second set of at least two
CC different (aa) side chains, or rotamers from two different (aa) side
CC chains; and (iv) analyzing the interaction of each of the rotamers in
CC each group or (aas), with all or part of the remainder of the protein to
CC generate a set of optimized protein sequences. Alternatively, the method
CC involves providing a sequence alignment of several related proteins,
CC generating frequencies of occurrence for individual (aas) in at a least
CC several of positions with the alignments, or proteins, creating a pseudo-
CC energy scoring function using the frequencies, and using the pseudo-
CC energy scoring function and at least one additional scoring function, to
CC generate a set of optimized protein sequences. The method is useful for
CC generating an optimized protein sequences using a computer under the
CC control of a program, and also in protein fold identification. The method
CC is also useful for computational screening of random peptide libraries
CC for the purpose of target identification, and for compounds that are
CC capable of inducing specific alterations in cellular physiology or
CC phenotype leading to the discovery of proteins that function in a variety
CC of biochemical and signal transduction pathways. The method is further
CC useful for generating secondary libraries of scaffold protein variants.
CC This sequence represents an example of a peptide sequence derived from
CC the method of the invention.
XX
XX Sequence 34 AA;

Query Match 34.4%; Score 33; DB 6; Length 34;
Best Local Similarity 41.7%; Pred. No. 9.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 FNDVTRLRENE 17
DB 20 FNDATNTMOESQ 31

RESULT 70

AAVS8596 standard; peptide; 16 AA.

XX AAVS8596;

XX 10-APR-2000 (first entry)

XX Toxoplasma gondii antigen SAG1 epitope #8.

XX SAG1; antigen; toxoplasmosis; subunit vaccine; Pichia pastoris; epitope; antibody.

XX Toxoplasma gondii.

XX WO9966043-A1.

XX 23-DEC-1999.

XX 08-JUN-1999; 99WO-EP003957.

XX 12-JUN-1998; 98GB-00012773.

XX 15-APR-1999; 99GB-00008564.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Biemanns R, Bollen A, Haumont M;

XX WPI; 2000-106101/09.

XX Method for production of toxoplasma antigen SAG1 for use in vaccines.

XX Example 1; Page 14; 47pp; English.

XX The invention relates to the recombinant production of the toxoplasma antigen SAG1 or a fragment thereof in the yeast Pichia pastoris. SAG1 is the major surface antigen of Toxoplasma gondii, an obligate intracellular protozoan parasite responsible for toxoplasmosis in mammals, including humans. SAG1 is anchored to the plasma membrane of T. gondii via a GPI (glycosylphosphatidylinositol) anchor, which is attached to the C-terminal anchor region (residues 308-336). The invention provides a truncated SAG1 protein, which lacks the anchor region and comprises amino acids 48-307, and a SAG protein N-terminally fused to a yeast secretion signal peptide. The SAG1 protein and its fragments can be used in the manufacture of a subunit vaccine for the prevention or treatment of toxoplasmosis in mammals. A live attenuated Toxoplasma vaccine is available, but cannot be administered to humans due to the risk of reversion of the attenuated strain to a virulent form. Prior art recombinant expression of SAG1 has been attempted in Escherichia coli, mammalian cells or S. cerevisiae, but has been associated with problems such as misfolding and insolubility, low yields of correctly folded SAG1, or heterogeneous protein production. In addition, purification of the native protein from tachyzoites is difficult and time-consuming, due to the GPI anchor. Sequences AAVS8595-Y58596 represent peptide epitopes of T. gondii SAG1, which were used to raise polyclonal antibodies in an exemplification of the present invention

XX Sequence 16 AA;

Query Match 33.9%; Score 32.5; DB 3; Length 16;
Best Local Similarity 43.8%; Pred. No. 5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 4 CN---FNDVTRLREN 16
DB 1 CNEKSFQDILPKLTEN 16

RESULT 71
ADP84196 standard; protein; 37 AA.
XX

AC ADP84196;
 XX
 DT 23-SEP-2004 (first entry)
 DE
 XX Human AAA1 splice variant X protein SeqID 39.
 XX
 XX AST-1; IGE mediated disease; human; GPRA;
 KW G-protein coupled receptor for asthma susceptibility; AAA1;
 KW asthma associated alternatively spliced gene 1;
 KW chronic obstructive pulmonary disease; cancer; rhinitis; dermatitis;
 KW cytosstatic; antiasthmatic; transgenic; asthma locus-1; asthma.
 XX
 OS Homo sapiens.
 XX
 XX WO2004056866-A1.
 PN
 XX 08-JUL-2004.
 PD
 XX 19-DEC-2003; 2003WO-FI000973.
 XX
 XX 20-DEC-2002; 2002US-0435846P.
 XX
 XX 03-JAN-2003; 2003US-0437895P.
 PR
 XX 26-MAR-2003; 2003US-0458767P.
 PR
 XX 09-JUL-2003; 2003US-0486000P.
 XX
 XX (GENE-) GENEOS OY.
 PA
 XX Laitinen T, Kere J, Laitinen LA, Polvi A, Maekelae S, Vendelin J;
 PI Pulkkinen V, Salmikangas P;
 PI
 XX WPI; 2004-500286/47.
 DR
 XX N-PSDB; ADP84195.
 DR
 XX New GPRA polypeptides, useful in preparing a composition for diagnosing,
 PT treating or preventing asthma, other IGE-mediated disease, chronic
 PT obstructive pulmonary disease or cancer.
 XX
 XX Claim 26; SEQ ID NO 39; 265pp; English.
 PS
 XX This invention relates to the identification of a novel susceptibility
 CC locus AST-1 for asthma and other IGE mediated diseases mapped to the
 CC human chromosome 7p14-p15. Specifically, it refers to two overlapping
 CC genes namely GPRA (G-protein coupled receptor for asthma susceptibility)
 CC and AAA1 (asthma associated alternatively spliced gene 1). The present
 CC invention describes identifying single nucleotide polymorphisms, as well
 CC as insertion or deletion polymorphisms, occurring at different positions
 CC in the AST-1 locus, and furthermore providing vectors, host cells,
 CC primers and probes in order to determine the status of an individual.
 CC Accordingly, it provides a kit to diagnose or assess predisposition to
 CC asthma, chronic obstructive pulmonary disease or cancer and other IGE
 CC mediated diseases including rhinitis and dermatitis, such that derived
 CC pharmaceutical compositions exhibit cytostatic and antiasthmatic
 CC activities. Furthermore, it provides a transgenic animal comprising the
 CC asthma locus-1 (AST-1) DNA. This polypeptide is a human AAA1 variant
 CC protein sequence of the invention.
 XX
 XX Sequence 37 AA;
 SQ
 Query Match 33.9%; Score 32.5; DB 8; Length 37;
 Best Local Similarity 35.0%; Pred. No. 1.2e+03;
 Matches 7; Conservative 4; Mismatches 6; Indels 3; Gaps 1;
 QY 1 PEHCNFDND---VTTRLRENE 17
 | | | | : : | : | :
 Db 17 FSHCNLHAHQFLVRRKQENK 36
 RESULT 72
 ADP84180
 ID ADP84180 standard; protein; 39 AA.
 XX
 XX ADP84180;
 AC
 XX

DT 23-SEP-2004 (first entry)
 XX
 DE Human AAA1 splice variant III protein SeqID 23.
 XX
 XX AST-1; IGE mediated disease; human; GPRA;
 KW G-protein coupled receptor for asthma susceptibility; AAA1;
 KW asthma associated alternatively spliced gene 1;
 KW chronic obstructive pulmonary disease; cancer; rhinitis; dermatitis;
 KW cytosstatic; antiasthmatic; transgenic; asthma locus-1; asthma.
 XX
 OS Homo sapiens.
 XX
 XX WO2004056866-A1.
 PN
 XX 08-JUL-2004.
 PD
 XX 19-DEC-2003; 2003WO-FI000973.
 XX
 XX 20-DEC-2002; 2002US-0435846P.
 XX
 XX 03-JAN-2003; 2003US-0437895P.
 PR
 XX 26-MAR-2003; 2003US-0458767P.
 PR
 XX 09-JUL-2003; 2003US-0486000P.
 XX
 XX (GENE-) GENEOS OY.
 PA
 XX Laitinen T, Kere J, Laitinen LA, Polvi A, Maekelae S, Vendelin J;
 PI Pulkkinen V, Salmikangas P;
 PI
 XX WPI; 2004-500286/47.
 DR
 XX N-PSDB; ADP84179.
 DR
 XX New GPRA polypeptides, useful in preparing a composition for diagnosing,
 PT treating or preventing asthma, other IGE-mediated disease, chronic
 PT obstructive pulmonary disease or cancer.
 XX
 XX Claim 26; SEQ ID NO 23; 265pp; English.
 PS
 XX This invention relates to the identification of a novel susceptibility
 CC locus AST-1 for asthma and other IGE mediated diseases mapped to the
 CC human chromosome 7p14-p15. Specifically, it refers to two overlapping
 CC genes namely GPRA (G-protein coupled receptor for asthma susceptibility)
 CC and AAA1 (asthma associated alternatively spliced gene 1). The present
 CC invention describes identifying single nucleotide polymorphisms, as well
 CC as insertion or deletion polymorphisms, occurring at different positions
 CC in the AST-1 locus, and furthermore providing vectors, host cells,
 CC primers and probes in order to determine the status of an individual.
 CC Accordingly, it provides a kit to diagnose or assess predisposition to
 CC asthma, chronic obstructive pulmonary disease or cancer and other IGE
 CC mediated diseases including rhinitis and dermatitis, such that derived
 CC pharmaceutical compositions exhibit cytostatic and antiasthmatic
 CC activities. Furthermore, it provides a transgenic animal comprising the
 CC asthma locus-1 (AST-1) DNA. This polypeptide is a human AAA1 variant
 CC protein sequence of the invention.
 XX
 XX Sequence 39 AA;
 SQ
 Query Match 33.9%; Score 32.5; DB 8; Length 39;
 Best Local Similarity 35.0%; Pred. No. 1.3e+03;
 Matches 7; Conservative 4; Mismatches 6; Indels 3; Gaps 1;
 QY 1 PEHCNFDND---VTTRLRENE 17
 | | | | : : | : | :
 Db 19 FSHCNLHAHQFLVRRKQENK 38
 RESULT 73
 ADC17406
 ID ADC17406 standard; peptide; 14 AA.
 XX
 XX ADC17406;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX

DE Type IV collagen NC1 domain related peptide SEQ ID NO:7.
 XX crystallised NC1 domain hexamer of type IV collagen;
 KW angiogenesis inhibitor; angiogenesis-mediated disease;
 KW tumour metastasis inhibitor; tumour growth inhibitor;
 KW endothelial cell interaction inhibitor;
 KW basal lamina membrane formation inhibitor; cytostatic; antipsoriatic;
 KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
 KW endothelial cell adhesion inhibitor;
 KW endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;
 KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
 KW blood-borne tumour.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003012122-A2.
 XX
 XX 13-FEB-2003.
 XX
 XX 26-JUL-2002; 2002WO-US023763.
 XX
 XX 27-JUL-2001; 2001US-0308523P.
 PR 29-OCT-2001; 2001US-0351289P.
 PR 22-MAR-2002; 2002US-0366854P.
 PR 03-JUN-2002; 2002US-0385362P.
 XX
 XX (UNIV) UNIV KANSAS MEDICAL CENT.
 PA (SUND/) SUNDARAMOORTHY M.
 PA (HUDS/) HUDSON B.
 XX
 XX Sundaramoorthy M, Hudson B;
 XX WPI; 2003-332730/31.
 XX
 XX New polypeptide, useful for treating an angiogenesis-mediated disease or
 PT condition consisting of glaucoma or blood-borne tumors or for inhibiting
 PT basal lamina membrane formation in cell or tissue development.
 XX
 XX Claim 5; SEQ ID NO 7; 168pp; English.
 XX
 CC The present invention describes a crystallised NC1 domain hexamer of type
 CC IV collagen (1). Also described: (1) a chimeric polypeptide; (2) a
 CC pharmaceutical composition comprising the polypeptide and a carrier; (3)
 CC inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
 CC disease or condition in a mammal; (5) inhibiting tumour metastasis or
 CC growth; (5) inhibiting endothelial cell interaction with the
 CC extracellular matrix in an animal tissue; (6) inhibiting basal lamina
 CC membrane formation in cell or tissue development; (7) a crystal of an NC1
 CC domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
 CC collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
 CC crystallised NC1 domain hexamer of type IV collagen (1) has cytostatic,
 CC antipsoriatic, antianaemic, ophthalmological, antiarteriosclerotic and
 CC antiulcer activities, and can be used as an inhibitor of angiogenesis,
 CC tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
 CC cell proliferation, and basal lamina assembly. A (1) polypeptide can be
 CC used for treating an angiogenesis-mediated disease or condition
 CC consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
 CC psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
 CC or for inhibiting basal lamina membrane formation in cell or tissue
 CC development. The methods are useful for inhibiting angiogenesis in
 CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
 CC cell interaction with the extracellular matrix in an animal tissue, and
 CC identifying inhibitors of type IV collagen assembly. The present sequence
 CC represents a peptide which is used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 33.3%; Score 32; DB 7; Length 14;
 Best Local Similarity 55.6%; Pred. No. 5.2e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEHCNPNV 9
 Db :|||:
 2 FYCINNEV 10
 RESULT 74
 ADC17402
 ID ADC17402 standard; peptide; 14 AA.
 XX
 AC ADC17402;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Type IV collagen NC1 domain related peptide SEQ ID NO:3.
 XX
 XX crystallised NC1 domain hexamer of type IV collagen;
 KW angiogenesis inhibitor; angiogenesis-mediated disease;
 KW tumour metastasis inhibitor; tumour growth inhibitor;
 KW endothelial cell interaction inhibitor;
 KW basal lamina membrane formation inhibitor; cytostatic; antipsoriatic;
 KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
 KW endothelial cell adhesion inhibitor;
 KW endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;
 KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
 KW blood-borne tumour.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003012122-A2.
 XX
 XX 13-FEB-2003.
 XX
 XX 26-JUL-2002; 2002WO-US023763.
 XX
 XX 27-JUL-2001; 2001US-0308523P.
 PR 29-OCT-2001; 2001US-0351289P.
 PR 22-MAR-2002; 2002US-0366854P.
 PR 03-JUN-2002; 2002US-0385362P.
 XX
 XX (UNIV) UNIV KANSAS MEDICAL CENT.
 PA (SUND/) SUNDARAMOORTHY M.
 PA (HUDS/) HUDSON B.
 XX
 XX Sundaramoorthy M, Hudson B;
 XX WPI; 2003-332730/31.
 XX
 XX New polypeptide, useful for treating an angiogenesis-mediated disease or
 PT condition consisting of glaucoma or blood-borne tumors or for inhibiting
 PT basal lamina membrane formation in cell or tissue development.
 XX
 XX Claim 5; SEQ ID NO 3; 168pp; English.
 XX
 CC The present invention describes a crystallised NC1 domain hexamer of type
 CC IV collagen (1). Also described: (1) a chimeric polypeptide; (2) a
 CC pharmaceutical composition comprising the polypeptide and a carrier; (3)
 CC inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
 CC disease or condition in a mammal; (5) inhibiting tumour metastasis or
 CC growth; (5) inhibiting endothelial cell interaction with the
 CC extracellular matrix in an animal tissue; (6) inhibiting basal lamina
 CC membrane formation in cell or tissue development; (7) a crystal of an NC1
 CC domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
 CC collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
 CC crystallised NC1 domain hexamer of type IV collagen (1) has cytostatic,
 CC antipsoriatic, antianaemic, ophthalmological, antiarteriosclerotic and
 CC antiulcer activities, and can be used as an inhibitor of angiogenesis,
 CC tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
 CC cell proliferation, and basal lamina assembly. A (1) polypeptide can be
 CC used for treating an angiogenesis-mediated disease or condition
 CC consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
 CC psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
 CC or for inhibiting basal lamina membrane formation in cell or tissue
 CC development. The methods are useful for inhibiting angiogenesis in
 CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
 CC cell interaction with the extracellular matrix in an animal tissue, and
 CC identifying inhibitors of type IV collagen assembly. The present sequence
 CC represents a peptide which is used in the exemplification of the present
 CC invention.

CC development. The methods are useful for inhibiting angiogenesis in
 CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
 CC cell interaction with the extracellular matrix in an animal tissue, and
 CC identifying inhibitors of type IV collagen assembly. The present sequence
 CC represents a peptide which is used in the exemplification of the present
 CC invention.

XX Sequence 14 AA;

Query Match 33.3%; Score 32; DB 7; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.2e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FEHCNFDV 9
 | | | | |
 Db 2 FLFCNVNDV 10

RESULT 75

ADRI8924 standard; peptide; 14 AA.

ID ADRI8924;

AC ADRI8924;

XX 04-NOV-2004 (first entry)

XX Human type IV collagen NC1 inter-CDSR alpha3 chain peptide.

XX angiogenesis; angiogenesis-mediated disease; tumour metastasis;
 KW tumour growth; type IV collagen; NC1 domain hexamer; angiogenic;
 KW cytosolic; antidiabetic; ophthalmological; antirheumatic; antiarthritic;
 KW immunosuppressive; antiseborrheic; dermatological; antibacterial;
 KW vulnary; antiulcer; fungicide; virucide; protozoacide; anti-HIV;
 KW antiinflammatory; antianaemic; antickling; osteopathic; vasotropic;
 KW gastrointestinal; antipsoriatic; antiatherosclerotic.

XX Homo sapiens.

XX WO2004067762-A2.

XX 12-AUG-2004.

XX 27-JAN-2004; 2004WO-US002187.

XX 27-JAN-2003; 2003US-0443133P.

XX (UNIV) UNIV KANSAS MEDICAL CENT.

XX Sundaramoorthy M, Hudson B;

XX WPI; 2004-594218/57.

XX Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions,
 PT tumor metastasis, and tumor growth, involves contacting subject with
 PT crystallized type IV collagen NC1 domain hexamer polypeptide.

PS Disclosure; SEQ ID NO 3; 178pp; English.

XX The invention relates to a novel method for inhibiting angiogenesis,
 CC angiogenesis-mediated diseases or conditions, tumour metastasis, and
 CC tumour growth, involving contacting a subject with a crystallised type IV
 CC collagen NC1 domain hexamer polypeptide. A polypeptide of the invention
 CC has angiogenic, cytosolic, antidiabetic, immunosuppressive, antiseborrheic,
 CC antirheumatic, antiarthritic, vulnary, antiulcer, fungicide, virucide,
 CC dermatological, antibacterial, immunosuppressive, ophthalmological,
 CC protozoacide, anti-HIV, antiinflammatory, antianaemic, antickling, and
 CC osteopathic, vasotropic, gastrointestinal, antipsoriatic, and
 CC antiatherosclerotic activity. The polypeptide inhibits assembly of type
 CC IV collagen heterotrimers and hexamers. The method of the invention is
 CC useful for inhibiting angiogenesis, angiogenesis-mediated diseases or
 CC conditions, tumour metastasis and tumour growth. The angiogenesis-
 CC mediated disease or condition is solid and blood-borne tumours, diabetic
 CC retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal

CC neovascularisation, macular degeneration, corneal neovascularisation,
 CC retinopathy of prematurity, corneal graft rejection, neovascular
 CC glaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis,
 CC pterygium keratitis sicca, Sjogren's, acne rosacea, phlyctenulosis,
 CC syphilis, Mycobacteria infections, lipid degeneration, chemical burns,
 CC bacterial ulcers, fungal ulcers, Herpes simplex infections, Herpes zoster
 CC infections, protozoan infections, Kaposi's sarcoma, Mooren ulcer,
 CC Terrien's marginal degeneration, marginal keratolysis, trauma, systemic
 CC lupus, polyarthritis, Wegeners sarcoidosis, scleritis, Steven's Johnson
 CC disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma
 CC elasticum, Paget's disease, vein occlusion, artery occlusion, carotid
 CC obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease,
 CC Bales disease, Bechet's disease, myopia, optic pits, Stargarts disease,
 CC pars planitis, chronic retinal detachment, hyperviscosity syndromes,
 CC toxoplasmosis, post-laser complications, abnormal proliferation of
 CC fibrovascular tissue, haemangiomas, Osler Weber-Rendu, AIDS, ocular
 CC neovascular disease, osteoarthritis, chronic inflammation, Crohn's
 CC disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid.
 CC The present sequence represents a peptide of the invention, derived from
 CC type IV collagen crystallised NC1 domain hexamer.

XX Sequence 14 AA;

Query Match 33.3%; Score 32; DB 8; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.2e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FEHCNFDV 9
 | | | | |
 Db 2 FLFCNVNDV 10

RESULT 76

ADRI8928 standard; peptide; 14 AA.

XX ADRI8928;

XX 04-NOV-2004 (first entry)

XX Human type IV collagen NC1 inter-CDSR alpha6 chain peptide.

XX angiogenesis; angiogenesis-mediated disease; tumour metastasis;
 KW tumour growth; type IV collagen; NC1 domain hexamer; angiogenic;
 KW cytosolic; antidiabetic; ophthalmological; antirheumatic; antiarthritic;
 KW immunosuppressive; antiseborrheic; dermatological; antibacterial;
 KW vulnary; antiulcer; fungicide; virucide; protozoacide; anti-HIV;
 KW antiinflammatory; antianaemic; antickling; osteopathic; vasotropic;
 KW gastrointestinal; antipsoriatic; antiatherosclerotic.

XX Homo sapiens.

XX WO2004067762-A2.

XX 12-AUG-2004.

XX 27-JAN-2004; 2004WO-US002187.

XX 27-JAN-2003; 2003US-0443133P.

XX (UNIV) UNIV KANSAS MEDICAL CENT.

XX Sundaramoorthy M, Hudson B;

XX WPI; 2004-594218/57.

XX Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions,
 PT tumor metastasis, and tumor growth, involves contacting subject with
 PT crystallized type IV collagen NC1 domain hexamer polypeptide.

PS Disclosure; SEQ ID NO 7; 178pp; English.

XX The invention relates to a novel method for inhibiting angiogenesis,

AA Sequence 15 AA:

Qy	6	FNDVTTRL	13
Db	2	FNVVTRL	9

AC ADK70613;

DE Human erythropoietin (EPO) protein-related epitope peptide #45.

XX

novum varietale.

FD
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04-MAR-2004.

XX
FY AUG-2002; 2002SF-00017317.
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PT useful in various therapeutic applications such as in the treatment of

XX

CC the same biological activity in an individual when used in vivo. The

CC is that of a human EPO epitope peptide which is related to the invention.

DR WPI; 2004-226801/21.
 XX New modified human erythropoietin molecules with reduced immunogenicity,
 PT useful in various therapeutic applications such as in the treatment of
 PT anemia.
 XX Example 1; Page 27; 38pp; English.
 XX This invention relates to a novel modified molecule comprising the
 CC biological activity of human erythropoietin (EPO) and being substantially
 CC non-immunogenic or less immunogenic than any non-modified molecule having
 CC the same biological activity in an individual when used in vivo. The
 CC invention is useful for manufacturing a modified human erythropoietin
 CC molecule. The modified EPO may be used in various therapeutic
 CC applications, such as in the treatment of anaemia. The present sequence
 CC is that of a human EPO epitope peptide which is related to the invention.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 33.3%; Score 32; DB 8; Length 15;
 Best Local Similarity 50.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
 |||: |: |
 DB 4 EHCSLNENIT 13

RESULT 82
 ADN65159
 ID ADN65159 standard; peptide; 15 AA.
 XX
 AC ADN65159;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE HLA binding peptide #1759.
 XX
 KW cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KW chondyloa acuminatum.
 XX
 OS Unidentified.
 XX
 PN WO2004031211-A2.
 XX
 PD 15-APR-2004.
 XX
 XX 03-OCT-2003; 2003WO-US031308.
 PF
 PR 03-OCT-2002; 2002US-0416207P.
 PR 08-OCT-2002; 2002US-0417569P.
 XX
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Sidney J, Southwood S, Sette A;
 PI
 XX WPI; 2004-347953/32.
 DR
 XX New composition of peptides and nucleic acids capable of binding Major
 PT Histocompatibility Complex molecules, useful for diagnosing, preventing
 PT or treating viral infections or cancer, such as prostate cancer,
 PT hepatitis B or AIDS.
 XX
 XX Claim 1; SEQ ID NO 1759; 186pp; English.
 PS
 XX The invention relates to a novel composition comprising one or more
 CC peptides or nucleic acids encoding an HLA binding peptide. The
 CC composition further comprises an HTL epitope. It also comprises a spacer

CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 CC are incorporated as part of a liposome. The peptide is from an antigen
 CC selected from prostate specific antigen (PSA), prostate specific membrane
 CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 CC Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
 CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 CC (TKP). The composition is useful for preventing or treating viral
 CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyloa
 CC acuminatum. The composition is also be used for diagnosing such diseases.
 CC This sequence represents a peptide of the invention.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 33.3%; Score 32; DB 8; Length 15;
 Best Local Similarity 50.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
 |||: |: |
 DB 1 EHCSLNENIT 10

RESULT 83
 ADT07746
 ID ADT07746 standard; peptide; 15 AA.
 XX
 AC ADT07746;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human erythropoietin derived peptide #6.
 XX
 KW Erythropoietin; EPO; reduced immunogenicity; reduced immunity;
 KW major histocompatibility complex class II; MHC;
 KW helper T lymphocyte response; HTL; fungal disease; viral disease;
 KW bacterial disease; parasitic disease; cancer; autoimmune disease;
 KW allograft rejection; allergy; Lyme disease; ulcerative colitis;
 KW transplantation; haemophilia; osteoporosis; metabolic disease;
 KW food hypersensitivity; cytostatic; immunosuppressive; antiinflammatory;
 KW human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2004089973-A2.
 XX
 PD 21-OCT-2004.
 XX
 XX 02-APR-2004; 2004WO-US010353.
 PF
 XX 02-APR-2003; 2003US-0459939P.
 PR
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Tangri S, Mothe B, Sette A, Southwood S, Briggs K, Chestnut RW;
 PI
 XX WPI; 2004-748719/73.
 DR
 XX New isolated or purified modified erythropoietin construct useful for
 PT treatment of anemia comprises a sequence selected from 5 sequences each
 PT containing 193 amino acids as given in specification, or truncated
 PT modified erythropoietin.
 XX
 XX Claim 11; SEQ ID NO 25; 223pp; English.
 PS
 XX The invention relates to isolated or purified modified erythropoietin
 CC (EPO) constructs (MSC), and truncated modified erythropoietin constructs.
 CC These constructs are peptides, polypeptides, proteins or antibodies
 CC having reduced immunogenicity as compared to the naturally occurring
 CC form. Also disclosed is a method of producing such peptides. The reduced

CC immunity is as a result of reduced binding to major histocompatibility
 CC complex (MHC) class II molecules. The peptides of the invention are
 CC useful for antagonising the erythropoietin (EPO) receptor or treating
 CC diseases or conditions associated with over-activation of the EPO
 CC receptor. The invention is useful for producing a peptide, polypeptide,
 CC protein and antibody having reduced immunogenicity, which is useful in
 CC the treatment and diagnosis of diseases, conditions and disorders. It is
 CC also useful for reducing the helper T lymphocyte (HTL) response against a
 CC candidate protein. The peptides, polypeptides, proteins and antibodies
 CC are useful for the treatment of pathological states (such as fungal,
 CC viral, bacterial and parasitic diseases, cancer (such as breast cancer,
 CC non-Hodgkin's lymphoma), autoimmune diseases (such as rheumatoid
 CC arthritis, multiple sclerosis, myasthenia gravis), allograft rejection,
 CC allergies (e.g. pollen allergies), Lyme disease, hepatitis B and C, LCMV,
 CC post-streptococcal endocarditis or glomerulonephritis, ulcerative
 CC colitis, Crohn's disease, psoriasis, chronic renal failure, asthma,
 CC transplantation, haemophilia, Paget's disease, osteoporosis, chronic
 CC granulomatous disease, genital warts, diabetes, defective tissue growth,
 CC metabolic disease and food hypersensitivities). The peptides,
 CC polypeptides, proteins and antibodies are modified so as to have reduced
 CC immunogenicity as a result of reduced binding to MHC class II against
 CC various DR and DQ molecules and the subsequent reduced helper T
 CC lymphocyte (HTL) response. Modified erythropoietin (EPO) construct
 CC inserts are useful for the construction of bacterial and eukaryotic
 CC expression vectors. The present sequence represents a peptide derived
 CC from human erythropoietin.

XX SQ Sequence 15 AA;

Query Match 33.3%; Score 32; DB 8; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.6e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFDNVT 11

Db 6 EHCSLNENIT 15

RESULT 84

ADT07747

ID ADT07747 standard; peptide; 15 AA.

XX AC ADT07747;

XX DT 13-JAN-2005 (first entry)

XX DE Human erythropoietin derived peptide #7.

XX KW Erythropoietin; EPO; reduced immunogenicity; reduced immunity;

XX KW major histocompatibility complex class II; MHC;

XX KW helper T lymphocyte response; HTL; fungal disease; viral disease;

XX KW bacterial disease; parasitic disease; cancer; autoimmune disease;

XX KW allograft rejection; allergy; Lyme disease; ulcerative colitis;

XX KW transplantation; haemophilia; osteoporosis; metabolic disease;

XX KW food hypersensitivity; cytostatic; immunosuppressive; antiinflammatory;

XX KW human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004089973-A2.

XX PD 21-OCT-2004.

XX PF 02-APR-2004; 2004WO-US010353.

XX PR 02-APR-2003; 2003US-0459939P.

XX FA (EPIM-) EPIMUNE INC.

XX PI Tangri S, Mothe B, Sette A, Southwood S, Briggs K, Chestnut RW;

XX DR WPI; 2004-748719/73.

XX PT New isolated or purified modified erythropoietin construct useful for
 PT treatment of anemia comprises a sequence selected from 5 sequences each
 PT containing 193 amino acids as given in specification, or truncated
 PT modified erythropoietin.

PS Claim 11; SEQ ID NO 26; 223pp; English.

XX CC The invention relates to isolated or purified modified erythropoietin
 CC (EPO) constructs (MEC), and truncated modified erythropoietin constructs.
 CC These constructs are peptides, polypeptides, proteins or antibodies
 CC having reduced immunogenicity as compared to the naturally occurring
 CC form. Also disclosed is a method of producing such peptides. The reduced
 CC immunity is as a result of reduced binding to major histocompatibility
 CC complex (MHC) class II molecules. The peptides of the invention are
 CC useful for antagonising the erythropoietin (EPO) receptor or treating
 CC diseases or conditions associated with over-activation of the EPO
 CC receptor. The invention is useful for producing a peptide, polypeptide,
 CC protein and antibody having reduced immunogenicity, which is useful in
 CC the treatment and diagnosis of diseases, conditions and disorders. It is
 CC also useful for reducing the helper T lymphocyte (HTL) response against a
 CC candidate protein. The peptides, polypeptides, proteins and antibodies
 CC are useful for the treatment of pathological states (such as fungal,
 CC viral, bacterial and parasitic diseases, cancer (such as breast cancer,
 CC non-Hodgkin's lymphoma), autoimmune diseases (such as rheumatoid
 CC arthritis, multiple sclerosis, myasthenia gravis), allograft rejection,
 CC allergies (e.g. pollen allergies), Lyme disease, hepatitis B and C, LCMV,
 CC post-streptococcal endocarditis or glomerulonephritis, ulcerative
 CC colitis, Crohn's disease, psoriasis, chronic renal failure, asthma,
 CC transplantation, haemophilia, Paget's disease, osteoporosis, chronic
 CC granulomatous disease, genital warts, diabetes, defective tissue growth,
 CC metabolic disease and food hypersensitivities). The peptides,
 CC polypeptides, proteins and antibodies are modified so as to have reduced
 CC immunogenicity as a result of reduced binding to MHC class II against
 CC various DR and DQ molecules and the subsequent reduced helper T
 CC lymphocyte (HTL) response. Modified erythropoietin (EPO) construct
 CC inserts are useful for the construction of bacterial and eukaryotic
 CC expression vectors. The present sequence represents a peptide derived
 CC from human erythropoietin.

XX SQ Sequence 15 AA;

Query Match 33.3%; Score 32; DB 8; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.6e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EHCNFDNVT 11

Db 1 EHCSLNENIT 10

RESULT 85

AAR70779

ID AAR70779 standard; peptide; 16 AA.

XX AC AAR70779;

XX DT 25-MAR-2003 (revised)

XX DT 30-AUG-1995 (first entry)

XX DE EPO neurotrophic peptide.

XX KW Erythropoietin; EPO; cytokine; myelination; nervous system;

XX KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;

XX KW adrenal leukodystrophy; neuroblastoma.

XX OS Homo sapiens.

XX PN WO9503821-A1.

XX PD 09-FEB-1995.

XX PF 28-JUL-1994; 94WO-US008453.

XX 30-JUL-1993; 93US-00100247.
PR 21-APR-1994; 94US-00232513.
XX (OBRI/) O'BRIEN J S.
XX O'brien JS, Kishimoto Y;
PI WPI; 1995-082029/11.
XX
XX Stimulating neural cell out-growth and myelination - with pro:saposin,
PT saposin C or new neurotrophic peptide(s) from cytokine(s), for treating
PT nervous system diseases.
XX
XX Disclosure; Page 36; 50pp; English.
XX
XX The peptide given in AAR70773, corresponding to amino acids 8-29 of human
CC saposin-C (AAR70784), promotes neurite outgrowth in vitro. A consensus
CC sequence was determined by comparing the peptide with hematopoietic and
CC neurotrophic cytokines, and neurotrophic peptides (AAR70774-82) were
CC identified in the AB loop of human ciliary neurotrophic factor,
CC interleukins-6, -2, -3 and -gamma, erythropoietin and leukocyte
CC inhibitory factor, and in helix C of human interleukin-1-beta and
CC oncostatin-M. Prosaoponin (AAR70783) and saposin-C also promoted nerve
CC cell myelination ex vivo. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
XX Sequence 16 AA;
SQ
Query Match 33.3%; Score 32; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 EHCNFNDVTT 11
DB 2 EHCSLNENIT 11
|||:|:|
RESULT 86
ADI38855
ID ADI38855 standard; peptide; 16 AA.
XX
AC ADI38855;
XX
XX 22-APR-2004 (first entry)
XX
XX Human erythropoietin mimetic.
XX
XX analgesic; erythropoietin receptor; neuropathic pain; erythropoietin;
KW Epo; nerve degeneration; pain; human; mimetic.
XX
XX Unidentified.
OS
XX US2004018978-A1.
PN
XX
XX 29-JAN-2004.
XX
XX 05-JUN-2003; 2003US-00455697.
PF
XX 05-JUN-2002; 2002US-0386286P.
PR
XX (CAMP/) CAMPANA W M.
PA (MYER/) MYERS R R.
PA
XX Campaña WM, Myers RR;
PI WPI; 2004-142542/14.
XX
XX Treatment of neuropathic pain comprising administration of erythropoietin
PT and erythropoietin mimetics.
XX
XX Disclosure; SEQ ID NO 3; 14pp; English.
PS

XX The invention describes a method of treating neuropathic pain by
CC administering erythropoietin (Epo). The method is used for treating
CC neuropathic pain. The method decreases nerve degeneration and pain, and
CC increases the rate of recovery. This is the amino acid sequence of a
CC human erythropoietin (EPO) mimetic.
XX
XX Sequence 16 AA;
SQ
Query Match 33.3%; Score 32; DB 8; Length 16;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 EHCNFNDVTT 11
DB 1 EHCSLNENIT 10
|||:|:|
RESULT 87
AAW30024
ID AAW30024 standard; peptide; 17 AA.
XX
AC AAW30024;
XX
XX 14-APR-1998 (first entry)
DT
XX
XX Cytokine hEPO AB loop derived peptide.
DE
XX Human; prosaposin; neural disorder; demyelination disorder;
KW neural cell death; inhibition; myelination; neurite outgrowth;
KW neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy;
KW polynuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus;
KW cytokine.
XX
XX Homo sapiens.
OS
XX WO9732895-A1.
PN
XX 12-SEP-1997.
PD
XX 05-MAR-1997; 97WO-US004143.
PF
XX 05-MAR-1996; 96US-00611307.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Obrien JS;
PI
XX WPI; 1997-470538/43.
DR
XX Prosaposin-derived peptide - useful for therapy of neural or
PT demyelination disorders in neural tissue.
PT
XX Claim 16; Page 56; 69pp; English.
PS
XX The present sequence represents a specifically claimed cytokine derived
CC peptide for use in the following method of the invention. A method has
CC been developed of alleviating or preventing neuropathic pain in a
CC subject, comprising administering an effective amount of an active
CC fragment of prosaposin to the subject. The prosaposin-derived peptide is
CC useful for therapy of neural or demyelination disorders in neural tissue.
CC It can be used to stimulate neurite outgrowth, inhibit neural cell death,
CC promote myelination or inhibit demyelination. The method is used to
CC alleviate neuropathic pain resulting from a peripheral nerve disorder,
CC such as neuroma, nerve compression, crush or stretch and incomplete nerve
CC transection, mononeuropathy or polyneuropathy. Alternatively the
CC neuropathic pain results from a disorder of the dorsal root ganglia,
CC spinal cord, brainstem, thalamus or cortex
XX
XX Sequence 17 AA;
SQ
Query Match 33.3%; Score 32; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 6.4e+02;
PS

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
 |||:|:|
 Db 2 EHCSLNENIT 11

RESULT 88
 AAW66142
 ID AAW66142 standard; peptide; 17 AA.
 XX AC AAW66142;
 XX DT 17-NOV-1998 (first entry)
 XX DE Prosaposin receptor agonist #16.
 XX KW prosaposin; receptor agonist; neuropathic pain; neurite outgrowth;
 KW neural cell death; nerve disorder; side effect.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9839357-A1.
 XX PD 11-SEP-1998.
 XX PF 11-SEP-1997; 97WO-US016062.
 XX PR 05-MAR-1997; 97WO-US004143.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Obrien JS;
 XX DR WPI; 1998-495790/42.
 XX PT Use of prosaposin receptor agonists - for alleviating neuropathic pain,
 PT inhibiting sensory or motor neuropathy, or inhibiting neural cell death.
 XX PS Claim 13; Page 19; 67pp; English.
 XX CC The invention relates to prosaposin receptor agonists. Also claimed are:
 CC (1) methods for alleviating neuropathic pain or inhibiting the onset of
 CC neuropathic pain, comprising administering a prosaposin receptor agonist;
 CC (2) inhibiting sensory or motor neuropathy, comprising contacting
 CC neuronal cells with a composition comprising a prosaposin receptor
 CC agonist; (3) methods for stimulating neurite outgrowth, inhibiting neural
 CC cell death, promoting myelination, or inhibiting demyelination comprising
 CC contacting neuronal cells with a composition comprising a prosaposin
 CC receptor agonist which has 14-50 amino acids and comprises the sequence
 CC of a prosaposin derived protein. The processes may be used for treatment
 CC of neuropathic pain resulting from peripheral nerve disorders (e.g.
 CC neuroma, nerve compression, nerve crush, nerve stretch, incomplete nerve
 CC transection, mononeuropathy or polyneuropathy) or disorders of dorsal
 CC root ganglia, the spinal cord, the brainstem, the thalamus or the cortex.
 CC The receptor agonists do not cause undesirable side effects. The present
 CC sequence represents a prosaposin receptor agonist
 XX SQ Sequence 17 AA;

Query Match 33.3%; Score 32; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
 |||:|:|
 Db 2 EHCSLNENIT 11

RESULT 89
 ADQ94321
 ID ADQ94321 standard; peptide; 17 AA.

XX AC ADQ94321;
 XX DT 23-SEP-2004 (first entry)
 XX DE Human prosaposin receptor agonist from EPO.
 XX KW Human; prosaposin; C-domain; prosaposin receptor agonist;
 KW neuropathic pain; neurite outgrowth; neural cell death; myelination;
 KW demyelination; neuropathy; peripheral nerve disorder; neuroma;
 KW nerve compression; nerve crush; nerve stretch;
 KW incomplete nerve transection; mononeuropathy; polyneuropathy; EPO.
 XX OS Homo sapiens.
 XX PN US2004121958-A1.
 XX PD 24-JUN-2004.
 XX PF 24-DEC-2003; 2003US-00746442.
 XX PR 05-MAR-1996; 96US-00611307.
 PR 05-MAR-1997; 97WO-US004143.
 PR 11-SEP-1997; 97US-00928074.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI O'brien JS;
 XX DR WPI; 2004-468194/44.
 XX PT New prosaposin receptor agonist, useful in alleviating or treating
 PT neuropathic pain, inhibiting the onset of neuropathic pain, neural cell
 PT death, demyelination, or sensory or motor neuropathy, and stimulating
 PT neurite outgrowth.
 XX PS Claim 13; SEQ ID NO 16; 33pp; English.
 XX CC The invention relates to a prosaposin receptor agonist comprising a
 CC defined amino acid sequence of 14-50 amino acids conforming to the
 CC consensus sequence appearing as ADQ94330. The agonists are based on
 CC peptides derived from the C domain of human prosaposin (or homologous
 CC peptides from other proteins). Also included are a pharmaceutical
 CC composition comprising the prosaposin receptor agonist in a
 CC pharmaceutical carrier, a method of alleviating neuropathic pain in a
 CC subject, a method of inhibiting the onset of neuropathic pain in a
 CC subject, a method of stimulating neurite outgrowth (or inhibiting neural
 CC cell death, promoting myelination or inhibiting demyelination) and a
 CC method of inhibiting sensory or motor neuropathy. The neuropathic pain
 CC results from a peripheral nerve disorder, e.g. neuroma, nerve
 CC compression, nerve crush, nerve stretch and incomplete nerve
 CC transection, mononeuropathy or polyneuropathy or results from a disorder
 CC of dorsal root ganglia, spinal cord, brainstem, thalamus, or cortex. The
 CC prosaposin receptor agonist, composition, and methods are useful in
 CC alleviating or treating neuropathic pain, inhibiting the onset of
 CC neuropathic pain, neural cell death, demyelination, or sensory or motor
 CC neuropathy, and in stimulating neurite outgrowth. The present sequence is
 CC prosaposin receptor agonist comprising a peptide derived from a
 CC prosaposin C domain-homologous peptide from another human protein.
 XX SQ Sequence 17 AA;

Query Match 33.3%; Score 32; DB 8; Length 17;
 Best Local Similarity 50.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EHCNFDVTT 11
 |||:|:|
 Db 2 EHCSLNENIT 11

RESULT 90
 ADW80720

ID ADW80720 standard; peptide; 17 AA.
 AC ADW80720;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Human erythropoietin (EPO) AB loop peptide, SEQ ID NO:16.
 XX
 KW Pharmaceutical; neuropathy; analgesic; cell death; diabetes;
 KW neurological disease; neuropathic pain; cytokine; erythropoietin.
 XX
 OS Homo sapiens.
 XX
 PN US6849602-B1.
 XX
 PD 01-FEB-2005.
 XX
 PF 11-SEP-1997; 97US-00928074.
 XX
 PR 05-MAR-1996; 96US-00611307.
 PR 05-MAR-1997; 97WO-US004143.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Obrien JS;
 XX
 DR WPI; 2005-129968/14.
 XX
 XX New pharmaceutical composition comprising a prosaposin receptor agonist and a carrier, where the composition is in a controlled release, PT liposomal or unit dosage form, useful for alleviating neuropathic pain PT resulting from diabetes.
 XX
 PS Disclosure; SEQ ID NO 16; 35pp; English.
 XX
 CC The invention relates to a pharmaceutical composition comprising a prosaposin receptor agonist and a carrier, where the composition is in a controlled release, liposomal or unit dosage form. The invention also relates to prosaposin receptor agonists and the use of these agonists for stimulating neurite outgrowth, inhibiting neural cell death, promoting myelination, inhibiting neural demyelination and inhibiting sensory or motor neuropathy. The pharmaceutical composition is useful for alleviating neuropathic pain resulting from diabetes. The present sequence is a human erythropoietin (EPO) AB loop peptide which shares similarity to residues 8-29 of human prosaposin. This sequence may be used in the method for alleviating neuropathic pain.
 XX
 SQ Sequence 17 AA;
 Query Match 33.3%; Score 32; DB 9; Length 17;
 Best Local Similarity 50.0%; Pred. No. 6.4e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EHCNFDVTT 11
 |||:|:|
 Db 2 EHCSLNEIT 11
 |||:|:|
 RESULT 91
 ADC17649
 ID ADC17649 standard; peptide; 18 AA.
 XX
 AC ADC17649;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Type IV collagen NC1 domain related peptide SEQ ID NO:254.
 XX
 KW crystallised NC1 domain hexamer of type IV collagen;
 KW angiogenesis inhibitor; angiogenesis-mediated disease;
 KW tumour metastasis inhibitor; tumour growth inhibitor;
 KW endothelial cell interaction inhibitor;
 KW basal lamina membrane formation inhibitor; cytostatic; antiprosoritic;

KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
 KW endothelial cell adhesion inhibitor;
 KW endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;
 KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
 KW blood-borne tumour.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003012122-A2.
 XX
 PD 13-FEB-2003.
 XX
 PF 26-JUL-2002; 2002WO-US023763.
 XX
 PR 27-JUL-2001; 2001US-0308523P.
 PR 29-OCT-2001; 2001US-0351289P.
 PR 22-MAR-2002; 2002US-0366854P.
 PR 03-JUN-2002; 2002US-0385362P.
 XX
 PA (UNIV) UNIV KANSAS MEDICAL CENT.
 PA (SUND/) SUNDARAMOORTHY M.
 PA (HUDS/) HUDSON B.
 XX
 PI Sundaramoorthy M, Hudson B;
 XX
 DR WPI; 2003-332730/31.
 XX
 XX New polypeptide, useful for treating an angiogenesis-mediated disease or condition consisting of glaucoma or blood-borne tumors or for inhibiting basal lamina membrane formation in cell or tissue development.
 XX
 PS Claim 57; SEQ ID NO 254; 168pp; English.
 XX
 CC The present invention describes a crystallised NC1 domain hexamer of type IV collagen (1). Also described: (1) a chimeric polypeptide; (2) a pharmaceutical composition comprising the polypeptide and a carrier; (3) inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated disease or condition in a mammal; (5) inhibiting tumour metastasis or growth; (5) inhibiting endothelial cell interaction with the extracellular matrix in an animal tissue; (6) inhibiting basal lamina membrane formation in cell or tissue development; (7) a crystal of an NC1 domain hexamer of type IV collagen; (8) identifying inhibitors of type IV collagen assembly; and (9) an inhibitor of type IV collagen assembly. A crystallised NC1 domain hexamer of type IV collagen (1) has cytostatic, antiprosoritic, antianaemic, ophthalmological, antiarteriosclerotic and antiulcer activities, and can be used as an inhibitor of angiogenesis, tumour growth, tumour metastasis, endothelial cell adhesion, endothelial cell proliferation, and basal lamina assembly. A (1) polypeptide can be used for treating an angiogenesis-mediated disease or condition consisting of glaucoma, sickle cell anaemia, ulcerative colitis, psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours or for inhibiting basal lamina membrane formation in cell or tissue development. The methods are useful for inhibiting angiogenesis in tissue, inhibiting tumour metastasis or growth, inhibiting endothelial cell interaction with the extracellular matrix in an animal tissue, and identifying inhibitors of type IV collagen assembly. The present sequence represents a peptide which is used in the exemplification of the present invention.
 XX
 SQ Sequence 18 AA;
 Query Match 33.3%; Score 32; DB 7; Length 18;
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FEHCNFDV 9
 |||:|:|
 Db 6 FLFCNVNDV 14
 |||:|:|
 RESULT 92
 ADC17653

ADCL17653 standard; peptide; 18 AA.

ADCL17653;

18-DEC-2003 (first entry)

Type IV collagen NC1 domain related peptide SEQ ID NO:258.

crystallised NC1 domain hexamer of type IV collagen;

angiogenesis inhibitor; angiogenesis-mediated disease;

tumour metastasis inhibitor; tumour growth inhibitor;

endothelial cell interaction inhibitor;

basal lamina membrane formation inhibitor; cytostatic; antiprosoriatic;

antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;

endothelial cell adhesion inhibitor;

endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;

ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;

blood-borne tumour.

Synthetic.

Homo sapiens.

WO2003012122-A2.

13-FEB-2003.

26-JUL-2002; 2002WO-US023763.

27-JUL-2001; 2001US-0308523P.

29-OCT-2001; 2001US-0351289P.

22-MAR-2002; 2002US-0366854P.

03-JUN-2002; 2002US-0385362P.

(UNIV) UNIV KANSAS MEDICAL CENT.

(SUND/) SUNDARAMOORTHY M.

(HUDS/) HUDSON B.

Sundaramoorthy M, Hudson B;

WPI; 2003-332730/31.

New polypeptide, useful for treating an angiogenesis-mediated disease or condition consisting of glaucoma or blood-borne tumors or for inhibiting basal lamina membrane formation in cell or tissue development.

Claim 57; SEQ ID NO 258; 168pp; English.

The present invention describes a crystallised NC1 domain hexamer of type IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a pharmaceutical composition comprising the polypeptide and a carrier; (3) inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated disease or condition in a mammal; (5) inhibiting tumour metastasis or growth; (6) inhibiting endothelial cell interaction with the extracellular matrix in an animal tissue; (6) inhibiting basal lamina membrane formation in cell or tissue development; (7) a crystal of an NC1 domain hexamer of type IV collagen; (8) identifying inhibitors of type IV collagen assembly; and (9) an inhibitor of type IV collagen assembly. A crystallised NC1 domain hexamer of type IV collagen (I) has cytostatic, antiprosoriatic, antianaemic, ophthalmological, antiarteriosclerotic and antiulcer activities, and can be used as an inhibitor of angiogenesis, tumour growth, tumour metastasis, endothelial cell adhesion, endothelial cell proliferation, and basal lamina assembly. A (I) polypeptide can be used for treating an angiogenesis-mediated disease or condition consisting of glaucoma, sickle cell anaemia, ulcerative colitis, psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours or for inhibiting basal lamina membrane formation in cell or tissue development. The methods are useful for inhibiting angiogenesis in tissue, inhibiting tumour metastasis or growth, inhibiting endothelial cell interaction with the extracellular matrix in an animal tissue, and identifying inhibitors of type IV collagen assembly. The present sequence represents a peptide which is used in the exemplification of the present invention.

SEQ Sequence 18 AA;

Query Match 33.3%; Score 32; DB 7; Length 18;

Best Local Similarity 55.6%; Pred. No. 6.8e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FEHCNFNDV 9

Db 6 FIYCNTINEV 14

RESULT 93

ADR19171

ID ADR19171 standard; peptide; 18 AA.

XX AC ADR19171;

XX DT 04-NOV-2004 (first entry)

XX DE Type IV collagen SR plus inter-CDSR region alpha3 chain peptide.

XX KW angiogenesis; angiogenesis-mediated disease; tumour metastasis;

XX KW tumour growth; type IV collagen; NC1 domain hexamer; angiogenic;

XX KW cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic;

XX KW immunosuppressive; antiseborrheic; dermatological; antibacterial;

XX KW vulnery; antiulcer; fungicide; virucide; protozoacide; anti-HIV;

XX KW antiinflammatory; antianaemic; antiskilling; osteopathic; vasotropic;

XX KW gastrointestinal; antipsoriatic; antiatherosclerotic.

OS Homo sapiens.

XX WO2004067762-A2.

XX PD 12-AUG-2004.

XX PF 27-JAN-2004; 2004WO-US002187.

XX PR 27-JAN-2003; 2003US-0443133P.

XX PA (UNIV) UNIV KANSAS MEDICAL CENT.

XX PI Sundaramoorthy M, Hudson B;

XX DR WPI; 2004-594218/57.

XX PT Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions, tumor metastasis, and tumor growth, involves contacting subject with crystallized type IV collagen NC1 domain hexamer polypeptide.

XX PS Disclosure; SEQ ID NO 254; 178pp; English.

XX CC The invention relates to a novel method for inhibiting angiogenesis, angiogenesis-mediated diseases or conditions, tumour metastasis, and tumour growth, involving contacting a subject with a crystallised type IV collagen NC1 domain hexamer polypeptide. A polypeptide of the invention has angiogenic, cytostatic, antidiabetic, ophthalmological, antirheumatic, antiarthritic, immunosuppressive, antiseborrheic, dermatological, antibacterial, vulnery, antiulcer, fungicide, virucide, protozoacide, anti-HIV, antiinflammatory, antianaemic, antiskilling, osteopathic, vasotropic, gastrointestinal, antipsoriatic, and antiatherosclerotic activity. The polypeptide inhibits assembly of type IV collagen heterotrimers and hexamers. The method of the invention is useful for inhibiting angiogenesis, angiogenesis-mediated diseases or conditions, tumour metastasis and tumour growth. The angiogenesis-mediated disease or condition is solid and blood-borne tumours, diabetic retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal neovascularisation, macular degeneration, corneal neovascularisation, retinopathy of prematurity, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis, pyerygium keratitis sicca, sjogren's, acne rosacea, phlyctenulosis, syphilis, Mycobacteria infections, lipid degeneration, chemical burns, bacterial ulcers, fungal ulcers, Herpes simplex infections, Herpes zoster infections, protozoan infections, Kaposi's sarcoma, Mooren ulcer,

CC Terrien's marginal degeneration, marginal keratolysis, trauma, systemic
 CC lupus, polyarthritis, Wegeners sarcoidosis, scleritis, Steven's Johnson
 CC disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma
 CC elasticum, Paget's disease, vein occlusion, artery occlusion, carotid
 CC obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease,
 CC Balse disease, Bechet's disease, myopia, optic pits, Stargardt disease,
 CC pars planitis, chronic retinal detachment, hyperviscosity syndromes,
 CC toxoplasmosis, post-laser complications, abnormal proliferation of
 CC fibrovascular tissue, haemangiomas, Oslar Weber-Rendu, AIDS, ocular
 CC neovascular disease, osteoarthritis, chronic inflammation, Crohn's
 CC disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid.
 CC The present sequence represents a peptide of the invention, derived from
 CC type IV collagen crystallised NCI domain hexamer.
 XX
 SQ Sequence 18 AA;
 Query Match 33.3%; Score 32; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FEHCNFDV 9
 Db 6 FLFCNVNDV 14
 RESULT 94
 ADR19175
 ID ADR19175 standard; peptide; 18 AA.
 XX
 AC ADR19175;
 XX
 XX
 DT 04-NOV-2004 (first entry)
 XX
 XX Type IV collagen SR plus inter-CDSR region alpha6 chain peptide.
 XX
 XX angiogenesis; angiogenesis-mediated disease; tumour metastasis;
 KW tumour growth; type IV collagen; NCI domain hexamer; angiogenic;
 KW cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic;
 KW immunosuppressive; antiseborrheic; dermatological; antibacterial;
 KW vulnery; antitumor; fungicide; virucide; protozoacide; anti-HIV;
 KW antinflammatory; antianemic; antiskinkling; osteopathic; vasotropic;
 KW gastrointestinal; antipsoriatic; antiatherosclerotic.
 XX
 OS Homo sapiens.
 XX
 XX WO2004067762-A2.
 PN
 XX
 XX 12-AUG-2004.
 PD
 XX
 PF 27-JAN-2004; 2004WO-US002187.
 XX
 XX 27-JAN-2003; 2003US-0443133P.
 PR
 XX (UNIV) UNIV KANSAS MEDICAL CENT.
 PA
 XX Sundaramoorthy M, Hudson B;
 PI
 XX WPI; 2004-594218/57.
 DR
 XX
 XX Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions,
 PT tumor metastasis, and tumor growth, involves contacting subject with
 PT crystallized type IV collagen NCI domain hexamer polypeptide.
 XX
 XX Disclosure; SEQ ID NO 258; 178pp; English.
 PS
 XX The invention relates to a novel method for inhibiting angiogenesis,
 CC angiogenesis-mediated diseases or conditions, tumour metastasis, and
 CC tumour growth, involving contacting a subject with a crystallised type IV
 CC collagen NCI domain hexamer polypeptide. A polypeptide of the invention
 CC has angiogenic, cytostatic, antidiabetic, ophthalmological,
 CC antirheumatic, antiarthritic, immunosuppressive, antiseborrheic,
 CC dermatological, antibacterial, vulnery, antitumor, fungicide, virucide,
 CC protozoacide, anti-HIV, antiinflammatory, antianemic, antiskinkling,

CC osteopathic, vasotropic, gastrointestinal, antipsoriatic, and
 CC antiatherosclerotic activity. The polypeptide inhibits assembly of type
 CC IV collagen heterotrimers and hexamers. The method of the invention is
 CC useful for inhibiting angiogenesis, angiogenesis-mediated diseases or
 CC conditions, tumour metastasis and tumour growth. The angiogenesis-
 CC mediated disease or condition is solid and blood-borne tumours, diabetic
 CC retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal
 CC neovascularisation, macular degeneration, corneal graft rejection, neovascular
 CC retinopathy of prematurity, corneal graft rejection, keratoconjunctivitis,
 CC glaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis,
 CC pterygium keratitis sicca, sjogren's, acne rosacea, phlyctenulosis,
 CC syphilis, Mycobacteria infections, lipid degeneration, chemical burns,
 CC bacterial ulcers, fungal ulcers, Herpes simplex infections, Herpes zoster
 CC infections, protozoan infections, Kaposi's sarcoma, Mooren ulcer,
 CC Terrien's marginal degeneration, marginal keratolysis, trauma, systemic
 CC lupus, polyarthritis, Wegeners sarcoidosis, scleritis, Steven's Johnson
 CC disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma
 CC elasticum, Paget's disease, vein occlusion, artery occlusion, carotid
 CC obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease,
 CC Balse disease, Bechet's disease, myopia, optic pits, Stargardt disease,
 CC pars planitis, chronic retinal detachment, hyperviscosity syndromes,
 CC toxoplasmosis, post-laser complications, abnormal proliferation of
 CC fibrovascular tissue, haemangiomas, Oslar Weber-Rendu, AIDS, ocular
 CC neovascular disease, osteoarthritis, chronic inflammation, Crohn's
 CC disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid.
 CC The present sequence represents a peptide of the invention, derived from
 CC type IV collagen crystallised NCI domain hexamer.
 XX
 SQ Sequence 18 AA;
 Query Match 33.3%; Score 32; DB 8; Length 18;
 Best Local Similarity 55.6%; Pred. No. 6.8e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FEHCNFDV 9
 Db 6 FYICNINEV 14
 RESULT 95
 AEE30424
 ID AEE30424 standard; peptide; 18 AA.
 XX
 AC AEE30424;
 XX
 XX 09-FEB-2006 (first entry)
 DT
 XX
 XX Representative binding module peptide, SEQ ID NO:21.
 DE
 XX Biofilter; purification; biocomputer.
 KW
 XX Unidentified.
 OS
 XX WO2005113037-A2.
 PN
 XX
 XX 01-DEC-2005.
 PD
 XX
 XX 14-APR-2005; 2005WO-US012540.
 PF
 XX
 XX 14-APR-2004; 2004US-0562166P.
 PR
 XX 22-JUL-2004; 2004US-0590184P.
 PR
 XX 13-APR-2005; 2005US-00105202.
 XX
 XX (AFFI-) AFFINERGY INC.
 PA
 XX Christensen DJ, Grinstaff MW, Kenan DJ;
 PI
 XX WPI; 2006-047173/05.
 DR
 XX New filter comprising an inlet or outlet, a filter assembly comprising an
 PT outer housing and filter surfaces or a coating bound to the filter
 PT surface, useful for removing at least one selected component from a fluid
 PT sample.

XX PS Disclosure; SEQ ID NO 21; 127pp; English.

XX CC The new invention relates to an improved filter assembly and improved

XX CC method for filtration of selected components from biological fluids,

XX CC including blood. Specifically described is a new filter for removing at

XX CC least one selected component from a fluid sample that passes through the

XX CC filter. The filter comprises an inlet; an outlet; a filter assembly

XX CC comprising an outer housing and filter surfaces located and contained

XX CC within the outer housing; or a coating bound to the at least one filter

XX CC surface. The coating further comprises a first binding module, configured

XX CC to selectively bind to the filter surfaces; and a second binding module,

XX CC configured to selectively bind to the first binding module and to the at

XX CC least one selected fluid component such that the at least one selected

XX CC fluid component is selectively bound to the filter surfaces via the

XX CC coating and a filtered fluid product emerges from the outlet into the

XX CC collection container. Also given are methods of removing at least one

XX CC selected component from a fluid sample to produce a filtered fluid

XX CC product; and removing at least two selected components from a fluid

XX CC sample to produce a filtered fluid product. The invention also provides

XX CC computers, computer readable media and systems including databases that

XX CC are composed of sequence records including character strings

XX CC corresponding to SEQ ID Nos: 1-462. The present sequence is a

XX CC representative binding module peptide that specifically binds to a non-

XX CC biological substrate which is a filter material.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 32; DB 10; Length 18;

Best Local Similarity 53.3%; Pred. No. 6.8e+02;

Matches 8; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 4 CNFN--DVTTLREN 16

DB 1 CNNNRDVMNLRDN 15

RESULT 96

AEF52040

ID AEF52040 standard; peptide; 18 AA.

AC AEF52040;

XX 23-MAR-2006 (first entry)

DT Interfacial biomaterial-associated peptide SEQ ID NO 117.

DE Interfacial biomaterial-associated peptide SEQ ID NO 117.

XX interfacial biomaterial; biofilm; antimicrobial;

KW RNA III inhibiting peptide; surgery.

KW Unidentified.

OS WO2006007368-A2.

XX 19-JAN-2006.

XX 15-JUN-2005; 2005WO-US021147.

XX 16-JUN-2004; 2004US-0580019P.

PR 09-FEB-2005; 2005US-0651338P.

PR 10-FEB-2005; 2005US-0651747P.

XX (AFFI-) AFFINERGY INC.

XX Hamilton PT, Grinstaff MW, Kenan DJ, Christensen DJ, Beyer WF;

PI Hyde-Deruysscher R, Benson RE;

XX WPI; 2006-118174/12.

XX Interfacial biomaterial for coating the surface of a medical device such

PT as an implant, comprises a surface binding molecule having a peptide, and

PT an affector module that inhibits biofilm formation.

XX

Claim 1; SEQ ID NO 117; 140pp; English.

XX This invention describes a novel interfacial biomaterial (IFBM) which

XX comprises surface binding module(s) and affector module(s) that inhibit

XX biofilm formation, where the surface-binding module comprises a peptide

XX having e.g. a 17 (SEQ ID Nos: 1, 150-206), 22 (SEQ ID Nos: 2-6, 40, 95-

XX 96), 14 (SEQ ID Nos: 7, 8), 23 (SEQ ID Nos: 39, 41, 42), or 15 (SEQ ID

XX No: 43), amino acid sequence. The affector module of the novel IFBM's

XX binds to human serum albumin. The surface-binding module and the affector

XX module are joined by a linker that comprises polyethylene glycol. The

XX affector module is a biofilm inhibitor that inhibits biofilm formation by

XX damaging cells or affects a regulatory mechanism of cells that is

XX involved in their establishment of or participation in a biofilm, and is

XX a quorum-sensing inhibitor. The biofilm inhibitor module is an anti-

XX microbial peptide. The affector module comprises magainin. The affector

XX module is RNA III inhibiting peptide (RIP). The products of the invention

XX are useful for inhibiting biofilm formation, and for coating the surface

XX of a medical device such as implants and catheters. The biomaterial is

XX applied easily, rapidly, and cost-effectively to the surface of a medical

XX device. This sequence represents a peptide used in the novel interfacial

XX biomaterial.

XX SQ Sequence 18 AA;

Query Match 33.3%; Score 32; DB 10; Length 18;

Best Local Similarity 53.3%; Pred. No. 6.8e+02;

Matches 8; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 4 CNFN--DVTTLREN 16

DB 1 CNNNRDVMNLRDN 15

RESULT 97

AAU75603

ID AAU75603 standard; peptide; 20 AA.

AC AAU75603;

XX 08-MAY-2002 (first entry)

DT Human type IV collagen alpha 3 chain, Tumstatin, mutant T3.

XX Human; type IV collagen alpha 3 chain; cytostatic; antiangiogenic;

KW non-Goodpasture fragment; alpha3(IV)NC1 domain; alphavbeta3 integrin;

KW endothelial cell proliferation; apoptosis; Arresten; Canstatin;

KW Tumstatin; angiogenesis; tumour; mutein; mutant.

OS Homo sapiens.

XX WO200151523-A2.

XX 19-JUL-2001.

XX 08-JAN-2001; 2001WO-US000565.

XX 07-JAN-2000; 2000US-00479118.

PR 04-APR-2000; 2000US-00543371.

PR 21-JUL-2000; 2000US-00625191.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Kalluri R;

XX WPI; 2002-188037/24.

XX A non-Goodpasture fragment of alpha3(IV)NC1 domain used in detecting and

XX treating disorders involving angiogenesis.

XX Claim 33; Page 153; 205pp; English.

XX The invention relates to a non-Goodpasture fragment of alpha3(IV)NC1

CC domain, having one or more of the characteristics selected from: (a) the

CC ability to bind alphavbeta3 integrin; (b) the ability to inhibit
 CC proliferation of endothelial cells; and (c) the ability to cause
 CC apoptosis of endothelial cells. Also described are the following: (1) use
 CC of Arresten, Canstatin or Tumstatin, or a fragment, mutant, homologue,
 CC analogue or allelic variant in the preparation of a medicament for
 CC treating a disorder involving: (a) inhibiting angiogenesis in a tissue,
 CC where the angiogenesis is mediated by one or more endothelial cell
 CC integrins or one or more endothelial cell integrin subunits; or (b) by
 CC promoting or inducing endothelial cell apoptosis in a tissue, where the
 CC endothelial cell apoptosis is mediated by one or more endothelial cell
 CC integrins or one or more endothelial cell integrin subunits; (2) use of
 CC an antibody or peptide that specifically binds the alpha1, alpha2, in the
 CC alpha3, alpha6, alpha8, alpha9, beta1 or beta2 subunit of integrin in the
 CC preparation of a medicament for inhibiting angiogenesis or cell
 CC proliferation; (3) use of an inhibitor, such as an antibody, antibody
 CC fragment or peptide of receptor-mediated angiogenesis in the preparation
 CC of a medicament for treating a proliferative disease in a vertebrate,
 CC where the disease is characterised by angiogenesis that is mediated by
 CC receptors to Arresten, Canstatin or Tumstatin and where the receptors
 CC inhibited are Arresten, Canstatin or Tumstatin receptors; (4) use of one
 CC or more soluble receptors that bind Arresten, Canstatin or Tumstatin in
 CC the presence of a medicament for promoting angiogenesis in a tissue; and
 CC (5) use of integrins in the preparation of a medicament for promoting or
 CC inducing angiogenesis or cell proliferation in a tissue. The fragments
 CC Arresten, Canstatin or Tumstatin and their mutants, homologues, analogues
 CC or allelic variants are useful in the preparation of a medicament for
 CC treating a disorder involving inhibiting angiogenesis in a tissue, where
 CC the angiogenesis is mediated by one or more endothelial cell integrins or
 CC one or more endothelial cell integrin subunits; or by promoting or
 CC inducing endothelial cell apoptosis in a tissue, where the endothelial
 CC cell apoptosis is mediated by one or more endothelial cell integrins or
 CC one or more endothelial cell integrin subunits. The medicament is useful
 CC in inhibiting tumour growth and for the regression of an established
 CC tumour. The present sequence represents the amino acid sequence of human
 CC type IV collagen alpha 3 chain mutant, T3, which consists of residues 69-
 CC 88 of Tumstatin
 XX

SQ Sequence 20 AA;
 Query Match 33.3%; Score 32; DB 5; Length 20;
 Best Local Similarity 66.7%; Pred. No. 7.6e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FEHCNFDV 9
 Db 9 FLFCNVNDV 17

RESULT 98
 ADA20267
 ID ADA20267 standard; peptide; 20 AA.

XX AC ADA20267;

XX XX 20-NOV-2003 (first entry)

XX DE Human tumstatin deletion peptide T3 amino acid sequence.

XX KW anti-angiogenic; undesirable angiogenesis; capillary; tumour growth;
 KW metastasis; basement membrane organisation; type IV collagen network;
 KW C-terminal globular non-collagenous domain; NC1; type IV collagen;
 KW cell surface receptor; integrin; angiogenic activity; protein synthesis;
 KW cytostatic; gene therapy; alpha 3 chain; tumstatin; human; T3.

XX OS Homo sapiens.

XX XX WO2003059257-A2.

XX XX 24-JUL-2003.

XX PF 20-DEC-2002; 2002WO-US040938.

XX PR 21-DEC-2001; 2001US-00032221.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Kalluri R;

XX WPI; 2003-587256/55.

DR N-PSDB; ADA20224.

XX New peptide, useful for preparing a composition for inhibiting tumor
 PT growth, angiogenic activity or protein synthesis in a mammalian tissue.

XX Claim 94; Page 131; 240pp; English.

XX This invention relates to novel isolated proteins and their fragments
 CC with anti-angiogenic properties. The invention also relates to the DNA
 CC sequences which encode the novel proteins. A wide variety of diseases are
 CC the result of undesirable angiogenesis. The formation of new capillaries
 CC from pre-existing vessels is essential for tumour growth and metastasis.
 CC Basement membrane organisation is dependent on the assembly of a type IV
 CC collagen network which may occur through the C-terminal globular non-
 CC collagenous (NC1) domain of type IV collagen. The alpha 1 and alpha 2
 CC forms are ubiquitously exhibited in human basement membranes. In the
 CC present invention, cell surface receptors (in particular integrins) which
 CC specifically bind anti-angiogenic proteins and peptides (in particular
 CC the alpha 1, alpha 2 and alpha 3 domains of the NC1 domain of type IV
 CC collagen) are disclosed. The proteins of the invention may inhibit tumour
 CC growth, angiogenic activity in mammalian tissue or protein synthesis in
 CC endothelial cells and thus may exhibit cytostatic activity. The DNA
 CC sequences of the invention may be useful in gene therapy. The present
 CC sequence is that of peptide T3, an abridged form of the "tumstatin"
 CC protein of the invention which was derived from the amino acid sequence
 CC of the alpha 3 chain of human type IV collagen.

SQ Sequence 20 AA;

Query Match 33.3%; Score 32; DB 6; Length 20;

Best Local Similarity 66.7%; Pred. No. 7.6e+02;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 FEHCNFDV 9

Db 9 FLFCNVNDV 17

RESULT 99

ADC17688

ID ADC17688 standard; peptide; 20 AA.

XX AC ADC17688;

XX XX 18-DEC-2003 (first entry)

XX DE Type IV collagen NC1 domain related peptide SEQ ID NO:293.

XX KW crystallised NC1 domain hexamer of type IV collagen;
 KW angiogenesis inhibitor; angiogenesis-mediated disease;
 KW tumour metastasis inhibitor; tumour growth inhibitor;
 KW endothelial cell interaction inhibitor;
 KW basal lamina membrane formation inhibitor; cytostatic; antiproliferative;
 KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
 KW endothelial cell adhesion inhibitor;
 KW endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;
 KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
 KW blood-borne tumour.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003012122-A2.

XX PD 13-FEB-2003.

XX XX 26-JUL-2002; 2002WO-US023763.

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XX PR 27-JUL-2001; 2001US-0308523P.
XX PR 29-OCT-2001; 2001US-0351289P.
XX PR 22-MAR-2002; 2002US-0366854P.
XX PR 03-JUN-2002; 2002US-0385362P.
XX PA (UNIV ) UNIV KANSAS MEDICAL CENT.
XX PA (SUND/) SUNDARAMOORTHY M.
XX PA (HUDS/) HUDSON B.
XX PI Sundaramoorthy M, Hudson B;
XX DR WPI; 2003-332730/31.
XX PR New polypeptide, useful for treating an angiogenesis-mediated disease or
XX PT condition consisting of glaucoma or blood-borne tumors or for inhibiting
XX PT basal lamina membrane formation in cell or tissue development.
XX PS Claim 57; SEQ ID NO 293; 168pp; English.
XX CC The present invention describes a crystallised NCI domain hexamer of type
XX CC IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a
XX CC pharmaceutical composition comprising the polypeptide and a carrier; (3)
XX CC inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
XX CC disease or condition in a mammal; (5) inhibiting tumour metastasis or
XX CC growth; (5) inhibiting endothelial cell interaction with the
XX CC extracellular matrix in an animal tissue; (6) inhibiting basal lamina
XX CC membrane formation in cell or tissue development; (7) a crystal of an NCI
XX CC domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
XX CC collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
XX CC crystallised NCI domain hexamer of type IV collagen (I) has cytostatic,
XX CC antiproliferative, antianaemic, ophthalmological, antiarteriosclerotic and
XX CC antiulcer activities, and can be used as an inhibitor of angiogenesis,
XX CC tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
XX CC cell proliferation, and basal lamina assembly. A (I) polypeptide can be
XX CC used for treating an angiogenesis-mediated disease or condition
XX CC consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
XX CC psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
XX CC or for inhibiting basal lamina membrane formation in cell or tissue
XX CC development. The methods are useful for inhibiting angiogenesis in
XX CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
XX CC cell interaction with the extracellular matrix in an animal tissue, and
XX CC identifying inhibitors of type IV collagen assembly. The present sequence
XX CC represents a peptide which is used in the exemplification of the present
XX CC invention.
XX SQ Sequence 20 AA;
Query Match 33.3%; Score 32; DB 7; Length 20;
Best Local Similarity 55.6%; Pred. No. 7.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 FEHCNFDV 9
Db 9 FYICNINEV 17
RESULT 100
ADCL17684
ID ADCL17684 standard; peptide; 20 AA.
XX AC ADCL17684;
XX DT 18-DEC-2003 (first entry)
XX DE Type IV collagen NCI domain related peptide SEQ ID NO:289.
XX KW crystallised NCI domain hexamer of type IV collagen;
XX KW angiogenesis inhibitor; angiogenesis-mediated disease;
XX KW tumour metastasis inhibitor; tumour growth inhibitor;
XX KW endothelial cell interaction inhibitor;
XX KW basal lamina membrane formation inhibitor; cytostatic; antiproliferative;
XX KW antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
XX KW endothelial cell adhesion inhibitor; glaucoma; sickle cell anaemia;
XX KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
XX KW blood-borne tumour.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX WO2003012122-A2.
XX PD 13-FEB-2003.
XX XX 26-JUL-2002; 2002WO-US023763.
XX PF 27-JUL-2001; 2001US-0308523P.
XX PR 29-OCT-2001; 2001US-0351289P.
XX PR 22-MAR-2002; 2002US-0366854P.
XX PR 03-JUN-2002; 2002US-0385362P.
XX PA (UNIV ) UNIV KANSAS MEDICAL CENT.
XX PA (SUND/) SUNDARAMOORTHY M.
XX PA (HUDS/) HUDSON B.
XX PI Sundaramoorthy M, Hudson B;
XX DR WPI; 2003-332730/31.
XX PR New polypeptide, useful for treating an angiogenesis-mediated disease or
XX PT condition consisting of glaucoma or blood-borne tumors or for inhibiting
XX PT basal lamina membrane formation in cell or tissue development.
XX PS Claim 57; SEQ ID NO 289; 168pp; English.
XX CC The present invention describes a crystallised NCI domain hexamer of type
XX CC IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a
XX CC pharmaceutical composition comprising the polypeptide and a carrier; (3)
XX CC inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated
XX CC disease or condition in a mammal; (5) inhibiting tumour metastasis or
XX CC growth; (5) inhibiting endothelial cell interaction with the
XX CC extracellular matrix in an animal tissue; (6) inhibiting basal lamina
XX CC membrane formation in cell or tissue development; (7) a crystal of an NCI
XX CC domain hexamer of type IV collagen; (8) identifying inhibitors of type IV
XX CC collagen assembly; and (9) an inhibitor of type IV collagen assembly. A
XX CC crystallised NCI domain hexamer of type IV collagen (I) has cytostatic,
XX CC antiproliferative, antianaemic, ophthalmological, antiarteriosclerotic and
XX CC antiulcer activities, and can be used as an inhibitor of angiogenesis,
XX CC tumour growth, tumour metastasis, endothelial cell adhesion, endothelial
XX CC cell proliferation, and basal lamina assembly. A (I) polypeptide can be
XX CC used for treating an angiogenesis-mediated disease or condition
XX CC consisting of glaucoma, sickle cell anaemia, ulcerative colitis,
XX CC psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours
XX CC or for inhibiting basal lamina membrane formation in cell or tissue
XX CC development. The methods are useful for inhibiting angiogenesis in
XX CC tissue, inhibiting tumour metastasis or growth, inhibiting endothelial
XX CC cell interaction with the extracellular matrix in an animal tissue, and
XX CC identifying inhibitors of type IV collagen assembly. The present sequence
XX CC represents a peptide which is used in the exemplification of the present
XX CC invention.
XX SQ Sequence 20 AA;
Query Match 33.3%; Score 32; DB 7; Length 20;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FEHCNFDV 9
Db 9 FLECNVDV 17
Search completed: July 15, 2006, 00:19:15
Job time : 211 secs

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